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(54) Title: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERETO

(57) Abstract: The sequences of nucleic acids encoding proteins required for E. coli proliferation are disclosed. The nucleic acids can be used to express proteins or portions thereof, to obtain antibodies capable of specifically binding to the expressed proteins, and to use those expressed proteins as a screen to isolate candidate molecules for rational drug discovery programs. The nucleic acids can also be used to screen for homologous genes that are required for proliferation in microorganisms other than E. coli. The nucleic acids can also be used to design expression vectors and secretion vectors. The nucleic acids of the present invention can also be used in various assay systems to screen for proliferation required genes in other organisms as well as to screen for antimicrobial agents.

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GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERETO**BACKGROUND OF THE INVENTION**

Since the discovery of penicillin, the use of antibiotics to treat the ravages of bacterial infections has saved millions of lives. With the advent of these "miracle drugs," for a time it was popularly believed that humanity might, once and for all, be saved from the scourge of bacterial infections. In fact, during the 1980s and early 1990s, many large pharmaceutical companies cut back or eliminated antibiotics research and development. They believed that infectious disease caused by bacteria finally had been conquered and that markets for new drugs were limited. Unfortunately, this belief was overly optimistic.

The tide is beginning to turn in favor of the bacteria as reports of drug resistant bacteria become more frequent. The United States Centers for Disease Control announced that one of the most powerful known antibiotics, vancomycin, was unable to treat an infection of the common *Staphylococcus aureus* (staph). This organism is commonly found in our environment and is responsible for many nosocomial infections. The import of this announcement becomes clear when one considers that vancomycin was used for years to treat infections caused by stubborn strains of bacteria, like staph. In short, the bacteria are becoming resistant to our most powerful antibiotics. If this trend continues, it is conceivable that we will return to a time when what are presently considered minor bacterial infections are fatal diseases.

There are a number of causes for the predicament in which practitioners of medical arts find themselves. Over-prescription and improper prescription habits by some physicians have caused an indiscriminate increase in the availability of antibiotics to the public. The patient is also partly responsible, for even in instances where an antibiotic is the appropriate treatment, patients will often improperly use the drug, the result being yet another population of bacteria that is resistant, in whole or in part, to traditional antibiotics.

The bacterial scourges that have haunted humanity remain, in spite of the development of modern scientific practices to deal with the diseases that they cause. Drug resistant bacteria are now advancing on the health of humanity. A new generation of antibiotics to once again deal with the pending health threat that bacteria present is required.

Discovery of New Antibiotics

As more and more bacterial strains become resistant to the panel of available antibiotics, new compounds are required. In the past, practitioners of pharmacology would have to rely upon traditional methods of drug discovery to generate novel, safe and efficacious compounds for the treatment of disease. Traditional drug discovery methods involve blindly testing potential drug candidate-molecules, often selected at random, in the hope that one might prove to be an effective treatment for some disease. The process is painstaking and laborious, with no guarantee of success. Today, the average cost to discover and develop a new drug is nearly US \$500 million, and the

average time is 15 years from laboratory to patient. Improving this process, even incrementally, would represent a huge advance in the generation of novel antimicrobial agents.

Newly emerging practices in drug discovery utilize a number of biochemical techniques to provide for directed approaches to creating new drugs, rather than discovering them at random. For example, gene sequences and proteins encoded thereby that are required for the proliferation of an organism make for excellent targets since exposure of bacteria to compounds active against these targets would result in the inactivation of the organism. Once a target is identified, biochemical analysis of that target can be used to discover or to design molecules that interact with and alter the functions of the target. Using physical and computational techniques, to analyze structural and biochemical targets in order to derive compounds that interact with a target is called rational drug design and offers great future potential. Thus, emerging drug discovery practices use molecular modeling techniques, combinatorial chemistry approaches, and other means to produce and screen and/or design large numbers of candidate compounds.

Nevertheless, while this approach to drug discovery is clearly the way of the future, problems remain. For example, the initial step of identifying molecular targets for investigation can be an extremely time consuming task. It may also be difficult to design molecules that interact with the target by using computer modeling techniques. Furthermore, in cases where the function of the target is not known or is poorly understood, it may be difficult to design assays to detect molecules that interact with and alter the functions of the target. To improve the rate of novel drug discovery and development, methods of identifying important molecular targets in pathogenic microorganisms and methods for identifying molecules that interact with and alter the functions of such molecular targets are urgently required.

Escherichia coli represents an excellent model system to understand bacterial biochemistry and physiology. The estimated 4288 genes scattered along the 4.6×10^6 base pairs of the *Escherichia coli* (*E. coli*) chromosome offer tremendous promise for the understanding of bacterial biochemical processes. In turn, this knowledge will assist in the development of new tools for the diagnosis and treatment of bacteria-caused human disease. The entire *E. coli* genome has been sequenced, and this body of information holds a tremendous potential for application to the discovery and development of new antibiotic compounds. Yet, in spite of this accomplishment, the general functions or roles of many of these genes are still unknown. For example, the total number of proliferation-required genes contained within the *E. coli* genome is unknown, but has been variously estimated at around 200 to 700 (Armstrong, K.A. and Fan, D.P. Essential Genes in the *metB-malB* Region of *Escherichia coli* K12, 1975, J. Bacteriol. 126: 48-55).

Novel, safe and effective antimicrobial compounds are needed in view of the rapid rise of antibiotic resistant microorganisms. However, prior to this invention, the characterization of even a single bacterial gene was a painstaking process, requiring years of effort. Accordingly, there is an urgent need for more novel methods to identify and characterize bacterial genomic sequences that

encode gene products required for proliferation and for methods to identify molecules that interact with and alter the functions of such genes and gene products.

SUMMARY OF THE INVENTION

One embodiment of the present invention is a purified or isolated nucleic acid sequence
5 consisting essentially of one of SEQ ID NOs: 1-127, wherein expression of said nucleic acid inhibits proliferation of a microorganism. The nucleic acid sequence may be complementary to at least a portion of a coding sequence of a gene whose expression is required for proliferation of a microorganism. The nucleic acid sequence may be complementary to at least a portion of an RNA required for proliferation of a microorganism. The RNA may be an RNA encoding more than one
10 gene product.

Another embodiment of the present invention is a nucleic acid comprising a fragment of one of SEQ ID NOs: 1-127, said fragment selected from the group consisting of fragments comprising at least 10, at least 20, at least 25, at least 30, at least 50 and more than 50 consecutive bases of one of SEQ ID NOs: 1-127.

15 Another embodiment of the present invention is a vector comprising a promoter operably linked to the nucleic acid sequences of each of the preceding paragraphs. The promoter may be active in a microorganism selected from the group consisting of *Aspergillus fumigatus*, *Bacillus anthracis*, *Campylobacter jejuni*, *Candida albicans*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Cryptococcus neoformans*, *Enterobacter cloacae*,
20 *Enterococcus faecalis*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Pseudomonas aeruginosa*, *Saccharomyces cerevisiae*, *Salmonella choleraesuis*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Treponema pallidum*, and *Yersinia pestis* or any species
25 falling within the genera of any of the above species.

Another embodiment of the present invention is a host cell containing the vectors of the preceding paragraph.

Another embodiment of the present invention is a purified or isolated nucleic acid consisting essentially of the coding sequence of one of SEQ ID NOs: 128-298.

30 Another embodiment of the present invention is a fragment of the nucleic acid of the preceding paragraph, said fragment comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive bases of one of SEQ ID NOs: 128-298.

Another embodiment of the present invention is a vector comprising a promoter operably linked to the nucleic acid of the preceding two paragraphs.

35 Another embodiment of the present invention is a purified or isolated antisense nucleic acid comprising a nucleic acid sequence complementary to at least a portion of an intragenic sequence, intergenic sequence, sequences spanning at least a portion of two or more genes, 5' noncoding

region, or 3' noncoding region within an operon comprising a proliferation-required gene whose activity or expression is inhibited by an antisense nucleic acid comprising one of SEQ ID NOs.: 1-127.

Another embodiment of the present invention is a purified or isolated nucleic acid comprising a nucleic acid having at least 70% identity to a sequence selected from the group consisting of SEQ ID NOs.: 1-127, fragments comprising at least 25 consecutive nucleotides of SEQ ID NOs.: 1-127, the sequences complementary to SEQ ID NOs.: 1-127 and the sequences complementary to fragments comprising at least 25 consecutive nucleotides of SEQ ID NOs.: 1-127 as determined using BLASTN version 2.0 with the default parameters. The nucleic acid may be from an organism selected from the group consisting of *Aspergillus fumigatus*, *Bacillus anthracis*, *Campylobacter jejuni*, *Candida albicans*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Staphylococcus aureus*, *Haemophilus influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Pseudomonas aeruginosa*, *Saccharomyces cerevisiae*, *Salmonella choleraesuis*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Treponema pallidum*, and *Yersinia pestis* or any species falling within the genera of any of the above species.

Another embodiment of the present invention is a vector comprising a promoter operably linked to a nucleic acid encoding a polypeptide whose expression is inhibited by an antisense nucleic acid comprising one of SEQ ID NOs.: 1-127. The polypeptide may comprise a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs: 299-469.

Another embodiment of the present invention is a host cell containing the vector of the preceding paragraph.

Another embodiment of the present invention is a purified or isolated polypeptide comprising a polypeptide whose expression is inhibited by an antisense nucleic acid comprising one of SEQ ID NOs.: 1-127, or a fragment selected from the group consisting of fragments comprising at least 5, at least 10, at least 20, at least 30, at least 40, at least 50, at least 60 or more than 60 consecutive amino acids of one of the said polypeptides. The polypeptide may comprise a polypeptide comprising one of SEQ ID NOs.: 299-469 or a fragment comprising at least 5, at least 10, at least 20, at least 30, at least 40, at least 50, at least 60 or more than 60 consecutive amino acids of a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 299-469.

Another embodiment of the present invention is a purified or isolated polypeptide comprising a polypeptide having at least 25% identity to a polypeptide whose expression is inhibited by a sequence selected from the group consisting of SEQ ID NOs.: 1-127, or at least 25% identity to a fragment comprising at least 5, at least 10, at least 20, at least 30, at least 40, at least

50, at least 60 or more than 60 consecutive amino acids of a polypeptide whose expression is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-127 as determined using FASTA version 3.0t78 with the default parameters. The polypeptide may have at least 25% identity to a polypeptide comprising one of SEQ ID NOs.: 299-469 or at least 25%
5 identity to a fragment comprising at least 5, at least 10, at least 20, at least 30, at least 40, at least 50, at least 60 or more than 60 consecutive amino acids of a polypeptide comprising one of SEQ ID NOs.: 299-469 as determined using FASTA version 3.0t78 with the default parameters.

Another embodiment of the present invention is an antibody capable of specifically binding one of the polypeptides of the preceding paragraph.

10 Another embodiment of the present invention is a method of producing a polypeptide, comprising introducing a vector comprising a promoter operably linked to a nucleic acid encoding a polypeptide whose expression is inhibited by an antisense nucleic acid comprising one of SEQ ID NOs.: 1-127 into a cell. The method may further comprise the step of isolating said polypeptide. The polypeptide may comprise a sequence selected from the group consisting of SEQ ID NOs.:
15 299-469.

Another embodiment of the present invention is a method of inhibiting proliferation of a microorganism comprising inhibiting the activity or reducing the amount of a gene product whose expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-127 or inhibiting the activity or reducing the amount of a nucleic acid
20 encoding said gene product. The gene product may comprise a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 299-469.

Another embodiment of the present invention is a method for identifying a compound which influences the activity of a gene product required for proliferation, said gene product comprising a gene product whose expression is inhibited by an antisense nucleic acid comprising a
25 sequence selected from the group consisting of SEQ ID NOs.: 1-127, said method comprising contacting said gene product with a candidate compound and determining whether said compound influences the activity of said gene product. The gene product may be a polypeptide and said activity may be an enzymatic activity. The gene product may be a polypeptide and said activity may be a carbon compound catabolism activity. The gene product may be a polypeptide and said
30 activity may be a biosynthetic activity. The gene product may be a polypeptide and said activity may be a transporter activity. The gene product may be a polypeptide and said activity may be a transcriptional activity. The gene product may be a polypeptide and said activity may be a DNA replication activity. The gene product may be a polypeptide and said activity may be a cell division activity. The gene product may be a polypeptide comprising a sequence selected from the group
35 consisting of SEQ ID NOs.: 299-469.

Another embodiment of the present invention is a compound identified using the methods of the preceding paragraph.

The method of Claim 28, wherein said gene product is a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 299-469.

method for identifying a compound or nucleic acid having the ability to reduce the activity or level of a gene product required for proliferation, said gene product comprising a gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-127, said method comprising:

(a) providing a target that is a gene or RNA, wherein said target comprises a nucleic acid encoding said gene product;

(b) contacting said target with a candidate compound or nucleic acid; and

(c) measuring an activity of said target.

The target may be a messenger RNA molecule and said activity may be translation of said messenger RNA. The target may be a messenger RNA molecule and said activity may be transcription of a gene encoding said messenger RNA. The target may be a gene and said activity may be transcription of said gene. The target may be a nontranslated RNA and said activity may be processing or folding of said nontranslated RNA or assembly of said nontranslated RNA into a protein/RNA complex. The target gene or RNA may encode a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 299-469.

Another embodiment of the present invention is a compound or nucleic acid identified using the methods of the preceding paragraph.

Another embodiment of the present invention is a method for identifying a compound which reduces the activity or level of a gene product required for proliferation of a microorganism, wherein the activity or expression of said gene product is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-127, said method comprising the steps of:

(a) expressing a sublethal level of an antisense nucleic acid complementary to a nucleic acid encoding said gene product in a cell to reduce the activity or amount of said gene product in said cell, thereby producing a sensitized cell;

(b) contacting said sensitized cell with a compound; and

(c) determining whether said compound inhibits the growth of said sensitized cell.

The determining step may comprise determining whether said compound inhibits the growth of said sensitized cell to a greater extent than said compound inhibits the growth of a nonsensitized cell.

The cell may be selected from the group consisting of bacterial cells, fungal cells, plant cells, and animal cells. The cell may be a Gram negative bacterium. The cell may be an *E. coli* cell. The cell may be from an organism selected from the group consisting of *Aspergillus fumigatus*, *Bacillus anthracis*, *Campylobacter jejuni*, *Candida albicans*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Haemophilus influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*,

Mycobacterium leprae, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Pseudomonas aeruginosa*, *Saccharomyces cerevisiae*, *Salmonella choleraesuis*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Treponema pallidum*, and *Yersinia pestis* or any species falling within the genera of any of the above species. The antisense nucleic acid may be transcribed from an inducible promoter. The method may further comprise the step of contacting said cell with a concentration of inducer which induces said antisense nucleic acid to a sublethal level. Growth inhibition may be measured by monitoring optical density of a culture growth solution. The gene product may be a polypeptide. The polypeptide may comprise a sequence selected from the group consisting of SEQ ID NOs.: 299-469. The gene product may be an RNA.

Another embodiment of the present invention is a compound identified using the methods of the preceding paragraph.

Another embodiment of the present invention is a method for inhibiting cellular proliferation comprising introducing a compound with activity against a gene whose activity or expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-127 or a compound with activity against the product of said gene into a population of cells expressing said gene. The compound may be an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-127, or a proliferation-inhibiting portion thereof. The proliferation inhibiting portion of one of SEQ ID NOs.: 1-127 may be a fragment comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 51 consecutive bases of one of SEQ ID NOs.: 1-127. The population may be a population selected from the group consisting of bacterial cells, fungal cells, plant cells, and animal cells. The population may be a population of Gram negative bacteria. The population may be a population of *E. coli* cells. The population may be a population selected from the group consisting of *Aspergillus fumigatus*, *Bacillus anthracis*, *Campylobacter jejuni*, *Candida albicans*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Haemophilus influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Pseudomonas aeruginosa*, *Saccharomyces cerevisiae*, *Salmonella choleraesuis*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Treponema pallidum*, and *Yersinia pestis* cells or cells from any species falling within the genera of any of the above species. The gene may encode a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 299-469.

Another embodiment of the present invention is a preparation comprising an effective concentration of an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-127, or a proliferation-inhibiting portion thereof in a pharmaceutically

acceptable carrier. The proliferation-inhibiting portion of one of SEQ ID NOs.: 1-127 may comprise at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive bases of one of SEQ ID NOs.: 1-127.

Another embodiment of the present invention is a method for inhibiting the activity or expression of a gene in an operon required for proliferation wherein the activity or expression of at least one gene in said operon is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-127, said method comprising contacting a cell in a cell population with an antisense nucleic acid comprising at least a proliferation-inhibiting portion of said operon. The antisense nucleic acid comprises a sequence selected from the group consisting of SEQ ID NOs.: 1-127 or a proliferation inhibiting portion thereof.

The method of Claim 68, wherein said cell is contacted with said antisense nucleic acid by introducing a plasmid which expresses said antisense nucleic acid into said cell population. The cell may be contacted with said antisense nucleic acid by introducing a phage which expresses said antisense nucleic acid into said cell population. The cell may be contacted with said antisense nucleic acid by expressing said antisense nucleic acid from the chromosome of cells in said cell population. The cell may be contacted with said antisense nucleic acid by introducing a promoter adjacent to a chromosomal copy of said antisense nucleic acid such that said promoter directs the synthesis of said antisense nucleic acid. The cell may be contacted with said antisense nucleic acid by introducing a retron which expresses said antisense nucleic acid into said cell population. The cell may be contacted with said antisense nucleic acid by introducing a ribozyme into said cell-population, wherein a binding portion of said ribozyme is complementary to said antisense oligonucleotide. The cell may be contacted with said antisense nucleic acid by introducing a liposome comprising said antisense oligonucleotide into said cell. The cell may be contacted with said antisense nucleic acid by electroporation of said antisense nucleic acid. The antisense nucleic acid may be a fragment comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive bases of one of SEQ ID NOs.: 1-127. The antisense nucleic acid may be an oligonucleotide.

Another embodiment of the present invention is a method for identifying a gene which is required for proliferation of a microorganism comprising:

- (a) contacting a microorganism other than *E. coli* with a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-127;
- (b) determining whether said nucleic acid inhibits proliferation of said microorganism;
- and
- (c) identifying the gene in said microorganism which is inhibited by said nucleic acid.

The microorganism may be a Gram negative bacterium. The microorganism may be selected from the group consisting of *Aspergillus fumigatus*, *Bacillus anthracis*, *Campylobacter jejuni*, *Candida albicans*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Cryptococcus*

neoformans, *Enterobacter cloacae*, *Enterococcus faecalis*, *Haemophilus influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Pseudomonas aeruginosa*, *Saccharomyces cerevisiae*, *Salmonella choleraesuis*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*,
 5 *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Treponema pallidum*, and *Yersinia pestis* or any species falling within the genera of any of the above species. The method may further comprise introducing said nucleic acid into a vector functional in said microorganism prior to introducing said inhibitory nucleic acid into said microorganism.

Another embodiment of the present invention is a method for identifying a compound
 10 having the ability to inhibit proliferation of a microorganism comprising:

- (a) identifying in a first microorganism a homolog of a gene or gene product present in a second microorganism which is different than said first microorganism, wherein the activity or level of said gene or gene product is inhibited by a nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs. 1-127 ;
- 15 (b) identifying an inhibitory nucleic acid sequence which inhibits the activity of said homolog in said first microorganism;
- (c) contacting said first microorganism with a sublethal level of said inhibitory nucleic acid, thus sensitizing said first microorganism;
- (d) contacting the sensitized microorganism of step (c) with a compound; and
- 20 (e) determining whether said compound inhibits proliferation of said sensitized microorganism.

The determining step may comprise determining whether said compound inhibits proliferation of said sensitized microorganism to a greater extent than said compound inhibits proliferation of a nonsensitized microorganism. Step (a) may comprise identifying a homologous nucleic acid to a
 25 gene or gene product whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs. 1-127 or a nucleic acid encoding a homologous polypeptide to a polypeptide whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs. 1-127 by using an algorithm selected from the group consisting of BLASTN version 2.0 with the default parameters and FASTA version 3.0t78 algorithm with the default
 30 parameters to identify said homologous nucleic acid or said nucleic acid encoding a homologous polypeptide in a database. Step (a) may comprise identifying a homologous nucleic acid or a nucleic acid encoding a homologous polypeptide by identifying nucleic acids which hybridize to said first gene. Step (a) may comprise expressing a nucleic acid selected from the group consisting of SEQ ID NOs. 1-127 in said microorganism. The inhibitory nucleic acid may be an antisense
 35 nucleic acid. The inhibitory nucleic acid may comprise an antisense nucleic acid to a portion of said homolog. The inhibitory nucleic acid may comprise an antisense nucleic acid to a portion of the operon encoding said homolog. The step of contacting the first microorganism with a sublethal

level of said inhibitory nucleic acid may comprise directly contacting said microorganism with said inhibitory nucleic acid. The step of contacting the first microorganism with a sublethal level of said inhibitory nucleic acid may comprise expressing an antisense nucleic acid to said homolog in said microorganism. The gene product may comprise a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 299-469.

Another embodiment of the present invention is a compound identified using the method of the preceding paragraph.

Another embodiment of the present invention is a method of identifying a compound having the ability to inhibit proliferation comprising:

- (a) contacting a microorganism other than *E. coli* with a sublethal level of a nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs. 1-127 or a portion thereof which inhibits the proliferation of *E. coli*, thus sensitizing said microorganism;
- (b) contacting the sensitized microorganism of step (a) with a compound; and
- (c) determining whether said compound inhibits proliferation of said sensitized microorganism.

The determining step may comprise determining whether said compound inhibits proliferation of said sensitized microorganism to a greater extent than said compound inhibits proliferation of a nonsensitized microorganism.

Another embodiment of the present invention is a compound identified using the methods of the preceding paragraph.

Another embodiment of the present invention is a method for identifying a compound having activity against a biological pathway required for proliferation comprising:

- (a) sensitizing a cell by expressing a sublethal level of an antisense nucleic acid complementary to a nucleic acid encoding a gene product required for proliferation, wherein the activity or expression of said gene product is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-127, in said cell to reduce the activity or amount of said gene product;
- (b) contacting the sensitized cell with a compound; and
- (c) determining whether said compound inhibits the growth of said sensitized cell.

The determining step may comprise determining whether said compound inhibits the growth of said sensitized cell to a greater extent than said compound inhibits the growth of a nonsensitized cell. The cell may be selected from the group consisting of bacterial cells, fungal cells, plant cells, and animal cells. The cell may be a Gram negative bacterium. The Gram negative bacterium may be *E. coli*. The cell may be selected from the group consisting of *Aspergillus fumigatus*, *Bacillus anthracis*, *Campylobacter jejuni*, *Candida albicans*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Haemophilus influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*,

Mycobacterium leprae, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Pseudomonas aeruginosa*, *Saccharomyces cerevisiae*, *Salmonella choleraesuis*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Treponema pallidum*, and *Yersinia pestis* or any species falling within the genera of any of the above species. The antisense nucleic acid may be transcribed from an inducible promoter. The method may further comprise contacting the cell with an agent which induces expression of said antisense nucleic acid from said inducible promoter, wherein said antisense nucleic acid is expressed at a sublethal level. The inhibition of proliferation may be measured by monitoring the optical density of a liquid culture. The gene product may comprise a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 299-469.

Another embodiment of the present invention is a compound identified using the methods of the preceding paragraph.

Another embodiment of the present invention is a method for identifying a compound having the ability to inhibit cellular proliferation comprising:

- (a) contacting a cell with an agent which reduces the activity or level of a gene product required for proliferation of said cell, wherein said gene product is a gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-127;
- (b) contacting said cell with a compound; and
- (c) determining whether said compound reduces proliferation of said contacted cell.

The determining step may comprise determining whether said compound reduces proliferation of said contacted cell to a greater extent than said compound reduces proliferation of cells which have not been contacted with said agent. The agent which reduces the activity or level of a gene product required for proliferation of said cell may comprise an antisense nucleic acid to a gene or operon required for proliferation. The agent which reduces the activity or level of a gene product required for proliferation of said cell may comprise a compound known to inhibit growth or proliferation of a microorganism. The cell may contain a mutation which reduces the activity or level of said gene product required for proliferation of said cell. The mutation may be a temperature sensitive mutation. The gene product may comprise a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 299-469.

Another embodiment of the present invention is a compound identified using the method of the preceding paragraph.

Another embodiment of the present invention is a method for identifying the biological pathway in which a proliferation-required gene or its gene product lies, wherein said gene or gene product comprises a gene or gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-127, said method comprising:

(a) expressing a sublethal level of an antisense nucleic acid which inhibits the activity of said proliferation-required gene or gene product in a cell;

(b) contacting said cell with a compound known to inhibit growth or proliferation of a microorganism, wherein the biological pathway on which said compound acts is known; and

5 (c) determining whether said cell is sensitive to said compound.

The determining step may comprise determining whether said cell has a substantially greater sensitivity to said compound than a cell which does not express said sublethal level of said antisense nucleic acid and wherein said gene or gene product lies in the same pathway on which said compound acts if said cell expressing said sublethal level of said antisense nucleic acid has a
10 substantially greater sensitivity to said compound than said cell which does not express said sublethal level of said antisense nucleic acid.

The gene product may comprise a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 299-469.

Another embodiment of the present invention is a method for determining the biological
15 pathway on which a test compound acts comprising:

(a) expressing a sublethal level of an antisense nucleic acid complementary to a proliferation-required nucleic acid in a cell, wherein the activity or expression of said proliferation-required nucleic acid is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-127 and wherein the biological pathway in which said
20 proliferation-required nucleic acid or a protein encoded by said proliferation-required polypeptide lies is known,

(b) contacting said cell with said test compound; and

(c) determining whether said cell is sensitive to said test compound.

The determining step may comprise determining whether said cell has a substantially greater
25 sensitivity to said test compound than a cell which does not express said sublethal level of said antisense nucleic acid. The method may further comprise:

(d) expressing a sublethal level of a second antisense nucleic acid complementary to a second proliferation-required nucleic acid in a second cell, wherein said second proliferation-required nucleic acid is in a different biological pathway than said proliferation-required nucleic
30 acid in step (a); and

(e) determining whether said second cell does not have a substantially greater sensitivity to said test compound than a cell which does not express said sublethal level of said second antisense nucleic acid, wherein said test compound is specific for the biological pathway against which the antisense nucleic acid of step (a) acts if said second cell does not have
35 substantially greater sensitivity to said test compound.

Another embodiment of the present invention is a purified or isolated nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-127.

Another embodiment of the present invention is a compound which interacts with a gene or gene product whose activity or expression is inhibited by an antisense nucleic acid comprising one of SEQ ID NOs.: 1-127 to inhibit proliferation.

Another embodiment of the present invention is a compound which interacts with a polypeptide whose expression is inhibited by an antisense nucleic acid comprising one of SEQ ID NOs.: 1-127 to inhibit proliferation.

Another embodiment of the present invention is a method for manufacturing an antibiotic comprising the steps of screening one or more candidate compounds to identify a compound that reduces the activity or level of a gene product required for proliferation, said gene product comprising a gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-127 and manufacturing the compound so identified.

The screening step may comprise performing any one of the methods of identifying a compound described above.

Another embodiment of the present invention is a method for inhibiting proliferation of a microorganism in a subject comprising administering a compound that reduces the activity or level of a gene product required for proliferation of said microorganism, said gene product comprising a gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-127 to said subject. The method of subject may be selected from the group consisting of vertebrates, mammals, avians, and human beings. The gene product may comprise a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 299-469.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is an IPTG dose response curve in *E. coli* transformed with an IPTG-inducible plasmid containing either an antisense clone to the *E. coli* ribosomal protein rplW (AS-rplW) which is required for protein synthesis and essential for cell proliferation, or an antisense clone to the *elaD* gene (AS-*elaD*) which is not known to be involved in protein synthesis and which is also essential for proliferation.

Figure 2A is a tetracycline dose response curve in *E. coli* transformed with an IPTG-inducible plasmid containing antisense to rplW gene (AS-rplW) carried out in the presence of 0, 20 or 50 μ M IPTG.

Figure 2B is a tetracycline dose response curve in *E. coli* transformed with an IPTG-inducible plasmid containing antisense to *elaD* gene (AS-*elaD*) carried out in the presence of 0, 20 or 50 μ M IPTG.

Figure 3 is a graph showing the fold increase in tetracycline sensitivity of *E. coli* transfected with antisense clones to essential ribosomal protein genes L23 (AS-rplW) and L7/L12

and L10 (AS-rplLrpLJ). Antisense clones to genes known not to be involved in protein synthesis (atpB/E(AS-atpB/E), visC (AS-visC, elaD (AS-elaD), yohH (AS-yohH) are much less sensitive to tetracycline.

5

Definitions

By "biological pathway" is meant any discrete cell function or process that is carried out by a gene product or a subset of gene products. Biological pathways include enzymatic, biochemical and metabolic pathways as well as pathways involved in the production of cellular structures such as cell walls. Biological pathways that are usually required for proliferation of microorganisms include, but are not limited to, cell division, DNA synthesis and replication, RNA synthesis (transcription), protein synthesis (translation), protein processing, protein transport, fatty acid biosynthesis, cell wall synthesis, cell membrane production, synthesis and maintenance, and the like.

By "inhibit activity of a gene or gene product" is meant having the ability to interfere with the function of a gene or gene product in such a way as to decrease expression of the gene or to reduce the level or activity of a product of the gene. Agents which inhibit the activity of a gene include agents that inhibit transcription of the gene, agents that inhibit processing of the transcript of the gene, agents that reduce the stability of the transcript of the gene, and agents that inhibit translation of the mRNA transcribed from the gene. In microorganisms, agents which inhibit the activity of a gene can act to decrease expression of the operon in which the gene resides or alter the folding or processing of operon RNA so as to reduce the level or activity of the gene product. The gene product can be a non-translated RNA such as ribosomal RNA, a translated RNA (mRNA) or the protein product resulting from translation of the gene mRNA. Of particular utility to the present invention are antisense RNAs that have activities against the operons or genes to which they specifically hybridize.

By "activity against a gene product" is meant having the ability to inhibit the function or to reduce the level or activity of the gene product in a cell.

By "activity against a protein" is meant having the ability to inhibit the function or to reduce the level or activity of the protein in a cell.

By "activity against a nucleic acid" is meant having the ability to inhibit the function or to reduce the level or activity of the nucleic acid in a cell.

By "activity against a gene" is meant having the ability to inhibit the function or expression of the gene in a cell.

By "activity against an operon" is meant having the ability to inhibit the function or reduce the level of one or more products of the operon in a cell.

By "antibiotic" is meant an agent which inhibits the proliferation of a microorganism.

By "identifying a compound" is meant to screen one or more compounds in a collection of compounds such as a combinatorial chemical library or other library of chemical compounds or to characterize a single compound by testing the compound in a given assay and determining whether it exhibits the desired activity.

5 By "inducer" is meant an agent or solution which, when placed in contact with a microorganism, increases transcription from a desired promoter.

As used herein, "nucleic acid" means DNA or RNA. Thus, the terminology "the nucleic acid of SEQ ID NO: X" includes both the DNA sequence of SEQ ID NO: X and an RNA sequence in which the thymidines in the DNA sequence have been substituted with uridines in the RNA sequence and in which the deoxyribose backbone of the DNA sequence has been substituted with a ribose backbone in the RNA sequence.

As used herein, "sublethal" means a concentration of an agent below the concentration required to inhibit all cell growth.

DETAILED DESCRIPTION OF THE INVENTION

15 The present invention describes a group of *E. coli* genes and gene families required for growth and/or proliferation. A proliferation-required gene or gene family is one where, in the absence of a gene transcript and/or gene product, growth or viability of the microorganism is reduced or eliminated. Thus, as used herein the terminology "proliferation-required" or "required for proliferation" encompasses sequences where the absence of a gene transcript and/or gene product completely eliminates cell growth as well as sequences where the absence of a gene transcript and/or gene product merely reduces cell growth. These proliferation-required genes can be used as potential targets for the generation of new antimicrobial agents. To achieve that goal, the present invention also encompasses novel assays for analyzing proliferation-required genes and for identifying compounds which interact with the gene products of the proliferation-required genes. In addition, the present invention contemplates the expression of genes and the purification of the proteins encoded by the nucleic acid sequences identified as required proliferation genes and reported herein. The purified proteins can be used to generate reagents and screen small molecule libraries or other candidate compound libraries for compounds that can be further developed to yield novel antimicrobial compounds. The present invention also describes methods for identification of homologous genes in organisms other than *E. coli*.

30 The present invention utilizes a novel method to identify proliferation-required *E. coli* sequences. Generally, a library of nucleic acid sequences from a given source are subcloned or otherwise inserted into an inducible expression vector, thus forming an expression library. Although the insert nucleic acids may be derived from the chromosome of the organism into which the expression vector is to be introduced, because the insert is not in its natural chromosomal location, the insert nucleic acid is an exogenous nucleic acid for the purposes of the discussion herein. The term expression is defined as the production of an RNA molecule from a gene, gene fragment, genomic

fragment, or operon. Expression can also be used to refer to the process of peptide or polypeptide synthesis. An expression vector is defined as a vehicle by which a ribonucleic acid (RNA) sequence is transcribed from a nucleic acid sequence carried within the expression vehicle. The expression vector can also contain features that permit translation of a protein product from the transcribed RNA message
5 expressed from the exogenous nucleic acid sequence carried by the expression vector. Accordingly, an expression vector can produce an RNA molecule as its sole product or the expression vector can produce a RNA molecule that is ultimately translated into a protein product.

Once generated, the expression library containing the exogenous nucleic acid sequences is introduced into an *E. coli* population to search for genes that are required for bacterial proliferation.

10 Because the library molecules are foreign to the population of *E. coli*, the expression vectors and the nucleic acid segments contained therein are considered exogenous nucleic acid.

Expression of the exogenous nucleic acid fragments in the test population of *E. coli* containing the expression vector library is then activated. Activation of the expression vectors consists of subjecting the cells containing the vectors to conditions that result in the expression of the exogenous
15 nucleic acid sequences carried by the expression vector library. The test population of *E. coli* cells is then assayed to determine the effect of expressing the exogenous nucleic acid fragments on the test population of cells. Those expression vectors that, upon activation and expression, negatively impact the growth of the *E. coli* screen population were identified, isolated, and purified for further study.

A variety of assays are contemplated to identify nucleic acid sequences that negatively impact
20 growth upon expression. In one embodiment, growth in *E. coli* cultures expressing exogenous nucleic acid sequences and growth in cultures not expressing these sequences is compared. Growth measurements are assayed by examining the extent of growth by measuring optical densities. Alternatively, enzymatic assays can be used to measure bacterial growth rates to identify exogenous nucleic acid sequences of interest. Colony size, colony morphology, and cell morphology are
25 additional factors used to evaluate growth of the host cells. Those cultures that failed to grow or grow with reduced efficiency under expression conditions are identified as containing an expression vector encoding a nucleic acid fragment that negatively affects a proliferation-required gene.

Once exogenous nucleic acid sequences of interest are identified, they are analyzed. The first step of the analysis is to acquire the nucleic acid sequence of the nucleic acid fragment of interest. To
30 achieve this end, the insert in those expression vectors identified as containing a sequence of interest is sequenced, using standard techniques well known in the art. The next step of the process is to determine the source of the nucleic acid sequence.

Determination of sequence source is achieved by comparing the obtained sequence data with known sequences in various genetic databases. The sequences identified are used to probe these gene
35 databases. The result of this procedure is a list of exogenous nucleic acid sequences corresponding to a list that included novel bacterial genes required for proliferation as well as genes previously identified as required for proliferation.

The number of DNA and protein sequences available in database systems has been growing exponentially for years. For example, at the end of 1998, the complete sequences of *Caenorhabditis elegans*, *Saccharomyces cerevisiae* and nineteen bacterial genomes, including *E. coli* were available. This sequence information is stored in a number of databanks, such as GenBank (the National Center
5 for Biotechnology Information (NCBI), and is publicly available for searching.

A variety of computer programs are available to assist in the analysis of the sequences stored within these databases. FastA, (W. R. Pearson (1990) "Rapid and Sensitive Sequence Comparison with FASTP and FASTA" Methods in Enzymology 183:63- 98), Sequence Retrieval System (SRS), (Etzold & Argos, SRS an indexing and retrieval tool for flat file data libraries. Comput. Appl.
10 Biosci. 9:49-57, 1993) are two examples of computer programs that can be used to analyze sequences of interest. In one embodiment of the present invention, the BLAST family of computer programs, which includes BLASTN version 2.0 with the default parameters, or BLASTX version 2.0 with the default parameters, is used to analyze nucleic acid sequences.

BLAST, an acronym for "Basic Local Alignment Search Tool," is a family of programs for
15 database similarity searching. The BLAST family of programs includes: BLASTN, a nucleotide sequence database searching program, BLASTX, a protein database searching program where the input is a nucleic acid sequence; and BLASTP, a protein database searching program. BLAST programs embody a fast algorithm for sequence matching, rigorous statistical methods for judging the significance of matches, and various options for tailoring the program for special situations. Assistance
20 in using the program can be obtained by e-mail at blast@ncbi.nlm.nih.gov.

Bacterial genes are often transcribed in polycistronic groups. These groups comprise operons, which are a collection of genes and intergenic sequences. The genes of an operon are co-transcribed and are often related functionally. Given the nature of the screening protocol, it is possible that the identified exogenous nucleic acid sequence corresponds to a gene or portion thereof with or without
25 adjacent noncoding sequences, an intragenic sequence (i.e. a sequence within a gene), an intergenic sequence (i.e. a sequence between genes), a sequence spanning at least a portion of two or more genes, a 5' noncoding region or a 3' noncoding region located upstream or downstream from the actual sequence that is required for bacterial proliferation. Accordingly, determining which of the genes that are encoded within the operons are individually required for proliferation is often desirable.

In one embodiment of the present invention, an operon is dissected to determine which gene or
30 genes are required for proliferation. For example, the RegulonDB DataBase described by Huerta et al. (*Nucl. Acids Res.* 26:55-59, 1998), which may also be found on the website http://www.cifn.unam.mx/Computational_Biology/regulondb/, may be used. to identify the boundaries of operons encoded within microbial genomes. A number of techniques that are well known in the art
35 can be used to dissect the operon. In one aspect of this embodiment, gene disruption by homologous recombination is used to individually inactivate the genes of an operon that is thought to contain a gene required for proliferation.

Several gene disruption techniques have been described for the replacement of a functional gene with a mutated, non-functional (null) allele. These techniques generally involve the use of homologous recombination. The method described by Link et al. (J. Bacteriol 1997 179:6228) serves as an excellent example of these methods as applicable to disruption of genes in *E. coli*. This technique uses crossover PCR to create a null allele with an in-frame deletion of the coding region of a target gene. The null allele is constructed in such a way that sequences adjacent to the wild type gene (ca. 500 bp) are retained. These homologous sequences surrounding the deletion null allele provide targets for homologous recombination so that the wild type gene on the *E. coli* chromosome can be replaced by the constructed null allele.

The crossover PCR amplification product is subcloned into the vector pKO3, the features of which include a chloramphenicol resistance gene, the counter-selectable marker *sacB*, and a temperature sensitive autonomous replication function. Following transformation of an *E. coli* cell population with such a vector, selection for cells that have undergone homologous recombination of the vector into the chromosome is achieved by growth on chloramphenicol at the non-permissive temperature of 43°C. Under these conditions, autonomous replication of the plasmid cannot occur and cell are resistant to chloramphenicol only if the chloramphenicol resistance gene has been integrated into the chromosome. Usually a single crossover event is responsible for this integration event such that the *E. coli* chromosome now contains a tandem duplication of the target gene consisting of one wild type allele and one deletion null allele separated by vector sequence.

This new *E. coli* strain containing the tandem duplication can be maintained at permissive temperatures in the presence of drug selection (chloramphenicol). Subsequently, cells of this new strain are cultured at the permissive temperature 30°C without drug selection. Under these conditions, the chromosome of some of the cells within the population will have undergone an internal homologous recombination event resulting in removal of the plasmid sequences. Subsequent culturing of the strain in growth medium lacking chloramphenicol but containing sucrose is used to select for such recombinative resolutions. In the presence of the counter-selectable marker *sacB*, sucrose is rendered into a toxic metabolite. Thus, cells that survive this counter-selection have lost both the plasmid sequences from the chromosome and the autonomously replicating plasmid that results as a byproduct of recombinative resolution.

There are two possible outcomes of the above recombinative resolution via homologous recombination. Either the wild type copy of the targeted gene is retained on the chromosome or the mutated null allele is retained on the chromosome. In the case of an essential gene, a single copy of the null allele would be lethal and such cells should not be obtained by the above procedure when applied to essential genes. In the case of a non-essential gene, roughly equal numbers of cells containing null alleles and cells containing wild type alleles should be obtained. Thus, the method serves as a test for essentiality of the targeted gene: when applied to essential genes, only cells with a wild type allele on the chromosome will be obtained.

Other techniques have also been described for the creation of disruption mutations in *E. coli*. For example, Link et al. also describe inserting an in-frame sequence tag concomitantly with an in-frame deletion in order to simplify analysis of recombinants obtained. Further, Link et al. describe disruption of genes with a drug resistance marker such as a kanamycin resistance gene.

5 Arigoni et al., (Arigoni, F. et al. A Genome-based Approach for the Identification of Essential Bacterial Genes, Nature Biotechnology 16: 851-856) describe the use of gene disruption combined with engineering a second copy of a test gene such that the expression of the gene is regulated by and inducible promoter such as the arabinose promoter to test the essentiality of the gene. Many of these techniques result in the insertion of large fragments of DNA into the gene of interest, such as

10 a drug selection marker. An advantage of the technique described by Link et al. is that it does not rely on an insertion into the gene to cause a functional defect, but rather results in the precise removal of the coding region. This insures the lack of polar effects on the expression of genes downstream from the target gene.

Recombinant DNA techniques can be used to express the entire coding sequences of the gene

15 identified as required for proliferation, or portions thereof. The over-expressed proteins can be used as reagents for further study. The identified exogenous sequences are isolated, purified, and cloned into a suitable expression vector using methods well known in the art. If desired, the nucleic acids can contain the sequences encoding a signal peptide to facilitate secretion of the expressed protein.

Expression of fragments of the bacterial genes identified as required for proliferation is also

20 contemplated by the present invention. The fragments of the identified genes can encode a polypeptide comprising at least 5, at least 10, at least 15, at least 20, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, at least 55, at least 60, at least 65, at least 75, or more than 75 consecutive amino acids of a gene complementary to one of the identified sequences of the present invention. The nucleic acids inserted into the expression vectors can also contain sequences upstream and downstream of the

25 coding sequence.

When expressing the coding sequence of an entire gene identified as required for bacterial proliferation or a fragment thereof, the nucleic acid sequence to be expressed is operably linked to a promoter in an expression vector using conventional cloning technology. The expression vector can be any of the bacterial, insect, yeast, or mammalian expression systems known in the art. Commercially

30 available vectors and expression systems are available from a variety of suppliers including Genetics Institute (Cambridge, MA), Stratagene (La Jolla, California), Promega (Madison, Wisconsin), and Invitrogen (San Diego, California). If desired, to enhance expression and facilitate proper protein folding, the codon usage and codon bias of the sequence can be optimized for the particular expression organism in which the expression vector is introduced, as explained by Hatfield, et al., U.S. Patent No.

35 5,082,767. Fusion protein expression systems are also contemplated by the present invention.

Following expression of the protein encoded by the identified exogenous nucleic acid sequence, the protein is purified. Protein purification techniques are well known in the art. Proteins

encoded and expressed from identified exogenous nucleic acid sequences can be partially purified using precipitation techniques, such as precipitation with polyethylene glycol. Chromatographic methods usable with the present invention can include ion-exchange chromatography, gel filtration, use of hydroxyapatite columns, immobilized reactive dyes, chromatofocusing, and use of high-
5 performance liquid chromatography. Electrophoretic methods such one-dimensional gel electrophoresis, high-resolution two-dimensional polyacrylamide electrophoresis, isoelectric focusing, and others are contemplated as purification methods. Also, affinity chromatographic methods, comprising antibody columns, ligand presenting columns and other affinity chromatographic matrices are contemplated as purification methods in the present invention.

10 The purified proteins produced from the gene coding sequences identified as required for proliferation can be used in a variety of protocols to generate useful antimicrobial reagents. In one embodiment of the present invention, antibodies are generated against the proteins expressed from the identified exogenous nucleic acid sequences. Both monoclonal and polyclonal antibodies can be generated against the expressed proteins. Methods for generating monoclonal and polyclonal
15 antibodies are well known in the art. Also, antibody fragment preparations prepared from the produced antibodies discussed above are contemplated.

Another application for the purified proteins of the present invention is to screen small molecule libraries for candidate compounds active against the various target proteins of the present invention. Advances in the field of combinatorial chemistry provide methods, well known in the art, to
20 produce large numbers of candidate compounds that can have a binding, or otherwise inhibitory effect on a target protein. Accordingly, the screening of small molecule libraries for compounds with binding affinity or inhibitory activity for a target protein produced from an identified gene sequence is contemplated by the present invention.

The present invention further contemplates utility against a variety of other pathogenic
25 organisms in addition to *E. coli*. For example, the invention has utility in identifying genes required for proliferation in prokaryotes and eukaryotes. For example, the invention has utility with protists, such as *Plasmodium* spp.; plants; animals, such as *Entamoeba* spp. and *Contracaecum* spp.; and fungi including *Candida* spp., (e.g., *Candida albicans*), *Saccharomyces cerevisiae*, *Cryptococcus neoformans*, and *Aspergillus fumigatus*. In one embodiment of the present invention, monera,
30 specifically bacteria are probed in search of novel gene sequences required for proliferation. This embodiment is particularly important given the rise of drug resistant bacteria.

The numbers of bacterial species that are becoming resistant to existing antibiotics are growing. A partial list of these organisms includes: *Staphylococcus* spp., such as *S. aureus*; *Enterococcus* spp., such as *E. faecalis*; *Pseudomonas* spp., such as *P. aeruginosa*, *Clostridium* spp.,
35 such as *C. botulinum*, *Haemophilus* spp., such as *H. influenzae*, *Enterobacter* spp., such as *E. cloacae*, *Vibrio* spp., such as *V. cholera*; *Moraxella* spp., such as *M. catarrhalis*; *Streptococcus* spp., such as *S. pneumoniae*, *Neisseria* spp., such as *N. gonorrhoeae*; *Mycoplasma* spp., such as

Mycoplasma pneumoniae; *Salmonella typhimurium*; *Helicobacter pylori*; *Escherichia coli*; and *Mycobacterium tuberculosis*. The sequences identified as required for proliferation in the present invention can be used to probe these and other organisms to identify homologous required proliferation genes contained therein.

5 In one embodiment of the present invention, the nucleic acid sequences disclosed herein are used to screen genomic libraries generated from bacterial species of interest other than *E. coli*. For example, the genomic library may be from *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Enterobacter cloacae*, *Helicobacter pylori*, *Neisseria gonorrhoeae*, *Enterococcus faecalis*, *Streptococcus pneumoniae*, *Haemophilus influenzae*, *Salmonella typhimurium*, *Saccharomyces*
10 *cerevisiae*, *Candida albicans*, *Cryptococcus neoformans*, *Aspergillus fumigatus*, *Klebsiella pneumoniae*, *Salmonella typhi*, *Salmonella paratyphi*, *Salmonella choleraesuis*, *Staphylococcus epidermidis*, *Mycobacterium tuberculosis*, *Mycobacterium leprae*, *Treponema pallidum*, *Bacillus anthracis*, *Yersinia pestis*, *Clostridium botulinum*, *Campylobacter jejuni*, *Chlamydia trachomatis*, *Chlamydia pneumoniae* or any species falling within the genera of any of the above species.
15 Standard molecular biology techniques are used to generate genomic libraries from various microorganisms. In one aspect, the libraries are generated and bound to nitrocellulose paper. The identified exogenous nucleic acid sequences of the present invention can then be used as probes to screen the libraries for homologous sequences. The homologous sequences identified can then be used as targets for the identification of new, antimicrobial compounds with activity against more than one
20 organism.

For example, the preceding methods may be used to isolate nucleic acids having a sequence with at least 97%, at least 95%, at least 90%, at least 85%, at least 80%, or at least 70% identity to a nucleic acid sequence selected from the group consisting of one of the sequences of SEQ ID NOS. 1-127, 128-298, fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300,
25 400, or 500 consecutive bases thereof, and the sequences complementary thereto. Identity may be measured using BLASTN version 2.0 with the default parameters. (Altschul, S.F. et al. Gapped BLAST and PSI-BLAST: A New Generation of Protein Database Search Programs, *Nucleic Acid Res.* 25: 3389-3402 (1997)). For example, the homologous polynucleotides may have a coding sequence which is a naturally occurring allelic variant of one of the coding sequences described
30 herein. Such allelic variants may have a substitution, deletion or addition of one or more nucleotides when compared to the nucleic acids of SEQ ID NOs: 1-127, 128-298 or the sequences complementary thereto.

Additionally, the above procedures may be used to isolate nucleic acids which encode polypeptides having at least 99%, 95%, at least 90%, at least 85%, at least 80%, at least 70%, at
35 least 60%, at least 50%, or at least 40% identity or similarity to a polypeptide having the sequence of one of SEQ ID NOs: 299-469 or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof as determined using the FASTA version 3.0t78

algorithm with the default parameters. Alternatively, protein identity or similarity may be identified using BLASTP with the default parameters, BLASTX with the default parameters, or TBLASTN with the default parameters. (Alschul, S.F. et al. Gapped BLAST and PSI-BLAST: A New Generation of Protein Database Search Programs, *Nucleic Acid Res.* 25: 3389-3402 (1997)).

5 Alternatively, homologous nucleic acids or polypeptides may be identified by searching a database to identify sequences having a desired level of homology to a nucleic acid or polypeptide involved in proliferation or an antisense nucleic acid to a nucleic acid involved in microbial proliferation. A variety of such databases are available to those skilled in the art, including GenBank and GenSeq. In some embodiments, the databases are screened to identify nucleic acids
10 or polypeptides having at least 97%, at least 95%, at least 90%, at least 85%, at least 80%, at least 70%, at least 60%, or at least 50%, at least 40% identity or similarity to a nucleic acid or polypeptide involved in proliferation or an antisense nucleic acid involved in proliferation. For example, the database may be screened to identify nucleic acids homologous to one of SEQ ID Nos. 1-127, 128-298 or polypeptides homologous to SEQ ID NOs. 299-469. In some embodiments, the
15 database may be screened to identify homologous nucleic acids or polypeptides from organisms other than *E. coli*, including organisms such as *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Enterobacter cloacae*, *Helicobacter pylori*, *Neisseria gonorrhoeae*, *Enterococcus faecalis*, *Streptococcus pneumoniae*, *Haemophilus influenzae*, *Salmonella typhimurium*, *Saccharomyces cerevisiae*, *Candida albicans*, *Cryptococcus neoformans*, *Aspergillus fumigatus*, *Klebsiella pneumoniae*, *Salmonella typhi*, *Salmonella paratyphi*, *Salmonella choleraesuis*, *Staphylococcus epidermidis*, *Mycobacterium tuberculosis*, *Mycobacterium leprae*, *Treponema pallidum*, *Bacillus anthracis*, *Yersinia pestis*, *Clostridium botulinum*, *Campylobacter jejuni*, *Chlamydia trachomatis*, *Chlamydia pneumoniae* or any species falling within the genera of any of the above species.

In another embodiment, gene expression arrays and microarrays can be employed. Gene
25 expression arrays are high density arrays of DNA samples deposited at specific locations on a glass chip, nylon membrane, or the like. Such arrays can be used by researchers to quantify relative gene expression under different conditions. Gene expression arrays are used by researchers to help identify optimal drug targets, profile new compounds, and determine disease pathways. An example of this technology is found in U.S. Patent No. 5807522.

30 It is possible to study the expression of all genes in the genome of a particular microbial organism using a single array. For example, the arrays from Genosys consist of 12 x 24 cm nylon filters containing PCR products corresponding to 4290 ORFs from *E. coli*. 10 ngs of each are spotted every 1.5 mm on the filter. Single stranded labeled cDNAs are prepared for hybridization to the array (no second strand synthesis or amplification step is done) and placed in contact with the
35 filter. Thus the labeled cDNAs are of "antisense" orientation. Quantitative analysis is done by phosphorimager.

Hybridization of cDNA made from a sample of total cell mRNA to such an array followed by detection of binding by one or more of various techniques known to those in the art results in a signal at each location on the array to which cDNA hybridized. The intensity of the hybridization signal obtained at each location in the array thus reflects the amount of mRNA for that specific gene that was present in the sample. Comparing the results obtained for mRNA isolated from cells grown under different conditions thus allows for a comparison of the relative amount of expression of each individual gene during growth under the different conditions.

Gene expression arrays may be used to analyze the total mRNA expression pattern at various time points after induction of an antisense nucleic acid against a proliferation-required gene. Analysis of the expression pattern indicated by hybridization to the array provides information on whether or not the target gene of the antisense nucleic acid is being affected by antisense induction, how quickly the antisense is affecting the target gene, and for later timepoints, what other genes are affected by antisense expression. For example, if the antisense is directed against a gene for ribosomal protein L7/L12 in the 50S subunit, its targeted mRNA may disappear first and then other mRNAs may be observed to increase, decrease or stay the same. Similarly, if the antisense is directed against a different 50S subunit ribosomal protein mRNA (e.g. L25), that mRNA may disappear first followed by changes in mRNA expression that are similar to those seen with the L7/L12 antisense expression. Thus, the mRNA expression pattern observed with an antisense nucleic acid against a proliferation required gene may identify other proliferation-required nucleic acids in the same pathway as the target of the antisense nucleic acid. In addition, the mRNA expression patterns observed with candidate drug compounds may be compared to those observed with antisense nucleic acids against a proliferation-required nucleic acid. If the mRNA expression pattern observed with the candidate drug compound is similar to that observed with the antisense nucleic acid, the drug compound may be a promising therapeutic candidate. Thus, the assay would be useful in assisting in the selection of candidate drug compounds for use in screening methods such as those described below.

In cases where the source of nucleic acid deposited on the array and the source of the nucleic acid being hybridized to the array are from two different organisms, gene expression arrays can identify homologous genes in the two organisms.

The present invention also contemplates additional methods for screening other microorganisms for proliferation-required genes. In this embodiment, the conserved portions of sequences identified as proliferation-required can be used to generate degenerate primers for use in the polymerase chain reaction (PCR). The PCR technique is well known in the art. The successful production of a PCR product using degenerate probes generated from the sequences identified herein would indicate the presence of a homologous gene sequence in the species being screened. This homologous gene is then isolated, expressed, and used as a target for candidate antibiotic compounds. In another aspect of this embodiment, the homologous gene is expressed in an autologous organism or

in a heterologous organism in such a way as to alter the level or activity of a homologous gene required for proliferation in the autologous or heterologous organism. In still another aspect of this embodiment, the homologous gene or portion is expressed in an antisense orientation in such a way as to alter the level or activity of a nucleic acid required for proliferation of an autologous or heterologous organism.

5 The homologous sequences to proliferation-required genes identified using the techniques described herein may be used to identify proliferation-required genes of organisms other than *E. coli*, to inhibit the proliferation of organisms other than *E. coli* by inhibiting the activity or reducing the amount of the identified homologous nucleic acid or polypeptide in the organism other than *E. coli*, or to identify compounds which inhibit the growth of organisms other than *E. coli* as described
10 below.

In another embodiment of the present invention, *E. coli* sequences identified as required for proliferation are transferred to expression vectors capable of function within non-*E. coli* species. As would be appreciated by one of ordinary skill in the art, expression vectors must contain certain elements that are species specific. These elements can include promoter sequences, operator
15 sequences, repressor genes, origins of replication, ribosomal binding sequences, termination sequences, and others. To use the identified exogenous sequences of the present invention, one of ordinary skill in the art would know to use standard molecular biology techniques to isolate vectors containing the sequences of interest from cultured bacterial cells, isolate and purify those sequences, and subclone those sequences into an expression vector adapted for use in the species of
20 bacteria to be screened.

Expression vectors for a variety of other species are known in the art. For example, Cao et al. report the expression of steroid receptor fragments in *Staphylococcus aureus*. *J. Steroid Biochem Mol Biol.* 44(1):1-11 (1993). Also, Pla et al. have reported an expression vector that is functional in a number of relevant hosts including: *Salmonella typhimurium*, *Pseudomonas putida*,
25 and *Pseudomonas aeruginosa*. *J. Bacteriol.* 172(8):4448-55 (1990). These examples demonstrate the existence of molecular biology techniques capable of constructing expression vectors for the species of bacteria of interest to the present invention.

Following the subcloning of the identified nucleic acid sequences into an expression vector functional in the microorganism of interest, the identified nucleic acid sequences are conditionally
30 transcribed to assay for bacterial growth inhibition. Those expression vectors found to contain sequences that, when transcribed, inhibit bacterial growth are compared to the known genomic sequence of the pathogenic microorganism being screened or, if the homologous sequence from the organism being screened is not known, it may be identified and isolated by hybridization to the proliferation-required *E. coli* sequence of interest or by amplification using primers based on the
35 proliferation-required *E. coli* sequence of interest as described above.

The antisense sequences from the second organism which are identified as described above may then be operably linked to a promoter, such as an inducible promoter, and introduced into the

second organism. The techniques described herein for identifying *E. coli* genes required for proliferation may thus be employed to determine whether the identified sequences from a second organism inhibit the proliferation of the second organism.

Antisense nucleic acids required for the proliferation of organisms other than *E. coli* or the
5 genes corresponding thereto, may also be hybridized to a microarray containing the *E. coli* ORFs to gauge the homology between the *E. coli* sequences and the proliferation-required nucleic acids from other organisms. For example, the proliferation-required nucleic acid may be from *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Enterobacter cloacae*, *Helicobacter pylori*, *Neisseria gonorrhoeae*, *Enterococcus faecalis*, *Streptococcus pneumoniae*, *Haemophilus influenzae*,
10 *Salmonella typhimurium*, *Saccharomyces cerevisiae*, *Candida albicans*, *Cryptococcus neoformans*, *Aspergillus fumigatus*, *Klebsiella pneumoniae*, *Salmonella typhi*, *Salmonella paratyphi*, *Salmonella choleraesuis*, *Staphylococcus epidermidis*, *Mycobacterium tuberculosis*, *Mycobacterium leprae*, *Treponema pallidum*, *Bacillus anthracis*, *Yersinia pestis*, *Clostridium botulinum*, *Campylobacter jejuni* or *Chlamydia trachomatis*, *Chlamydia pneumoniae* or any species falling within the genera
15 of any of the above species. The proliferation-required nucleic acids from an organism other than *E. coli* may be hybridized to the array under a variety of conditions which permit hybridization to occur when the probe has different levels of homology to the sequence on the microarray. This would provide an indication of homology across the organisms as well as clues to other possible essential genes in these organisms.

20 In still another embodiment, the exogenous nucleic acid sequences of the present invention that are identified as required for bacterial growth or proliferation can be used as antisense therapeutics for killing bacteria. The antisense sequences can be directed against the proliferation-required genes whose sequence corresponds to the exogenous nucleic acid probes identified here (i.e. the antisense nucleic acid may hybridize to the gene or a portion thereof). Alternatively, antisense therapeutics can
25 be directed against operons in which proliferation-required genes reside (i.e. the antisense nucleic acid may hybridize to any gene in the operon in which the proliferation-required genes reside). Further, antisense therapeutics can be directed against a proliferation-required gene or portion thereof with or without adjacent noncoding sequences, an intragenic sequence (i.e. a sequence within a gene), an intergenic sequence (i.e. a sequence between genes), a sequence spanning at least a portion of two or
30 more genes, a 5' noncoding region or a 3' noncoding region located upstream or downstream from the actual sequence that is required for bacterial proliferation or an operon containing a proliferation-required gene.

In addition to therapeutic applications, the present invention encompasses the use of nucleic acid sequences complementary to sequences required for proliferation as diagnostic tools. For
35 example, nucleic acid probes complementary to proliferation-required sequences that are specific for particular species of microorganisms can be used as probes to identify particular microorganism species in clinical specimens. This utility provides a rapid and dependable method by which to identify

the causative agent or agents of a bacterial infection. This utility would provide clinicians the ability to prescribe species specific antimicrobial compounds to treat such infections. In an extension of this utility, antibodies generated against proteins translated from mRNA transcribed from proliferation-required sequences can also be used to screen for specific microorganisms that produce such proteins in a species-specific manner.

The following examples teach the genes of the present invention and a subset of uses for the *E. coli* genes identified as required for proliferation. These examples are illustrative only and are not intended to limit the scope of the present invention.

EXAMPLES

The following examples are directed to the identification and exploitation of *E. coli* genes required for proliferation. Methods of gene identification are discussed as well as a variety of methods to utilize the identified sequences.

Genes Identified as Required for Proliferation of *E. coli*

Exogenous nucleic acid sequences were cloned into an inducible expression vector and assayed for growth inhibition activity. Example 1 describes the examination of a library of exogenous nucleic acid sequences cloned into the IPTG-inducible expression vector pLex5BA (Krause et al., J. Mol. Biol. 274: 365 (1997)). Upon activation or induction, the expression vectors produced an RNA molecule corresponding to the subcloned exogenous nucleic acid sequences. The RNA product was in an antisense orientation with respect to the *E. coli* genes from which it was originally derived. This antisense RNA then interacted with sense mRNA produced from various *E. coli* genes and interfered with or inhibited the translation of the sense messenger RNA (mRNA) thus preventing protein production from these sense mRNA molecules. In cases where the sense mRNA encoded a protein required for the proliferation, bacterial cells containing an activated expression vector failed to grow or grew at a substantially reduced rate. Similar results have also be obtained in cases where the gene encodes a non-translated RNA, such as a ribosomal RNA.

EXAMPLE 1

Inhibition of Bacterial Proliferation after IPTG induction

To study the effects of transcriptional induction in liquid medium, growth curves were carried out by back diluting cultures 1:200 into fresh media with or without 1 mM IPTG and measuring the OD₄₅₀ every 30 minutes (min). To study the effects of transcriptional induction on solid medium, 10², 10³, 10⁴, 10⁵, 10⁶, 10⁷ and 10⁸ fold dilutions of overnight cultures were prepared. Aliquots of from 0.5 to 3 µl of these dilutions were spotted on selective agar plates with or without 1 mM IPTG. After overnight incubation, the plates were compared to assess the sensitivity of the clones to IPTG.

Of the numerous clones tested, some clones were identified as containing a sequence that inhibited *E. coli* growth after IPTG induction. Accordingly, the gene to which the inserted nucleic acid

sequence corresponds, or a gene within the operon containing the inserted nucleic acid, may be required for proliferation in *E. coli*.

Characterization of Isolated Clones Negatively Affecting *E. coli* Proliferation

- 5 Following the identification of those expression vectors that, upon expression, negatively impacted *E. coli* growth or proliferation, the inserts or nucleic acid fragments contained in those expression vectors were isolated for subsequent characterization. Inserts in expression vectors of interest were subjected to nucleic acid sequence determination.

EXAMPLE 2

10 Nucleic Acid Sequence Determination of Identified Clones Expressing Nucleic Acid Fragments with Detrimental Effects of *E. coli* Proliferation

- The nucleotide sequences for the exogenous identified sequences were determined using plasmid DNA isolated using QIAPREP (Qiagen, Valencia, CA) and methods supplied by the manufacturer. The primers used for sequencing the inserts were 5' - TGTTTATCAGACCGCTT - 3' (SEQ ID NO: 1) and 5' - ACAATTTACACAGCCTC - 3' (SEQ ID NO: 2). These sequences flank the polylinker in pLEX5BA. Sequence identification numbers (SEQ ID NOs) for the identified inserts are listed in Table I and discussed below.

EXAMPLE 3

Comparison Of Isolated Sequences to Known Sequences

- 20 The nucleic acid sequences of the subcloned fragments obtained from the expression vectors discussed above were compared to known *E. coli* sequences in GenBank using BLAST version 1.4 or version 2.0.6 using the following default parameters: Filtering off, cost to open a gap=5, cost to extend a gap=2, penalty for a mismatch in the blast portion of run=-3, reward for a match in the blast portion of run=1, expectation value (e)=10.0, word size=11, number of one-line descriptions=100, number of alignments to show (B)=100. BLAST is described in Altschul, J Mol Biol. 215:403-10 (1990). Expression vectors were found to contain nucleic acid sequences in both the sense and antisense orientations. The presence of known genes, open reading frames, and ribosome binding sites was determined by comparison to public databases holding genetic information and various computer programs such as the Genetics Computer Group programs FRAMES and CODONPREFERENCE.
- 25 Clones were designated as "antisense" if the cloned fragment was oriented to the promoter such that the RNA transcript produced was complementary to the expressed mRNA from a chromosomal locus. Clones were designated as "sense" if they coded for an RNA fragment that was identical to a portion of a wild type mRNA from a chromosomal locus.

- The sequences described in Examples 1-2 that inhibited bacterial proliferation and contained gene fragments in an antisense orientation are listed in Table I. This table lists each identified sequence by: a sequence identification number; a Molecule Number; a gene to which the identified sequence corresponds, listed according to the National Center for Biotechnology Information (NCBI), Blattner
- 35

(Science 277:1453-1474(1997); also contains the *E. coli* K-12 genome sequence), or Rudd (Micro. and Mol. Rev. 62:985-1019 (1998)), nomenclatures. The CONTIG numbers for each identified sequence is shown, as well as the location of the first and last base pairs located on the *E. coli* chromosome. A Molecule Number with a "***" indicates a clone corresponding to an intergenic sequence.

5

10

TABLE I

Identified Clones with Corresponding Genes and Operons

Clone Name	Seq ID	Molecule No.	Gene (NCBI)	Gene (Blattner)	Gene (Rudd)	Contig	Start	Stop
626.O24	1	EcXA056	f320	b1113	ycfS	AE000211	7631	7971
E1M10000116B1	2	EcXA056b	ycfS	b1113	ycfS	AE000211	7658	7847
E1M10000155F12	3	EcXA056c	ycfS	b1113	ycfS	AE000211	7649	8037
Z56-D2	4	EcXA057	arp	b4017	arp	AE000474	14059	14440
E1M10000144B6	5	EcXA057b	arp	b4017	arp	AE000474	14187	14385
Z60-P16	6	EcXA058	rplC	b3320	rplC	AE000408	10002	10338
Z80-D10	7	EcXA059	ypjA	b2647	ypjA	AE000349	10402	10493
						AE000350	1	728
P33-1.C22	8	EcXA060	rplR	b3304	rplR	AE000408	2763	2958
E1M10000161C06	9	EcXA060b	RplR; rplF	b3304; b3305	RplR; rplF	AE000408	3006	3477
P35-7	10	EcXA061	malE	b4034	malE	AE000476	11925	12089
P35-8	11	EcXA062	rep	b3778	rep	AE000454	4438	4111
P38-1.G20	12	EcXA063	elaD	b2269	elaD	AE000316	9912	9581
E1M10000107H4	13	EcXA063b	elaD	b2269	elaD	AE000316	9520	9389
E1M10000122B03	14	EcXA063c	elaD	b2269	elaD	AE000316	9979	9715
E1M10000139B07	15	EcXA063d	elaD	b2269	elaD	AE000316	10171	9533
E1M10000152G3	16	EcXA063e	elaD	b2269	elaD	AE000316	9535	9406
E1M10000143G03	17	EcXA063f	elaD	b2269	elaD	AE000316	10104	9869
E1M10000131H01	18	EcXA063h	elaD	b2269	elaD	AE000316	9953	9746
P319-4.O6	19	EcXA064	CyoE	b0428	cyoE	AE000149	2140	2293
P323-1.M10	20	EcXA065	DgoA	b3692	YidU	AE000446	6005	6272
E1M10000111E4	21	EcXA065b	DgoA	b3692	YidU	AE000446	6005	6133
P323-8.P1	22	EcXA066	RpmI	b1717	RpmI	AE000266	10240	10390

Clone Name	Seq ID	Molecule No.	Gene (NCBI)	Gene (Blat- tner)	Gene (Rudd)	Contig	Start	Stop
E1M10000137G09	23	EcXA066b	RplT;r pmI	b1716; b1717	RplT; RpmI	AE000266	9947	10525
P326-22.E17	24	EcXA067	xylF	b3566	XylF	AE000434	288	95
P326-9.K2	25	EcXA068	YhfL; yhfM	b3369; b3370	yhfL; yhfM	AE000413	581	306
P327-50.M10	26	EcXA069	RplD; rplC	b3319; b3320	rplD; rplC	AE000408	9747	9900
E1M10000110G1	27	EcXA069b	RplD; rplC	b3319; b3320	rplD; rplC	AE000408	9789	9933
E1M10000121D08	28	EcXA069c	RplD; rplC	b3319; b3320	RplD; rplC	AE000408	9737	10002
E1M10000136H1	29	EcXA069d	RplD; rplC	b3319; b3320	RplD; rplC	AE000408	9707	10241
E1M10000126E08	30	EcXA069e	rplC	b3320	RplC	AE000408	10157	10379
E1M10000137C04	31	EcXA069f	RplD; rplC	b3319; b3320	RplD; RplC	AE000408	9783	10007
E1M10000106G02	32	EcXA069g	rplC	b3320	RplC	AE000408	9814	10154
E1M10000146H01	33	EcXA069h	RplD; rplC	b3319; b3320	RplD; RplC	AE000408	9715	9890
E1M10000148C02	34	EcXA069i	RplD; rplC	b3319; b3320	RplD; RplC	AE000408	9740	9980
P328-20.P20	35	EcXA070	YbcQ	b0551	YbcQ	AE000160	7883	7661
1065-12	36	EcXA071	ffh	b2610	Ffh	AE000346	11978	12129
						AE000347	1	319
E1M10000101D6	37	EcXA071b	RpsP; ffh	b2609; b2610	RpsP; ffh	AE000346	11911	12129
						AE000347	1	348
P332-11.C20	38	EcXA072	recJ	b2892	recJ	AE000372	12047	12144
						AE000273	1	108
P334-5.H2	39	EcXA073	htrE	b0139	htrE	AE000123	5431	5548
P338-4.M21	40	EcXA073b	htrE	b0139	htrE	AE000123	5447	5593
E1M10000119A04	41	EcXA073c	htrE	b0139	htrE	AE000123	5419	5642
E1M10000137C03	42	EcXA073d	htrE; ecpD	b0139; b0140	htrE; ecpD	AE000123	5414	5919
E1M10000124G03	43	EcXA073e	htrE	b0139	htrE	AE000123	5332	5515
P334-8.L7	44	EcXA074	yciR	b1285	yciR	AE000226	8045	8371
1053-37	45	EcXA074b	yciR	b1285	yciR	AE000226	6079	6293
P335-3.J14	46	EcXA075	SfmD	b0532	sfmD	AE000159	3235	3115
P335-8.H8	47	EcXA076	mviM	b1068	mviM	AE000207	11140	10983
						AE000208	50	1
P342-3	48	EcXA077	B2145	b2145	yciS	AE000303	9025	8831

Clone Name	Seq ID	Molecule No.	Gene (NCBI)	Gene (Blat-tner)	Gene (Rudd)	Contig	Start	Stop
E1M10000106G10	49	EcXA077b	B2145	b2145	yeiS	AE000303	9007	8841
E1M10000144F3	50	EcXA077c	B2145	b2145	yeiS	AE000303	9052	8827
X3S177-4	51	EcXA078	ycgB	b1188	ycgB	AE000217	3945	4129
P317-2.A3	52	EcXA079	yedV	b1968	yedX	AE000288	5289	5475
E1M10000151C04	53	EcXA079b	yedV	b1968	yedV	AE000288	5179	5515
E1M10000162G05	54	EcXA079c	yedV	b1968	yedV	AE000288	5313	5503
E1M10000167F04	55	EcXA079d	yedV	b1968	yedV	AE000288	5293	5531
E1M10000167G04	56	EcXA079e	yedV	b1968	yedV	AE000288	5293	5531
X3S204-7	57	EcXA080	rplV	b3315	RplV	AE000408	7444	7770
E1M10000111C3	58	EcXA080b	RplV; rpsS	b3315; b3316	RplV; rpsS	AE000408	7633	7898
E1M10000131B07	59	EcXA080c	RplV; rpsS	b3315; b3316	RplV; rpsS	AE000408	7686	7871
E1M10000131C07	60	EcXA080d	RplV; rpsS	b3315; b3316	RplV; rpsS	AE000408	7723	7860
E1M10000144G6	61	EcXA080e	rplV	b3315	RplV	AE000408	7580	7762
E1M10000144C2	62	EcXA080f	RplV; rpsS	b3315; b3316	RplV; rpsS	AE000408	7650	7784
E1M10000107G2	63	EcXA081	rpsP	b2609	RpsP	AE000346	11957	12097
MC9.6	64	EcXA082	hybC; hybB	b2994; b2995	HybC; hybB	AE000382	4419	4562
B18-2.N21	65	EcXA083	hrpB	b0148	HrpB	AE000124	3024	2955
P336-14.F20	66	EcXA084	B1399	b1399	PaaX	AE000237	164	1
						AE000236	12073	12006
985.P21	67	EcXA085	AgaZ; agaV	b3132; b3133	agaZ; agaV	AE000394	10111	10705
Z92-K24	68	EcXA086	rplQ	b3294	RplQ	AE000407	7653	8349
E1M10000101C12	69	EcXA086b	rplQ	b3294	RplQ	AE000407	7748	8075
E1M10000103D11	70	EcXA086c	RplQ	b3294	RplQ	AE000407	7652	8051
E1M10000127D09	71	EcXA086d	rplQ; rpoA	b3294; b3295	RplQ; rpoA	AE000407	7806	8129
E1M10000152D8	72	EcXA086e	rplQ; rpoA	b3294; b3295	rplQ; rpoA	AE000407	7950	8146
SC17.1	73	EcXA087	YehW	b2128	YehW	AE000302	915	1226
SC21.1	74	EcXA088	RplO	b3301	RplO	AE000408	1743	1907
E1M10000107G8	75	EcXA089	YadT	b0158	YadT	AE000125	4489	4639
E1M10000115C6	76	EcXA090	DnaE	b0184	DnaE	AE000127	10980	10830
E1M10000107B2	77	EcXA091	YkgE	b0306	YkgE	AE000137	9375	9261
E1M10000107C3	78	EcXA092	b1497	b1497	YdeM	AE000247	689	908
E1M10000107H9	79	EcXA093	YohM	b2106	YohM	AE000299	9423	9166
E1M10000109A11	80	EcXA094	YfjW	b2642	YfjW	AE000349	7160	6851

Clone Name	Seq ID	Molecule No.	Gene (NCBI)	Gene (Blat- tner)	Gene (Rudd)	Contig	Start	Stop
E1M10000160D07	81	EcXA094b	YfjW	b2642	YfjW	AE000349	7118	6932
E1M10000161A05	82	EcXA094c	YfjW	b2642	YfjW	AE000349	6381	5980
E1M10000155A06	83	EcXA094d	YfjW	b2642	YfjW	AE000349	6893	6749
E1M10000111A7	84	EcXA095	b2758	b2758	YgcJ	AE000359	4983	5069
E1M10000107E2	85	EcXA096	YgcM; ygcN	b2765; b2766	ygcM; ygcN	AE000360	5320	5190
E1M10000115E3	86	EcXA097	yhcB	b3233	YhcB	AE000402	8070	7864
E1M10000107B3	87	EcXA097b	yhcB; degQ	b3233; b3234	yhcB; degQ	AE000402	8168	7922
E1M10000162F03	88	EcXA097c	yhcB	b3233	yhcB	AE000402	8111	7874
E1M10000127H07	89	EcXA097d?	yhcB	b3233	yhcB	AE000402	8092	7808
E1M10000163C04	90	EcXA097e	yhcB; degQ?	b3233; b3234	yhcB; degQ	AE000402	8159	7874
E1M10000115G2	91	EcXA098	rpoA	b3295	RpoA	AE000407	8254	8453
E1M10000144A8	92	EcXA098b	RplQ; rpoA	b3294; b3295	RplQ; rpoA	AE000407	7841	8118
E1M10000101H9	93	EcXA099	RpsN; rplE	b3307; b3308	RpsN; RplE	AE000408	4403	4826
E1M10000111F9	94	EcXA100	RpmH; rnpA	b3703; b3704	RpmH; RnpA	AE000447	7555	7395
E1M10000119D02	95	EcXA100b	rpmH; rnpA	b3703; b3704	RpmH; RnpA	AE000447	7581	7395
E1M10000106F05	96	EcXA100c	rpmH; rnpA	b3703; b3704	RpmH; RnpA	AE000447	7594	7359
E1M10000152H8	97	EcXA100d	RpmH; rnpA	b3703; b3704	RpmH; RnpA	AE000447	7630	7340
E1M10000115H1	98	EcXA101	yihK	b3871	TypA	AE000462	8811	8629
E1M10000101H7	99	EcXA102	adiY	b4116	AdiY	AE000484	1980	2171
E1M10000109A02	100	EcXA103	yjhB	b4279	YjhB	AE000498	8776	8536
E1M10000113A11	101	EcXA104	hsdS	b4348	HsdS	AE000505	6319	6495
E1M10000125A2	102	EcXA104b	hsdS	b4348	HsdS	AE000505	6277	6526
E1M10000103A5	103	EcXA105	ydaU	b1359	YdaU	AE000233	4497	4306
E1M10000135B2	104	EcXA106	ybbV	b0510	YbbV	AE000157	3796	3624
E1M10000131G10	105	EcXA106	ybbV	b0510	YbbV	AE000157	3796	3624
E1M10000110A12	106	EcXA107	yegO	b2076	YegO	AE000297	14471	14330
E1M10000110E9	107	EcXA108	yigK	b3824	YigK	AE000458	3709	3964
E1M10000133A06	108	EcXA109	modC	b0765	ModC	AE000179	2414	2180
E1M10000133B08	109	EcXA110	ynaF; b1377	b1376; b1377	YnaF; OmpN	AE000234	8011	8149
E1M10000106E09	110	EcXA110b	ynaF; b1377	b1376; b1377	YnaF; OmpN	AE000234	7967	8207

Clone Name	Seq ID	Molecule No.	Gene (NCBI)	Gene (Blattner)	Gene (Rudd)	Contig	Start	Stop
E1M10000160G07	111	EcXA110c	ynaF;	b1376;	YnaF;	AE000234	7990	8114
SC13.1	112	EcXA110d	b1377 ynaF	b1377 b1376	OmpN YnaF	AE000234	8027	8243
E1M10000155B05	113	EcXA110e	ynaF;	b1376;	YnaF;	AE000234	7992	8139
			b1377	b1377	ompN			
E1M10000133D09	114	EcXA111	ppdA	b2826	PpdA	AE000366	4876	5068
E1M10000162B08	115	EcXA111b	ppdA	b2826	PpdA	AE000366	4968	5084
E1M10000133E01	116	EcXA112	yrfF	b3398	YrfF	AE000415	5835	5712
E1M10000101A7	117	EcXA113	ybbQ;	b0509;	YbbQ;	AE000157	3753	3466
			ybbV	b0510	ybbV			
E1M10000131F04	118	EcXA113b	ybbQ;	b0509;	YbbQ;	AE000157	3781	3536
			ybbV	b0510	ybbV			
E1M10000159A09	119	EcXA113c	ybbQ;	b0509;	YbbQ;	AE000157	3781	3257
			ybbV	b0510	ybbV			
E1M10000166F09	120	EcXA113d	ybbV	b0510	YbbV	AE000157	3784	3624
E1M10000121E07	121	EcXA114	b2352;	b2352;	YfdH;	AE000323	10110	9882
			b2353	b2353	yfdI			
						AE000324	357	1
E1M10000121F06	122	EcXA115	ygeF	b2850	YgeF	AE000369	570	304
E1M10000140B05	123	EcXA115b	ygeF	b2850	YgeF	AE000369	512	312
E1M10000148H09	124	EcXA115c	ygeF	b2850	YgeF	AE000369	607	361
E1M10000164A02	125	EcXA115d	ygeF	b2850	YgeF	AE000369	555	411
E1M10000121G05	126	EcXA116	insB_3	b0021		AE000135	5258	5726
E1M10000136D3	127	EcXA117	rhsA	b3593	RhsA	AE000437	4125	3529

EXAMPLE 4

Identification of Genes and their Corresponding Operons Affected by Antisense Inhibition

The sequencing of the entire *E. coli* genome is described in Blattner et al., Science 277:1453-1474(1997) and the sequence of the genome is listed in GenBank Accession No.U00096. The operons to which the proliferation-inhibiting nucleic acids correspond were identified using RegulonDB and information in the literature. The coordinates of the boundaries of these operons on the *E. coli* genome are listed in Table III. Table II lists the molecule numbers of the inserts containing the growth inhibiting nucleic acid fragments, the genes in the operons corresponding to the inserts, the SEQ ID NOs of the genes containing the inserts, the SEQ ID NOs of the proteins encoded by the genes, the start and stop points of the genes on the *E. coli* genome, the orientation of the genes on the genome, whether the operons are predicted or documented, and the predicted functions of the genes. The identified operons, their putative functions, and whether or not the genes are presently thought to be required for proliferation are discussed below.

Functions for the identified genes were determined by using either Blattner functional class designations or by comparing identified sequence with known sequences in various databases. A variety of biological functions were noted for the genes to which the clones of the present invention correspond. The functions for the genes of interest appear in Table II.

5 The proteins that are listed in Table II are involved in a wide range of biological functions.

TABLE II
All Operon Data with Whole Chromosome Coordinates

Molecule Number	Gene	Seq ID No. (gene)	Seq ID No. (protein)	Start	Stop	Operon	Blattner Functional Class	Predicted Function
EcXA056	<i>ycfS</i>	128	299	1168635	1169597	predicted operon	hypothetical, unclassified, unknown	
EcXA057	<i>arp</i>	129	300	4217880	4220066	predicted operon	Fatty acid and phospholipid metabolism	ankyrin repeat protein
EcXA058	<i>rpsQ</i>	130	301	3445951	3446205	documented	Translation, post-translational modification	
	<i>rpmC</i>	131	302	3446205	3446396		Translation, post-translational modification	
	<i>rplP</i>	132	303	3446396	3446806		Translation, post-translational modification	
	<i>rpsC</i>	133	304	3446819	3447520		Translation, post-translational modification	
	<i>rplV</i>	134	305	3447538	3447870		Translation, post-translational modification	
	<i>rpsS</i>	135	306	3447885	3448163		Translation, post-translational modification	
	<i>rplB</i>	136	307	3448180	3449001		Translation, post-translational modification	translation
	<i>rplW</i>	137	308	3449019	3449321		Translation, post-translational modification	translation
	<i>rplD</i>	138	309	3449318	3449923		Translation, post-translational modification	
	<i>rplC</i>	139	310	3449934	3450563		Translation, post-translational modification	
	<i>rpsJ</i>	140	311	3450596	3450907		Translation, post-translational modification	
EcXA059	<i>ypjA</i>	141	312	2776167	2780876	predicted operon	Translation, post-translational modification	
EcXA060	<i>rpmJ</i>	142	313	3440255	3440371	documented	Translation, post-translational modification	
	<i>prlA</i>	143	314	3440403	3441734		Putative transport proteins	
	<i>rplO</i>	144	315	3441742	3442176		Translation, post-translational modification	
	<i>rpmD</i>	145	316	3442180	3442359		Translation, post-translational modification	
	<i>rpsE</i>	146	317	3442363	3442866		Translation, post-translational modification	

Molecule Number	Gene	Seq ID No. (gene)	Seq ID No. (protein)	Start	Stop	Operon	Blattner Functional Class	Predicted Function
	<i>rplR</i>	147	318	3442881	3443234		Translation, post-translational modification	
	<i>rplF</i>	148	319	3443244	3443777		Translation, post-translational modification	translation
	<i>rpsH</i>	149	320	3443790	3444182		Translation, post-translational modification	
	<i>rpsN</i>	150	321	3444216	3444521		Translation, post-translational modification	
	<i>rplE</i>	151	322	3444536	3445075		Translation, post-translational modification	translation
	<i>rplX</i>	152	323	3445090	3445404		Translation, post-translational modification	
	<i>rplN</i>	153	324	3445415	3445786		Translation, post-translational modification	
EcXA061	malE	154	325	4242808	4243998	documented	Transport and binding proteins	
	malF	155	326	4241110	4242654		Transport and binding proteins	
	malG	156	327	4240205	4241095		Transport and binding proteins	
EcXA062	rcp	157	328	3958292	3960313	predicted operon	DNA replication, recombination, modification and repair	
EcXA063	b2269	158	329	2380733	2381944	predicted operon	Putative enzymes	putative phosphatase/sul fatase
EcXA064	cyoE	159	330	446039	446929	documented	Energy metabolism	
	cyoA	160	331	449887	450834		Energy metabolism	
	cyoB	161	332	447874	449865		Energy metabolism	
	cyoC	162	333	447270	447884		Energy metabolism	
	cyoD	163	334	446941	447270		Energy metabolism	
EcXA065	dgoA	164	335	3869477	3871240	predicted	Carbon compound catabolism	2-Oxo-3-deoxygalactonate 6-phosphate aldolase
	dgoK	165	336	3871224	3872401		Carbon compound catabolism	
	yidW	166	337	3872401	3872787		Hypothetical, unclassified, unknown	
	b3694	167	338	3872099	3872395		Putative regulatory protein	
EcXA066	<i>rplT</i>	168	339	1797417	1797773	documented	Translation, post-translational modification	
	<i>rplM</i>	169	340	1797826	1798023		Translation, post-translational modification	
	<i>infC</i>	170	341	1798120	1798662		Translation, post-translational modification	translation
	<i>thrS</i>	171	342	1798666	1800594		Translation, post-translational modification	
EcXA067	xylF	172	343	3728760	3729752		Transport and binding proteins	
EcXA068	yhfL	173	344	3497085	3497252	predicted operon	Hypothetical, unclassified, unknown	

Molecule Number	Gene	Seq ID No. (gene)	Seq ID No. (protein)	Start	Stop	Operon	Blattner Functional Class	Predicted Function
	yhfM	174	345	3497496	3498884	predicted operon	Putative Transport	
	yhfN	175	346	3498884	3499927		Putative Transport	
	yhfO	176	347	3499890	3500339		Hypothetical, unclassified, unknown	
EcXA069		x	x			same operon as EcXA058		
EcXA070	ybcQ	177	348	573179	573562	predicted operon	Hypothetical, unclassified, unknown	
EcXA071	ffh	178	349	2744454	2745815	predicted operon	Transport and binding proteins	
EcXA072	recJ	179	350	3034393	3036126	predicted operon	Transcription, RNA processing and degradation	
	dsbC	180	351	3036132	3036842		Cell structure	
	xerD	181	352	3036867	3037763		DNA replication, recombination, modification and repair	
EcXA073	ecpD	182	353	155461	156201	documented	Cell structure	
	htrE	183	354	152829	155426		Cell structure	
EcXA074	yciR	184	355	1342781	1344766	predicted operon	Hypothetical, unclassified, unknown	
EcXA075	sfmC	185	356	558197	558889	predicted operon	Putative chaperonin	
	sfmD	186	357	558920	561523		Cell structure	
	sfmH	187	358	561565	562542		Cell processes (incl. adaptation, protection)	
	sfmF	188	359	562553	563068		Cell processes (incl. adaptation, protection)	
EcXA076	rimJ	189	360	1124785	1125369	predicted operon	Translation, post-translational modification	
	yccH	190	361	1125380	1126027		Hypothetical, unclassified, unknown	
	mviM	191	362	1126029	1126952		Cell processes (incl. adaptation, protection)	
EcXA077	sanA	192	363	2230898	2231617	predicted		
	b2145	193	364	2231620	2231859		Hypothetical, unclassified, unknown	
EcXA078	ycgB	194	365	1234932	1236464	predicted operon	Hypothetical, unclassified, unknown	
EcXA079	yedV	195	366	2034816	2036174	predicted	Hypothetical, unclassified, unknown	
	yedW	196	367	2036174	2036893		Hypothetical, unclassified, unknown	
EcXA080		x	x			same operon as EcXA058		
EcXA081	b2107	197	368	2184800	2185318	predicted	Hypothetical, unclassified, unknown	
	b2106	198	369	2183937	2184761		Hypothetical, unclassified, unknown	
EcXA082	hybG	199	370	3137731	3137979	documented	Energy metabolism	
	hybF	200	371	3137992	3138333		Energy metabolism	
	hybE	201	372	3138326	3138814		Energy metabolism	

Molecule Number	Gene	Seq ID No. (gene)	Seq ID No. (protein)	Start	Stop	Operon	Blattner Functional Class	Predicted Function
EcXA083	hybD	202	373	3138807	3139301		Energy metabolism	
	hybC	203	374	3139301	3141004		Energy metabolism	
	hybB	204	375	3141001	3142179		Energy metabolism	
	hybA	205	376	3142169	3143155		Energy metabolism	
	hrpB	206	377	162060	164534		Transcription, RNA processing and degradation	
EcXA084	b1399	207	378	1461563	1462513		Hypothetical, unclassified, unknown	
	b1400	208	379	1462495	1463085		Hypothetical, unclassified, unknown	
EcXA085	agaZ	209	380	3276555	3277835	predicted	Carbon compound catabolism	putative tagatose 6-phosphate kinase 2
	agaV	210	381	3277822	3278331		Central intermediary metabolism	PTS system, (EIIB-AGA)
	agaW	211	382	3278342	3278743		Central intermediary metabolism	PTS system (EIIC)
	agaA	212	383	3278763	3279266		Central intermediary metabolism	putative N-NAG-6-phosphatideacetylase
	agaS	213	384	3279617	3280771		Central intermediary metabolism	putative tagatose-6-phosphate aldose/ketose isomerase
	agaY	214	385	3280784	3281644		Central intermediary metabolism	tagatose-bisphosphate aldolase 2
EcXA086	rpsM	215	386	3439752	3440108	documented	Translation, post-translational modification	
	rpsK	216	387	3439346	3439735		Translation, post-translational modification	
	rpsD	217	388	3438692	3439312		Translation, post-translational modification	
	rpoA	218	389	3437677	3438666		Translation, post-translational modification	
	rplQ	219	390	3437253	3437636		Translation, post-translational modification	
EcXA087	yehW	220	391	2213765	2214496	predicted	Hypothetical, unclassified, unknown	
	yehX	221	392	2214501	2215427		Hypothetical, unclassified, unknown	
	yehY	222	393	2215420	2216577		Hypothetical, unclassified, unknown	
	yehZ	223	394	2216584	2217501		Hypothetical, unclassified, unknown	
EcXA088	x	x	x			same as EcXAO60		
EcXA089	yadS	224	395	177662	178462	predicted operon	Hypothetical, unclassified, unknown	
	yadT	225	396	177662	178462		Hypothetical, unclassified, unknown	
	pfs	226	397	178455	179153			

Molecule Number	Gene	Seq ID No. (gene)	Seq ID No. (protein)	Start	Stop	Operon	Blattner Functional Class	Predicted Function
EcXA090	lpxA	227	398	202560	203348	predicted operon		
	lpxB	228	399	203348	204496			
	mhB	229	400	204493	205089			RnaaseH 2
	dnaE	230	401	205126	208608			DNA pol III subunit
EcXA091	ykgE	231	402	320832	321551	predicted	Hypothetical, unclassified, unknown	
	ykgF	232	403	321562	322989		Hypothetical, unclassified, unknown	
	ykgG	233	404	322829	323677		Hypothetical, unclassified, unknown	
EcXA092	b1497	234	405	1577657	1578829	predicted	Hypothetical, unclassified, unknown	
	b1498	235	406	1578866	1580581		Hypothetical, unclassified, unknown	
EcXA093	yohM	236	407	2183937	2184761	predicted	Hypothetical, unclassified, unknown	
	b2107	237	408	2184800	2185318		Hypothetical, unclassified, unknown	
EcXA094	yfjW	238	409	2771339	2773042	predicted	Hypothetical, unclassified, unknown	
EcXA095	b2758	239	410	2879074	2880165	predicted	Hypothetical, unclassified, unknown	
EcXA096	ygcM	240	411	2890237	2890602	predicted	Hypothetical, unclassified, unknown	
	ygcN	241	412	2890650	2891951		Hypothetical, unclassified, unknown	
	b2767	242	413	2891906	2892202		Hypothetical, unclassified, unknown	
	b2768	243	414	2892219	2892794		Hypothetical, unclassified, unknown	
							Hypothetical, unclassified, unknown	
EcXA097	yhcB	244	415	3377820	3378224	predicted operon	Hypothetical, unclassified, unknown	
	hhoA (degQ)	245	416	3378378	3379745	predicted operon	Translation, post-translational modification	
	hhoB	246	417	3379835	3380902		Translation, post-translational modification	
EcXA098	rpsM	247	418	3439752	3440108	documented	Translation, post-translational modification	
	rpsK	248	419	3439346	3439735		Translation, post-translational modification	
	rpsD	249	420	3438692	3439312		Translation, post-translational modification	
	rpoA	250	421	3437677	3438666		Translation, post-translational modification	
	rplQ	251	422	3437253	3437636		Translation, post-translational modification	
EcXA099		x	x			same as EcXA060		
EcXA100	rpmH	252	423	3881965	3882105	documented	Translation, post-translational modification	
	mpA	253	424	3882122	3882481		DNA replication, recombination, modification and repair	

Molecule Number	Gene	Seq ID No. (gene)	Seq ID No. (protein)	Start	Stop	Operon	Blattner Functional Class	Predicted Function
EcXA101	yihK	254	425	4055987	4057762	predicted operon	Hypothetical, unclassified, unknown	
EcXA102	adi	255	426	4335832	4338102	documented	Putative regulatory proteins	biodegradative acid-induced arginine decarboxylase
	adiY	256	427	4334746	4335507		Amino acid biosynthesis and metabolism	
EcXA103	yjhB	257	428	4501566	4502843	predicted operon	Hypothetical, unclassified, unknown	
	yjhC	258	429	4502840	4503973		Hypothetical, unclassified, unknown	
EcXA104	hsdS	259	430	4577638	4579032	documented	DNA replication, recombination, modification and repair	host specificity
	hsdM	260	431	4579029	4580618		DNA replication, recombination, modification and repair	
EcXA105	b1357	261	432	1418389	1418685	predicted	Hypothetical, unclassified, unknown	
	b1358	262	433	1418708	1419130		Hypothetical, unclassified, unknown	
	ydaU	263	434	1419143	1420000		Hypothetical, unclassified, unknown	
	b1360	264	435	1420007	1420753		Hypothetical, unclassified, unknown	
	b1361	265	436	1420725	1421336		Hypothetical, unclassified, unknown	
	b1362	266	437	1421363	1421668		Hypothetical, unclassified, unknown	
EcXA106	ybbQ	267	438	535810	536688	predicted	Hypothetical, unclassified, unknown	
	ybbV	268	439	536720	536998		Hypothetical, unclassified, unknown	
	b0511	269	440	536998	538311		Hypothetical, unclassified, unknown	
EcXA107	yegM	270	441	2151891	2153285	predicted	Hypothetical, unclassified, unknown	
	yegN	271	442	2153285	2156407		Hypothetical, unclassified, unknown	
	yegO	272	443	2156408	2159485		Hypothetical, unclassified, unknown	
	yegB	273	444	2159486	2160901		Hypothetical, unclassified, unknown	
EcXA108	yigK	274	445	4006046	4006462		Hypothetical, unclassified, unknown	
EcXA109	modA	275	446	794312	795085	documented	Transport and binding proteins	molybdate uptake
	modB	276	447	795085	795774		Transport and binding proteins	
	modC	277	448	795777	796835		Transport and binding proteins	
EcXA110	ynaF	278	449	1433209	1433715	predicted	Hypothetical, unclassified, unknown	
	b1377	279	450	1433784	1434917	predicted	Hypothetical, unclassified, unknown	
EcXA111	recC	280	451	2957082	2960450	predicted	Transcription, RNA processing and	

Molecule Number	Gene	Seq ID No. (gene)	Seq ID No. (protein)	Start	Stop	Operon	Blattner Functional Class	Predicted Function
							degradation	
	ppdC	281	452	2960463	2960786		Other known genes	prepilin peptidase dependent protein C
	ygdB	282	453	2960771	2961136		Hypothetical, unclassified, unknown	
	ppdB	283	454	2961175	2961738		Other known genes	prepilin peptidase dependent protein B
	ppdA	284	455	2961729	2962199		Other known genes	prepilin peptidase dependent protein A
EcXA112	yrfI	285	456	3524107	3526242	predicted	Hypothetical, unclassified, unknown	
	yrfG	286	457	3526262	3526975		Hypothetical, unclassified, unknown	
	yrfH	287	458	3526986	3527387		Hypothetical, unclassified, unknown	
	yrfI	288	459	3527406	3528290		Hypothetical, unclassified, unknown	
EcXA113	x	x				same as EcXA106		
EcXA114	b2350	289	460	2465875	2466237	predicted	Hypothetical, unclassified, unknown	
	b2351	290	461	2466234	2467154		Hypothetical, unclassified, unknown	
	b2352	291	462	2467151	2468482		Hypothetical, unclassified, unknown	
	b2353	292	463	2468781	2469125	predicted	Hypothetical, unclassified, unknown	
EcXA115	ygeF	293	464	2988576	2989022	predicted	Hypothetical, unclassified, unknown	
EcXA116	insB_3	294	465	289873	290376	predicted	phage, transposon, or plasmid	
	insA_3	295	466	290295	290570		phage, transposon, or plasmid	
EcXA117	rhsA	296	467	3759810	3763943	predicted	Hypothetical, unclassified, unknown	
	yibA	297	468	3763964	3763806		Hypothetical, unclassified, unknown	
	yibJ	298	469	3764848	3765549		Hypothetical, unclassified, unknown	

Functions for the identified genes were determined by using either Blattner functional class designations or by comparing identified sequence with known sequences in various databases. A variety of biological functions were noted for the genes to which the clones of the present invention correspond. Biological functions for genes that lie on the same operon as an identified gene have also been made. The functions for the genes of interest appear in Table II.

The genes of interest have a variety of biological functions. For example, genes that are thought to function as transport or binding proteins, that participate in translation or post-translational modification, that are involved in carbon compound catabolism, that are thought to be enzymes,

participate in cell processes, energy metabolism and biosynthetic functions appear in Table II. Genes that are involved in cell structure, transcription, RNA processing and degradation also appear in Table II.

Several of the expression vectors contain fragments that correspond to genes of unknown function or if the function is known, it is not known whether the gene is essential. For example, EcXA056, 057, 059, 063, 064, 065, 067, 068, 070, 073, 074, 075, 076, 077, 078, 079, 081, 084, 085, 087, 089, 091, 092, 093, 094, 095, 096, 097, 101, 102, 103, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115 and 117 are all exogenous nucleic acid sequences that correspond to *E. coli* proteins that have no known function or where the function has not been shown to be essential or nonessential.

The present invention reports a number of novel *E. coli* genes and operons that are required for proliferation. From the list of clone sequences identified here, each was identified to be a portion of a gene in an operon required for the proliferation of *E. coli*. Cloned sequences corresponding to genes already known to be required for proliferation in *E. coli* include EcXA058, 060, 066, 069, 071, 080, 086, 088, 090, 098, 099 and 100 are exogenous nucleic acid sequences that correspond to *E. coli* genes that are known to be required for cellular proliferation. The remaining identified sequences correspond to *E. coli* genes previously undesigned as required for proliferation in the art.

An interesting observation of the present invention is that there are also several sequence fragments that correspond to *E. coli* genes that are not thought to be required for *E. coli* proliferation. Nevertheless, under the conditions described above, the antisense expression of these gene fragments causes a reduction in cell growth. This result implies that the genes corresponding to the identified sequences are actually required for proliferation or are in operons required for proliferation. Molecule Nos. corresponding to these genes are EcXA061, 062, 072, 082, 083, 104 and 116.

Following identification of the sequences of interest, these sequences were localized into operons. Since bacterial genes are expressed in a polycistronic manner, the antisense inhibition of a single gene in an operon might effect the expression of all the other genes on the operon or the genes down stream from the single gene identified. In order to determine which of the gene products in an operon are required for proliferation, each of the genes contained within an operon may be analyzed for their effect on viability as described below.

TABLE III
Operon Boundaries

Molecule Number	Start	Stop
EcXA056	1168635	1169597
EcXA057	4217880	4220066
EcXA059	2776167	2780876
EcXA061	4240205	4243998
EcXA062	3958292	3960313
EcXA063	2380733	2381944
EcXA064	446039	450834
EcXA065	3869477	3872395
EcXA067	3728760	3729752
EcXA068	3497085	3500339
EcXA070	573179	573562
EcXA071	2744454	2745815
EcXA072	3034393	3037763
EcXA073	152829	156201
EcXA074	1342781	1344766
EcXA075	558197	563068
EcXA076	1124785	1126952
EcXA077	2230898	2231859
EcXA078	1234932	1236464
EcXA079	2034816	2036893
EcXA081	2183937	2185318
EcXA082	3137731	3143155
EcXA083	162060	164534
EcXA084	1461563	1463085
EcXA085	3276555	3280771
EcXA086	3437253	3440108
EcXA087	2213765	2217501
EcXA089	177662	179153
EcXA090	202560	208608
EcXA091	320832	323677
EcXA092	1577657	1580581
EcXA093	2183937	2185318
EcXA094	2771339	2773042
EcXA095	2879074	2880165
EcXA096	2890237	2892794

Molecule Number	Start	Stop
EcXA097	3377820	3380902
EcXA098	3437253	3438666
EcXA100	3881965	3882481
EcXA101	4055987	4057762
EcXA102	4334746	4338102
EcXA103	4501566	4503973
EcXA104	4577638	4580618
EcXA105	1418389	1421668
EcXA106	535810	538311
EcXA107	2151891	2160901
EcXA108	4006046	4006462
EcXA109	794312	796835
EcXA110	1433209	1434917
EcXA111	2957082	2962199
EcXA112	3524107	3528290
EcXA114	2465875	2469125
EcXA115	2988576	2989022
EcXA116	289873	290570
EcXA117	3759810	3765549

EXAMPLE 5

Identification of Individual Genes within an Operon Required for Proliferation

5 The following example illustrates a method for determining which gene in an operon is required for proliferation. The clone insert corresponding to Molecule No. EcXA066 possesses nucleic acid sequence homology to the *E. coli* genes *rplT* and *rpml*. These genes are located in an operon containing two additional genes, *infC* and *thrS*. To determine which gene or genes in this operon are required for proliferation, each gene is selectively inactivated using homologous recombination. Gene *rplT* is the first gene to be inactivated.

10 Deletion inactivation of a chromosomal copy of a gene in *E. coli* can be accomplished by integrative gene replacement. The principle of this method (Hamilton, C. M., et al 1989. *J. Bacteriol.* 171: 4617-4622) is to construct a mutant allele of the targeted gene, introduce that allele into the chromosome using a conditional suicide vector, and then force the removal of the native wild type allele and vector sequences. This will replace the native gene with a desired mutation(s) but leave promoters, operators, etc. intact. Essentiality of a gene is determined either by deduction from genetic analysis or by conditional expression of a wild type copy of the targeted gene (trans complementation).

The first step is to generate a mutant *rplT* allele using PCR amplification. Two sets of PCR primers are chosen to produce a copy of *rplT* with a large central deletion to inactivate the gene. In order to eliminate polar effects, it is desirable to construct a mutant allele comprising an in-frame deletion of most or all of the coding region of the *rplT* gene. Each set of PCR primers is chosen such that a region flanking the gene to be amplified is sufficiently long to allow recombination (typically at least 500 nucleotides on each side of the deletion). The targeted deletion or mutation will be contained within this fragment. To facilitate cloning of the PCR product, the PCR primers may also contain restriction endonuclease sites found in the cloning region of a conditional knockout vector such as pKO3 (Link, et al 1997 *J. Bacteriol.* 179 (20): 6228-6237). Suitable sites include NotI, SalI, BamHI and SmaI. The *rplT* gene fragments are produced using standard PCR conditions including, but not limited to, those outlined in the manufacturers directions for the Hot Start Taq PCR kit (Qiagen, Inc., Valencia, CA). The PCR reactions will produce two fragments that can be fused together. Alternatively, crossover PCR can be used to generate a desired deletion in one step (Ho, S. N., et al 1989. *Gene* 77: 51-59, Horton, R. M., et al 1989. *Gene* 77: 61-68). The mutant allele thus produced is called a "null" allele because it cannot produce a functional gene product.

The mutant allele obtained from PCR amplification is cloned into the multiple cloning site of pKO3. Directional cloning of the *rplT* null allele is not necessary. The pKO3 vector has a temperature-sensitive origin of replication derived from pSC101. Therefore, clones are propagated at the permissive temperature of 30°C. The vector also contains two selectable marker genes: one that confers resistance to chloramphenicol and another, the *Bacillus subtilis sacB* gene, that allows for counter-selection on sucrose containing growth medium. Clones that contain vector DNA with the null allele inserted are confirmed by restriction endonuclease analysis and DNA sequence analysis of isolated plasmid DNA. The plasmid containing the *rplT* null allele insert is known as a knockout plasmid.

Once the knockout plasmid has been constructed and its sequence verified, it is transformed into a Rec⁺ *E. coli* host cell. Transformation can be by any standard method such as electroporation. In some fraction of the transformed cells, plasmids will integrate into the *E. coli* chromosome by homologous recombination between the *rplT* null allele in the plasmid and the *rplT* gene in the chromosome. Transformant colonies in which such an event has occurred are readily selected by growth at the non-permissive temperature of 43°C and in the presence of chloramphenicol. At this temperature, the plasmid will not replicate as an episome and will be lost from cells as they grow and divide. These cells are no longer resistant to chloramphenicol and will not grow when it is present. However, cells in which the knockout plasmid has integrated into the *E. coli* chromosome remain resistant to chloramphenicol and propagate.

Cells containing integrated knock-out plasmids are usually the result of a single crossover event that creates a tandem repeat of the mutant and native wild type alleles of *rplT* separated by the

vector sequences. A consequence of this is that *rplT* will still be expressed in these cells. In order to determine if the gene is essential for growth, the wild type copy must be removed. This is accomplished by selecting for plasmid excision, a process in which homologous recombination between the two alleles results in looping out of the plasmid sequences. Cells that have undergone
5 such an excision event and have lost plasmid sequences including *sacB* gene are selected for by addition of sucrose to the medium. The *sacB* gene product converts sucrose to a toxic molecule. Thus counter selection with sucrose ensures that plasmid sequences are no longer present in the cell. Loss of plasmid sequences is further confirmed by testing for sensitivity to chloramphenicol (loss of the chloramphenicol resistance gene). The latter test is important because occasionally a
10 mutation in the *sacB* gene can occur resulting in a loss of *sacB* function with no effect on plasmid replication (Link, et. al., 1997 *J. Bacteriol.* 179 (20): 6228-6237). These artifact clones retain plasmid sequences and are therefore still resistant to chloramphenicol.

In the process of plasmid excision, one of the two *rplT* alleles is lost from the chromosome along with the plasmid DNA. In general, it is equally likely that the null allele or the wild type
15 allele will be lost. Therefore, if the *rplT* gene is not essential, half of the clones obtained in this experiment will have the wild type allele on the chromosome and half will have the null allele. However, if the *rplT* gene is essential, cells containing the null allele will not be obtained as a single copy of the null allele would be lethal.

To determine the essentiality of *rplT*, a statistically significant number of the resulting
20 clones, at least 20, are analyzed by PCR amplification of the *rplT* gene. Since the null allele is missing a significant portion of the *rplT* gene, its PCR product is significantly shorter than that of the wild type gene and the two are readily distinguished by gel electrophoretic analysis. The PCR products may also be subjected to sequence determination for further confirmation by methods well known to those in the art.

The above experiment is generally adequate for determining the essentiality of a gene such as *rplT*. However, it may be necessary or desirable to more directly confirm the essentiality of the gene. There are several methods by which this can be accomplished. In general, these involve three steps: 1) construction of an episome containing a wild type allele, 2) isolation of clones containing a single chromosomal copy of the mutant null allele as described above but in the
25 presence of the episomal wild type allele, and then 3) determining if the cells survive when the expression of the episomal allele is shut off. In this case, the trans copy of wild type *rplT* is made by PCR cloning of the entire coding region of *rplT* and inserting it in the sense orientation downstream of an inducible promoter such as the *E. coli lac* promoter. Transcription of this allele of *rplT* will be induced in the presence of IPTG which inactivates the *lac* repressor. Under IPTG
30 induction *rplT* protein will be expressed as long as the recombinant gene also possesses a ribosomal binding site, also known as a "Shine-Dalgarno Sequence". The trans copy of *rplT* is cloned on a plasmid that is compatible with pSC101. Compatible vectors include p15A, pBR322, and the pUC

plasmids, among others. Replication of the compatible plasmid will not be temperature-sensitive. The entire process of integrating the null allele of *rplT* and subsequent plasmid excision is carried out in the presence of IPTG to ensure the expression of functional *rplT* protein is maintained throughout. After the null *rplT* allele is confirmed as integrated on the chromosome in place of the wild type *rplT* allele, then IPTG is withdrawn and expression of functional *rplT* protein shut off. If the *rplT* gene is essential, cells will cease to proliferate under these conditions. However, if the *rplT* gene is not essential, cells will continue to proliferate under these conditions. In this experiment, essentiality is determined by conditional expression of a wild type copy of the gene rather than inability to obtain the intended chromosomal disruption.

An advantage of this method over some other gene disruption techniques is that the targeted gene can be deleted or mutated without the introduction of large segments of foreign DNA. Therefore, polar effects on downstream genes are eliminated or minimized. There are methods described to introduce inducible promoters upstream of potential essential bacterial genes. However in such cases, polarity from multiple transcription start points can be a problem. One way of preventing this is to insert a gene disruption cassette that contains strong transcriptional terminators upstream of the integrated inducible promoter (Zhang, Y, and Cronan, J. E. 1996 *J. Bacteriol.* 178 (12): 3614-3620). The described techniques will all be familiar to one of ordinary skill in the art.

Following the analysis of the *rplT* gene, the other genes of the operon are investigated to determine if they are required for proliferation.

EXAMPLE 6

Expression of the Proteins Encoded by Genes Identified as Required for *E. coli* Proliferation

The following is provided as one exemplary method to express the proliferation-required proteins encoded by the identified sequences described above. First, the initiation and termination codons for the gene are identified. If desired, methods for improving translation or expression of the protein are well known in the art. For example, if the nucleic acid encoding the polypeptide to be expressed lacks a methionine codon to serve as the initiation site, a strong Shine-Delgarno sequence, or a stop codon, these sequences can be added. Similarly, if the identified nucleic acid sequence lacks a transcription termination signal, this sequence can be added to the construct by, for example, splicing out such a sequence from an appropriate donor sequence. In addition, the coding sequence may be operably linked to a strong promoter or an inducible promoter if desired. The identified nucleic acid sequence or portion thereof encoding the polypeptide to be expressed is obtained by PCR from the bacterial expression vector or genome using oligonucleotide primers complementary to the identified nucleic acid sequence or portion thereof and containing restriction endonuclease sequences for *NcoI* incorporated into the 5' primer and *BglII* at the 5' end of the corresponding 3'-primer, taking care to ensure that the identified nucleic acid sequence is positioned in frame with the termination signal. The

purified fragment obtained from the resulting PCR reaction is digested with *NcoI* and *BglII*, purified and ligated to an expression vector.

The ligated product is transformed into DH5 α or some other *E. coli* strain suitable for the over expression of potential proteins. Transformation protocols are well known in the art. For example, transformation protocols are described in: **Current Protocols in Molecular Biology**, Vol. 1, Unit 1.8, (Ausubel, et al., Eds.) John Wiley & Sons, Inc. (1997). Positive transformants are selected after growing the transformed cells on plates containing 50-100 μ g/ml Ampicillin (Sigma, St. Louis, Missouri). In one embodiment, the expressed protein is held in the cytoplasm of the host organism. In an alternate embodiment, the expressed protein is released into the culture medium. In still another alternative, the expressed protein can be sequestered in the periplasmic space and liberated therefrom using any one of a number of cell lysis techniques known in the art. For example, the osmotic shock cell lysis method described in Chapter 16 of **Current Protocols in Molecular Biology**, Vol. 2, (Ausubel, et al., Eds.) John Wiley & Sons, Inc. (1997). Each of these procedures can be used to express a proliferation-required protein.

Expressed proteins, whether in the culture medium or liberated from the periplasmic space or the cytoplasm, are then purified or enriched from the supernatant using conventional techniques such as ammonium sulfate precipitation, standard chromatography, immunoprecipitation, immunochromatography, size exclusion chromatography, ion exchange chromatography, and HPLC. Alternatively, the secreted protein can be in a sufficiently enriched or pure state in the supernatant or growth media of the host to permit it to be used for its intended purpose without further enrichment. The purity of the protein product obtained can be assessed using techniques such as Coomassie or silver staining or using antibodies against the control protein. Coomassie and silver staining techniques are familiar to those skilled in the art.

Antibodies capable of specifically recognizing the protein of interest can be generated using synthetic peptides using methods well known in the art. See, **Antibodies: A Laboratory Manual**, (Harlow and Lane, Eds.) Cold Spring Harbor Laboratory (1988). For example, 15-mer peptides having a sequence encoded by the appropriate identified gene sequence of interest or portion thereof can be chemically synthesized. The synthetic peptides are injected into mice to generate antibodies to the polypeptide encoded by the identified nucleic acid sequence of interest or portion thereof. Alternatively, samples of the protein expressed from the expression vectors discussed above can be purified and subjected to amino acid sequencing analysis to confirm the identity of the recombinantly expressed protein and subsequently used to raise antibodies. An Example describing in detail the generation of monoclonal and polyclonal antibodies appears in Example 7.

The protein encoded by the identified nucleic acid sequence of interest or portion thereof can be purified using standard immunochromatography techniques. In such procedures, a solution containing the secreted protein, such as the culture medium or a cell extract, is applied to a column having antibodies against the secreted protein attached to the chromatography matrix. The secreted

protein is allowed to bind the immunochromatography column. Thereafter, the column is washed to remove non-specifically bound proteins. The specifically bound secreted protein is then released from the column and recovered using standard techniques. These procedures are well known in the art.

5 In an alternative protein purification scheme, the identified nucleic acid sequence of interest or portion thereof can be incorporated into expression vectors designed for use in purification schemes employing chimeric polypeptides. In such strategies the coding sequence of the identified nucleic acid sequence of interest or portion thereof is inserted in-frame with the gene encoding the other half of the chimera. The other half of the chimera can be maltose binding protein (MBP) or a nickel binding polypeptide encoding sequence. A chromatography matrix having antibody to MBP or nickel attached
10 thereto is then used to purify the chimeric protein. Protease cleavage sites can be engineered between the MBP gene or the nickel binding polypeptide and the identified expected gene of interest, or portion thereof. Thus, the two polypeptides of the chimera can be separated from one another by protease digestion.

One useful expression vector for generating maltose binding protein fusion proteins is pMAL
15 (New England Biolabs), which encodes the *malE* gene. In the pMal protein fusion system, the cloned gene is inserted into a pMal vector downstream from the *malE* gene. This results in the expression of an MBP-fusion protein. The fusion protein is purified by affinity chromatography. These techniques as described are well known to those skilled in the art of molecular biology.

EXAMPLE 7

20 Production of an Antibody to an isolated *E. coli* Protein

Substantially pure protein or polypeptide is isolated from the transformed cells as described in Example 6. The concentration of protein in the final preparation is adjusted, for example, by concentration on a 10,000 molecular weight cut off AMICON filter device (Millipore, Bedford, MA), to the level of a few micrograms/ml. Monoclonal or polyclonal antibody to the protein can then be
25 prepared as follows:

Monoclonal Antibody Production by Hybridoma Fusion

Monoclonal antibody to epitopes of any of the peptides identified and isolated as described can be prepared from murine hybridomas according to the classical method of Kohler, G. and Milstein, C., *Nature* 256:495 (1975) or any of the well-known derivative methods thereof. Briefly, a mouse is
30 repetitively inoculated with a few micrograms of the selected protein or peptides derived therefrom over a period of a few weeks. The mouse is then sacrificed, and the antibody producing cells of the spleen isolated. The spleen cells are fused by means of polyethylene glycol with mouse myeloma cells, and the excess unfused cells destroyed by growth of the system on selective media comprising aminopterin (HAT media). The successfully fused cells are diluted and aliquots of the dilution placed
35 in wells of a microtiter plate where growth of the culture is continued. Antibody-producing clones are identified by detection of antibody in the supernatant fluid of the wells by immunoassay procedures, such as ELISA, as described by Engvall, E., "Enzyme immunoassay ELISA and EMIT," *Meth.*

Enzymol. 70:419 (1980), and derivative methods thereof. Selected positive clones can be expanded and their monoclonal antibody product harvested for use. Detailed procedures for monoclonal antibody production are described in Davis, L. et al. **Basic Methods in Molecular Biology** Elsevier, New York. Section 21-2.

5 **Polyclonal Antibody Production by Immunization**

Polyclonal antiserum containing antibodies to heterogeneous epitopes of a single protein or a peptide can be prepared by immunizing suitable animals with the expressed protein or peptides derived therefrom described above, which can be unmodified or modified to enhance immunogenicity. Effective polyclonal antibody production is affected by many factors related both to the antigen and the
10 host species. For example, small molecules tend to be less immunogenic than larger molecules and can require the use of carriers and adjuvant. Also, host animals vary in response to site of inoculations and dose, with both inadequate or excessive doses of antigen resulting in low titer antisera. Small doses (ng level) of antigen administered at multiple intradermal sites appears to be most reliable. An effective immunization protocol for rabbits can be found in Vaitukaitis, J. et al. **J. Clin. Endocrinol. Metab.**
15 **33:988-991** (1971).

Booster injections can be given at regular intervals, and antiserum harvested when antibody titer thereof, as determined semi-quantitatively, for example, by double immunodiffusion in agar against known concentrations of the antigen, begins to fall. See, for example, Ouchterlony, O. et al., Chap. 19 in: **Handbook of Experimental Immunology** D. Wier (ed) Blackwell (1973). Plateau
20 concentration of antibody is usually in the range of 0.1 to 0.2 mg/ml of serum (about 12 μ M). Affinity of the antisera for the antigen is determined by preparing competitive binding curves, as described, for example, by Fisher, D., Chap. 42 in: **Manual of Clinical Immunology**, 2d Ed. (Rose and Friedman, Eds.) Amer. Soc. For Microbiol., Washington, D.C. (1980).

Antibody preparations prepared according to either protocol are useful in quantitative
25 immunoassays which determine concentrations of antigen-bearing substances in biological samples; they are also used semi-quantitatively or qualitatively to identify the presence of antigen in a biological sample. The antibodies can also be used in therapeutic compositions for killing bacterial cells expressing the protein.

EXAMPLE 8

30 **Screening Chemical Libraries**

A. Protein-Based Assays

Having isolated and expressed bacterial proteins shown to be required for bacterial proliferation, the present invention further contemplates the use of these expressed proteins in assays to screen libraries of compounds for potential drug candidates. The generation of chemical libraries is
35 well known in the art. For example combinatorial chemistry can be used to generate a library of compounds to be screened in the assays described herein. A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological

synthesis by combining a number of chemical "building blocks" reagents. For example, a linear combinatorial chemical library such as a polypeptide library is formed by combining amino acids in every possible combination to yield peptides of a given length. Millions of chemical compounds theoretically can be synthesized through such combinatorial mixings of chemical building blocks. For example, one commentator observed that the systematic, combinatorial mixing of 100 interchangeable chemical building blocks results in the theoretical synthesis of 100 million tetrameric compounds or 10 billion pentameric compounds. (Gallop et al., "Applications of Combinatorial Technologies to Drug Discovery, Background and Peptide Combinatorial Libraries," *Journal of Medicinal Chemistry*, Vol. 37, No. 9, 1233-1250 (1994). Other chemical libraries known to those in the art may also be used, including natural product libraries.

Once generated, combinatorial libraries can be screened for compounds that possess desirable biological properties. For example, compounds which may be useful as drugs or to develop drugs would likely have the ability to bind to the target protein identified, expressed and purified as discussed above. Further, if the identified target protein is an enzyme, candidate compounds would likely interfere with the enzymatic properties of the target protein. Any enzyme can be a target protein. For example, the enzymatic function of a target protein can be to serve as a protease, nuclease, phosphatase, dehydrogenase, transporter protein, transcriptional enzyme, and any other type of enzyme known or unknown. Thus, the present invention contemplates using the protein products described above to screen combinatorial and other chemical libraries.

Those in the art will appreciate that a number of techniques exist for characterizing target proteins in order to identify molecules useful for the discovery and development of therapeutics. For example, some techniques involve the generation and use of small peptides to probe and analyze target proteins both biochemically and genetically in order to identify and develop drug leads. Such techniques include the methods described in PCT publications No. WO9935494, WO9819162, WO9954728.

In another example, the target protein is a serine protease and the substrate of the enzyme is known. The present example is directed towards the analysis of libraries of compounds to identify compounds that function as inhibitors of the target enzyme. First, a library of small molecules is generated using methods of combinatorial library formation well known in the art. U.S. Patent NOs. 5,463,564 and 5,574, 656, to Agraftotis, et al., entitled "System and Method of Automatically Generating Chemical Compound with Desired Properties," are two such teachings. Then the library compounds are screened to identify library compounds that possess desired structural and functional properties. U.S. Patent No. 5,684,711 also discusses a method for screening libraries.

To illustrate the screening process, the combined target and chemical compounds of the library are exposed to and permitted to interact with the purified enzyme. A labeled substrate is added to the incubation. The label on the substrate is such that a detectable signal is emitted from metabolized substrate molecules. The emission of this signal permits one to measure the effect of the combinatorial

library compounds on the enzymatic activity of target enzymes. The characteristics of each library compound is encoded so that compounds demonstrating activity against the enzyme can be analyzed and features common to the various compounds identified can be isolated and combined into future iterations of libraries.

- 5 Once a library of compounds is screened, subsequent libraries are generated using those chemical building blocks that possess the features shown in the first round of screen to have activity against the target enzyme. Using this method, subsequent iterations of candidate compounds will possess more and more of those structural and functional features required to inhibit the function of the target enzyme, until a group of enzyme inhibitors with high specificity for the enzyme can be found.
- 10 These compounds can then be further tested for their safety and efficacy as antibiotics for use in mammals.

 It will be readily appreciated that this particular screening methodology is exemplary only. Other methods are well known to those skilled in the art. For example, a wide variety of screening techniques are known for a large number of naturally-occurring targets when the biochemical

15 function of the target protein is known.

B. Cell Based Assays

- Current cell-based assays used to identify or to characterize compounds for drug discovery and development frequently depend on detecting the ability of a test compound to inhibit the activity of a target molecule located within a cell or located on the surface of a cell. Most often
- 20 such target molecules are proteins such as enzymes, receptors and the like. However, target molecules may also include other molecules such as DNAs, lipids, carbohydrates and RNAs including messenger RNAs, ribosomal RNAs, tRNAs and the like. A number of highly sensitive cell-based assay methods are available to those of skill in the art to detect binding and interaction of test compounds with specific target molecules. However, these methods are generally not highly
- 25 effective when the test compound binds to or otherwise interacts with its target molecule with moderate or low affinity. In addition, the target molecule may not be readily accessible to a test compound in solution, such as when the target molecule is located inside the cell or within a cellular compartment such as the periplasm of a bacterial cell. Thus, current cell-based assay methods are limited in that they are not effective in identifying or characterizing compounds that
- 30 interact with their targets with moderate to low affinity or compounds that interact with targets that are not readily accessible.

- Cell-based assay methods of the present invention have substantial advantages over current cell-based assays practiced in the art. These advantages derive from the use of sensitized cells in which the level or activity of a proliferation-required gene product (the target molecule) has been
- 35 specifically reduced to the point where the presence or absence of its function becomes a rate-determining step for cellular proliferation. Bacterial, fungal, plant, or animal cells can all be used with the present method. Such sensitized cells become much more sensitive to compounds that are

active against the affected target molecule. Thus, cell-based assays of the present invention are capable of detecting compounds exhibiting low or moderate potency against the target molecule of interest because such compounds are substantially more potent on sensitized cells than on non-sensitized cells. The affect may be such that a test compound may be two to several times more
5 potent, at least 10 times more potent or even at least 100 times more potent when tested on the sensitized cells as compared to the non-sensitized cells.

Due in part to the increased appearance of antibiotic resistance in pathogenic microorganisms and to the significant side-effects associated with some currently used antibiotics, novel antibiotics acting at new targets are highly sought after in the art. Yet, another limitation in
10 the current art related to cell-based assays is the problem of identifying hits against the same kinds of target molecules in the same limited set of biological pathways over and over again. This may occur when compounds acting at such new targets are discarded, ignored or fail to be detected because compounds acting at the "old" targets are encountered more frequently and are more potent than compounds acting at the new targets. As a result, the majority of antibiotics in use currently
15 interact with a relatively small number of target molecules within an even more limited set of biological pathways.

The use of sensitized cells of the current invention provides a solution to the above problem in two ways. First, desired compounds acting at a target of interest, whether a new target or a previously known but poorly exploited target, can now be detected above the "noise" of compounds
20 acting at the "old" targets due to the specific and substantial increase in potency of such desired compounds when tested on the sensitized cells of the current invention. Second, the methods used to sensitize cells to compounds acting at a target of interest may also sensitize these cells to compounds acting at other target molecules within the same biological pathway. For example, expression of an antisense molecule to a gene encoding a ribosomal protein is expected to sensitize
25 the cell to compounds acting at that ribosomal protein and may also sensitize the cells to compounds acting at any of the ribosomal components (proteins or rRNA) or even to compounds acting at any target which is part of the protein synthesis pathway. Thus an important advantage of the present invention is the ability to reveal new targets and pathways that were previously not readily accessible to drug discovery methods.

30 Sensitized cells of the present invention are prepared by reducing the activity or level of a target molecule. The target molecule may be a gene product, such as an RNA or polypeptide produced from the proliferation-required nucleic acids described herein. Alternatively, the target may be a gene product such as an RNA or polypeptide which is produced from a sequence within the same operon as the proliferation-required nucleic acids described herein. In addition, the target
35 may be an RNA or polypeptide in the same biological pathway as the proliferation-required nucleic acids described herein. Such biological pathways include, but are not limited to, enzymatic,

biochemical and metabolic pathways as well as pathways involved in the production of cellular structures such the cell wall.

Current methods employed in the arts of medicinal and combinatorial chemistries are able to make use of structure-activity relationship information derived from testing compounds in various biological assays including direct binding assays and cell-based assays. Occasionally compounds are directly identified in such assays that are sufficiently potent to be developed as drugs. More often, initial hit compounds exhibit moderate or low potency. Once a hit compound is identified with low or moderate potency, directed libraries of compounds are synthesized and tested in order to identify more potent leads. Generally these directed libraries are combinatorial chemical libraries consisting of compounds with structures related to the hit compound but containing systematic variations including additions, subtractions and substitutions of various structural features. When tested for activity against the target molecule, structural features are identified that either alone or in combination with other features enhance or reduce activity. This information is used to design subsequent directed libraries containing compounds with enhanced activity against the target molecule. After one or several iterations of this process, compounds with substantially increased activity against the target molecule are identified and may be further developed as drugs. This process is facilitated by use of the sensitized cells of the present invention since compounds acting at the selected targets exhibit increased potency in such cell-based assays, thus; more compounds can now be characterized providing more useful information than would be obtained otherwise.

Thus, it is now possible using cell-based assays of the present invention to identify or characterize compounds that previously would not have been readily identified or characterized including compounds that act at targets that previously were not readily exploited using cell-based assays. The process of evolving potent drug leads from initial hit compounds is also substantially improved by the cell-based assays of the present invention because, for the same number of test compounds, more structure-function relationship information is likely to be revealed.

The method of sensitizing a cell entails selecting a suitable gene or operon. A suitable gene or operon is one whose expression is required for the proliferation of the cell to be sensitized. The next step is to introduce into the cells to be sensitized, an antisense RNA capable of hybridizing to the suitable gene or operon or to the RNA encoded by the suitable gene or operon. Introduction of the antisense RNA can be in the form of an expression vector in which antisense RNA is produced under the control of an inducible promoter. The amount of antisense RNA produced is limited by varying the inducer concentration to which the cell is exposed and thereby varying the activity of the promoter driving transcription of the antisense RNA. Thus, cells are sensitized by exposing them to an inducer concentration that results in a sub-lethal level of antisense RNA expression.

In one embodiment of the cell-based assays, the identified exogenous *E. coli* nucleotide sequences of the present invention are used to inhibit the production of a proliferation-required

protein. Expression vectors producing antisense RNA against identified genes required for proliferation are used to limit the concentration of a proliferation-required protein without severely inhibiting growth. To achieve that goal, a growth inhibition dose curve of inducer is calculated by plotting various doses of inducer against the corresponding growth inhibition caused by the antisense expression. From this curve, various percentages of antisense induced growth inhibition, from 1 to 100% can be determined. If the promoter contained in the expression vector contains a *lac* operator the transcription is regulated by *lac* repressor and expression from the promoter is inducible with IPTG. For example, the highest concentration of the inducer IPTG that does not reduce the growth rate (0% growth inhibition) can be predicted from the curve. Cellular proliferation can be monitored by growth medium turbidity via OD measurements. In another example, the concentration of inducer that reduces growth by 25% can be predicted from the curve. In still another example, a concentration of inducer that reduces growth by 50% can be calculated. Additional parameters such as colony forming units (cfu) can be used to measure cellular viability.

Cells to be assayed are exposed to the above-determined concentrations of inducer. The presence of the inducer at this sub-lethal concentration reduces the amount of the proliferation required gene product to a low amount in the cell that will limit but not prevent growth. Cells grown in the presence of this concentration of inducer are therefore specifically more sensitive to inhibitors of the proliferation-required protein or RNA of interest or to inhibitors of proteins or RNAs in the same biological pathway as the proliferation-required protein or RNA of interest but not to inhibitors of unrelated proteins or RNAs.

Cells pretreated with sub-inhibitory concentrations of inducer and thus containing a reduced amount of proliferation-required target gene product are then used to screen for compounds that reduce cell growth. The sub-lethal concentration of inducer may be any concentration consistent with the intended use of the assay to identify candidate compounds to which the cells are more sensitive. For example, the sub-lethal concentration of the inducer may be such that growth inhibition is at least about 5%, at least about 8%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60% at least about 75%, 90%, 95% or more. Cells which are pre-sensitized using the preceding method are more sensitive to inhibitors of the target protein because these cells contain less target protein to be inhibited than do wild-type cells.

In another embodiment of the cell based assays of the present invention, the level or activity of a proliferation required gene product is reduced using a mutation, such as a temperature sensitive mutation, in the proliferation-required sequence and an antisense nucleic acid against the proliferation-required sequence. Growing the cells at an intermediate temperature between the permissive and restrictive temperatures of the temperature sensitive mutant where the mutation is in a proliferation-required gene produces cells with reduced activity of the proliferation-required gene product. The antisense RNA directed against the proliferation-required sequence further reduces

the activity of the proliferation required gene product. Drugs that may not have been found using either the temperature sensitive mutation or the antisense nucleic acid alone may be identified by determining whether cells in which expression of the antisense nucleic acid has been induced and which are grown at a temperature between the permissive temperature and the restrictive temperature are substantially more sensitive to a test compound than cells in which expression of the antisense nucleic acid has not been induced and which are grown at a permissive temperature. Also drugs found previously from either the antisense nucleic acid alone or the temperature sensitive mutation alone may have a different sensitivity profile when used in cells combining the two approaches, and that sensitivity profile may indicate a more specific action of the drug in inhibiting one or more activities of the gene product.

Temperature sensitive mutations may be located at different sites within the gene and correspond to different domains of the protein. For example, the *dnaB* gene of *Escherichia coli* encodes the replication fork DNA helicase. DnaB has several domains, including domains for oligomerization, ATP hydrolysis, DNA binding, interaction with primase, interaction with DnaC, and interaction with DnaA [(Biswas, E.E. and Biswas, S.B. 1999. Mechanism and DnaB helicase of *Escherichia coli*: structural domains involved in ATP hydrolysis, DNA binding, and oligomerization. *Biochem.* 38:10919-10928; Hiasa, H. and Marians, K.J. 1999. Initiation of bidirectional replication at the chromosomal origin is directed by the interaction between helicase and primase. *J. Biol. Chem.* 274:27244-27248; San Martin, C., Rademacher, M., Wolpensinger, B., Engel, A., Miles, C.S., Dixon, N.E., and Carazo, J.M. 1998. Three-dimensional reconstructions from cryoelectron microscopy images reveal an intimate complex between helicase DnaB and its loading partner DnaC. *Structure* 6:501-9; Sutton, M.D., Carr, K.M., Vicente, M., and Kaguni, J.M. 1998. *Escherichia coli* DnaA protein. The N-terminal domain and loading of DnaB helicase at the *E. coli* chromosomal. *J. Biol. Chem.* 273:34255-62.)). Temperature sensitive mutations in different domains of DnaB confer different phenotypes at the restrictive temperature, which include either an abrupt stop or slow stop in DNA replication with or without DNA breakdown (Wechsler, J.A. and Gross, J.D. 1971. *Escherichia coli* mutants temperature-sensitive for DNA synthesis. *Mol. Gen. Genetics* 113:273-284) and termination of growth or cell death. Combining the use of temperature sensitive mutations in the *dnaB* gene that cause cell death at the restrictive temperature with an antisense to the *dnaB* gene could lead to the discovery of very specific and effective inhibitors of one or a subset of activities exhibited by DnaB.

When screening for antimicrobial agents against a gene product required for proliferation, growth inhibition of cells containing a limiting amount of that proliferation-required gene product can be assayed. Growth inhibition can be measured by directly comparing the amount of growth, measured by the optical density of the growth medium, between an experimental sample and a control sample. Alternative methods for assaying cell proliferation include measuring green

fluorescent protein (GFP) reporter construct emissions, various enzymatic activity assays, and other methods well known in the art.

It will be appreciated that the above method may be performed in solid phase, liquid phase or a combination of the two. For example, cells grown on nutrient agar containing the inducer of the antisense construct may be exposed to compounds spotted onto the agar surface. A compound's effect may be judged from the diameter of the resulting killing zone, the area around the compound application point in which cells do not grow. Multiple compounds may be transferred to agar plates and simultaneously tested using automated and semi-automated equipment including but not restricted to multi-channel pipettes (for example the Beckman Multimek) and multi-channel spotters (for example the Genomic Solutions Flexys). In this way multiple plates and thousands to millions of compounds may be tested per day.

The compounds may also be tested entirely in liquid phase using microtiter plates as described below. Liquid phase screening may be performed in microtiter plates containing 96, 384, 1536 or more wells per microtiter plate to screen multiple plates and thousands to millions of compounds per day. Automated and semi-automated equipment may be used for addition of reagents (for example cells and compounds) and determination of cell density.

EXAMPLE 9

Cell Based Assay Using Antisense Complementary to Genes Encoding Ribosomal Proteins

The effectiveness of the above cell based assay was validated using constructs expressing antisense RNA to the proliferation required *E. coli* genes *rplL*, *rplJ*, and *rplW* encoding ribosomal proteins L7/L12, L10 and L23 respectively. These proteins are part of the protein synthesis apparatus of the cell and as such are required for proliferation. These constructs were used to test the effect of antisense expression on cell sensitivity to antibiotics known to bind to the ribosome and thereby inhibit protein synthesis. Constructs expressing antisense RNA to several other genes (*elaD*, *visC*, *yohH*, and *atpE/B*), the products of which are not involved in protein synthesis were used for comparison.

First pLex5BA (Krause et al., J. Mol. Biol. 274: 365 (1997)) expression vectors containing antisense constructs to either *rplW* or to *elaD* were introduced into separate *E. coli* cell populations. Vector introduction is a technique well known to those of ordinary skill in the art. The expression vectors of this example contain IPTG inducible promoters that drive the expression of the antisense RNA in the presence of the inducer. However, those skilled in the art will appreciate that other inducible promoters may also be used. Suitable expression vectors are also well known in the art. The *E. coli* antisense clones encoding ribosomal proteins L7/L12, L10 and L23 were used to test the effect of antisense expression on cell sensitivity to the antibiotics known to bind to these proteins. First, expression vectors containing antisense to either the genes encoding L7/L12 and L10 or L23 were introduced into separate *E. coli* cell populations.

The cell populations were exposed to a range of IPTG concentrations in liquid medium to obtain the growth inhibitory dose curve for each clone (Fig. 1). First, seed cultures were grown to a particular turbidity that is measured by the optical density (OD) of the growth solution. The OD of the solution is directly related to the number of bacterial cells contained therein. Subsequently, sixteen 200 ul liquid medium cultures were grown in a 96 well microtiter plate at 37 C with a range of IPTG concentrations in duplicate two-fold serial dilutions from 1600 uM to 12.5 uM (final concentration). Additionally, control cells were grown in duplicate without IPTG. These cultures were started from equal amounts of cells derived from the same initial seed culture of a clone of interest. The cells were grown for up to 15 hours and the extent of growth was determined by measuring the optical density of the cultures at 600 nm. When the control culture reached mid-log phase the percent growth of the control for each of the IPTG containing cultures was plotted against the log concentrations of IPTG to produce a growth inhibitory dose response curve for the IPTG. The concentration of IPTG that inhibits cell growth to 50% (IC₅₀) as compared to the 0 mM IPTG control (0% growth inhibition) was then calculated from the curve. Under these conditions, an amount of antisense RNA was produced that reduced the expression levels of *rplW* and *elaD* to a degree such that growth was inhibited by 50%.

Alternative methods of measuring growth are also contemplated. Examples of these methods include measurements of proteins, the expression of which is engineered into the cells being tested and can readily be measured. Examples of such proteins include green fluorescent protein (GFP) and various enzymes.

Cells were pretreated with the selected concentration of IPTG and then used to test the sensitivity of cell populations to tetracycline, erythromycin and other protein synthesis inhibitors. Figure 2 is an IPTG dose response curve in *E. coli* transformed with an IPTG-inducible plasmid containing either an antisense clone to the *E. coli* ribosomal protein *rplW* (AS-*rplW*) which is required for protein synthesis and essential for cell proliferation, or an antisense clone to the *elaD* (AS-*elaD*) gene which is not known to be involved in protein synthesis and which is also essential for proliferation.

An example of a tetracycline dose response curve is shown in Figures 2A and 2B for the *rplW* and *elaD* genes, respectively. Cells were grown to log phase and then diluted into media alone or media containing IPTG at concentrations which give 20% and 50% growth inhibition as determined by IPTG dose response curves. After 2.5 hours, the cells were diluted to a final OD₆₀₀ of 0.002 into 96 well plates containing (1) +/- IPTG at the same concentrations used for the 2.5 hour pre-incubation; and (2) serial two-fold dilutions of tetracycline such that the final concentrations of tetracycline range from 1 µg/ml to 15.6 ng/ml and 0 µg/ml. The 96 well plates were incubated at 37°C and the OD₆₀₀ was read by a plate reader every 5 minutes for up to 15 hours. For each IPTG concentration and the no IPTG control, tetracycline dose response curves were determined when the control (absence of tetracycline) reached 0.1 OD₆₀₀. To compare tetracycline sensitivity with and without IPTG, tetracycline IC_{50s} were

determined from the dose response curves (Figs. 3A-B). Cells with reduced levels of L23 (*rplW*) showed increased sensitivity to tetracycline (Fig. 2A) as compared to cells with reduced levels of *elaD* (Fig. 2B). Figure 3 shows a summary bar chart in which the ratios of tetracycline IC_{50s} determined in the presence of IPTG which gives 50% growth inhibition versus tetracycline IC_{50s} determined without IPTG (fold increase in tetracycline sensitivity) were plotted. Cells with reduced levels of either L7/L12 (genes *rplL*, *rplJ*) or L23 (*rplW*) showed increased sensitivity to tetracycline (Fig. 3). Cells expressing antisense to genes not known to be involved in protein synthesis (*atpB/E*, *visC*, *elaD*, *yohH*) did not show the same increased sensitivity to tetracycline, validating the specificity of this assay (Fig. 3).

In addition to the above, it has been observed in initial experiments that clones expressing antisense RNA to genes involved in protein synthesis (including genes encoding ribosomal proteins L7/L12 & L10, L7/L12 alone, L22, and L18, as well as genes encoding rRNA and Elongation Factor G) have increased sensitivity to the macrolide, erythromycin, whereas clones expressing antisense to the non-protein synthesis genes *elaD*, *atpB/E* and *visC* do not. Furthermore, the clone expressing antisense to *rplL* and *rplJ* does not show increased sensitivity to nalidixic acid and ofloxacin, antibiotics which do not inhibit protein synthesis.

The results with the ribosomal protein genes *rplL*, *rplJ*, and *rplW* as well as the initial results using various other antisense clones and antibiotics show that limiting the concentration of an antibiotic target makes cells more sensitive to the antimicrobial agents that specifically interact with that protein. The results also show that these cells are sensitized to antimicrobial agents that inhibit the overall function in which the protein target is involved but are not sensitized to antimicrobial agents that inhibit other functions.

The cell based assay described above may also be used to identify the biological pathway in which a proliferation-required nucleic acid or its gene product lies. In such methods, cells expressing a sub-lethal level of antisense to a target proliferation-required nucleic acid and control cells in which expression of the antisense has not been induced are contacted with a panel of antibiotics known to act in various pathways. If the antibiotic acts in the pathway in which the target proliferation-required nucleic acid or its gene product lies, cells in which expression of the antisense has been induced will be more sensitive to the antibiotic than cells in which expression of the antisense has not been induced.

As a control, the results of the assay may be confirmed by contacting a panel of cells expressing antisense nucleic acids to many different proliferation-required genes including the target proliferation-required gene. If the antibiotic is acting specifically, heightened sensitivity to the antibiotic will be observed only in the cells expressing antisense to a target proliferation-required gene (or cells expressing antisense to other proliferation-required genes in the same pathway as the target proliferation-required gene) but will not be observed generally in all cells expressing antisense to proliferation-required genes.

Similarly, the above method may be used to determine the pathway on which a test compound, such as a test antibiotic acts. A panel of cells, each of which expresses antisense to a proliferation-required nucleic acid in a known pathway, is contacted with a compound for which it is desired to determine the pathway on which it acts. The sensitivity of the panel of cells to the test compound is determined in cells in which expression of the antisense has been induced and in control cells in which expression of the antisense has not been induced. If the test compound acts on the pathway on which an antisense nucleic acid acts, cells in which expression of the antisense has been induced will be more sensitive to the compound than cells in which expression of the antisense has not been induced. In addition, control cells in which expression of antisense to proliferation-required genes in other pathways has been induced will not exhibit heightened sensitivity to the compound. In this way, the pathway on which the test compound acts may be determined.

The Example below provides one method for performing such assays.

EXAMPLE 10

Identification of the Pathway in which a Proliferation-Required Gene Lies or the Pathway on which an Antibiotic Acts

A. Preparation of Bacterial Stocks for Assay

To provide a consistent source of cells to screen, frozen stocks of host bacteria containing the desired antisense construct are prepared using standard microbiological techniques. For example, a single clone of the organism can be isolated by streaking out a sample of the original stock onto an agar plate containing nutrients for cell growth and an antibiotic for which the antisense construct contains a gene which confers resistance. After overnight growth an isolated colony is picked from the plate with a sterile needle and transferred to an appropriate liquid growth media containing the antibiotic required for maintenance of the plasmid. The cells are incubated at 30°C to 37°C with vigorous shaking for 4 to 6 hours to yield a culture in exponential growth. Sterile glycerol is added to 15% (volume to volume) and 100µL to 500 µL aliquots are distributed into sterile cryotubes, snap frozen in liquid nitrogen, and stored at -80°C for future assays.

B. Growth of Bacteria for Use in the Assay

A day prior to an assay, a stock vial is removed from the freezer, rapidly thawed (37°C water bath) and a loop of culture is streaked out on an agar plate containing nutrients for cell growth and an antibiotic to which the antisense construct confers resistance. After overnight growth at 37°C, ten randomly chosen, isolated colonies are transferred from the plate (sterile inoculum loop) to a sterile tube containing 5 mL of LB medium containing the antibiotic to which the antisense vector confers resistance. After vigorous mixing to form a homogeneous cell suspension, the optical density of the suspension is measured at 600 nm (OD600) and if necessary an aliquot of the suspension is diluted into a second tube of 5 mL, sterile, LB medium plus antibiotic to achieve an

OD600 \leq 0.02 absorbance units. The culture is then incubated at 37° C for 1-2 hrs with shaking until the OD600 reaches OD 0.2 – 0.3. At this point the cells are ready to be used in the assay.

5 **C. Selection of Media to be Used in Assay**

Two fold dilution series of the inducer are generated in culture media containing the appropriate antibiotic for maintenance of the antisense construct. Several media are tested side by side and three to four wells are used to evaluate the effects of the inducer at each concentration in each media. For example, M9 minimal media, LB broth, TBD broth and Muller-Hinton media may
10 be tested with the inducer IPTG at the following concentrations, 50 μ M, 100 μ M, 200 μ M, 400 μ M, 600 μ M, 800 μ M and 1000 μ M. Equal volumes of test media-inducer and cells are added to the wells of a 384 well microtiter plate and mixed. The cells are prepared as described above and diluted 1:100 in the appropriate media containing the test antibiotic immediately prior to addition to the microtiter plate wells. For a control, cells are also added to several wells of each media that do
15 not contain inducer, for example 0 μ M IPTG. Cell growth is monitored continuously by incubation at 37°C in a microtiter plate reader monitoring the OD600 of the wells over an 18-hour period. The percent inhibition of growth produced by each concentration of inducer is calculated by comparing the rates of logarithmic growth against that exhibited by cells growing in media without inducer. The medium yielding greatest sensitivity to inducer is selected for use in the assays described
20 below.

D. Measurement of Test Antibiotic Sensitivity in the Absence of Antisense Construct Induction

Two-fold dilution series of antibiotics of known mechanism of action are generated in the culture media selected for further assay development that has been supplemented with the antibiotic used to maintain the construct. A panel of test antibiotics known to act on different pathways is
25 tested side by side with three to four wells being used to evaluate the effect of a test antibiotic on cell growth at each concentration. Equal volumes of test antibiotic and cells are added to the wells of a 384 well microtiter plate and mixed. Cells are prepared as described above using the media selected for assay development supplemented with the antibiotic required to maintain the antisense construct and are diluted 1:100 in identical media immediately prior to addition to the microtiter
30 plate wells. For a control, cells are also added to several wells that contain the solvent used to dissolve the antibiotics but no antibiotic. Cell growth is monitored continuously by incubation at 37°C in a microtiter plate reader monitoring the OD600 of the wells over an 18-hour period. The percent inhibition of growth produced by each concentration of antibiotic is calculated by comparing the rates of logarithmic growth against that exhibited by cells growing in media without
35 antibiotic. A plot of percent inhibition against log[antibiotic concentration] allows extrapolation of an IC₅₀ value for each antibiotic.

E. Measurement of Test Antibiotic Sensitivity in the Presence of Antisense Construct Inducer

The culture media selected for use in the assay is supplemented with inducer at concentrations shown to inhibit cell growth by 50 and 80% as described above and the antibiotic used to maintain the construct. Two fold dilution series of the panel of test antibiotics used above are generated in each of these media. Several antibiotics are tested side by side with three to four wells being used to evaluate the effects of an antibiotic on cell growth at each concentration, in each media. Equal volumes of test antibiotic and cells are added to the wells of a 384 well microtiter plate and mixed. Cells are prepared as described above using the media selected for use in the assay supplemented with the antibiotic required to maintain the antisense construct. The cells are diluted 1:100 into two 50 mL aliquots of identical media containing concentrations of inducer that have been shown to inhibit cell growth by 50% and 80 % respectively and incubated at 37°C with shaking for 2.5 hours. Immediately prior to addition to the microtiter plate wells, the cultures are adjusted to an appropriate OD₆₀₀ (typically 0.002) by dilution into warm (37°C) sterile media supplemented with identical concentrations of the inducer and antibiotic used to maintain the antisense construct. For a control, cells are also added to several wells that contain solvent used to dissolve test antibiotics but which contain no antibiotic. Cell growth is monitored continuously by incubation at 37°C in a microtiter plate reader monitoring the OD₆₀₀ of the wells over an 18-hour period. The percent inhibition of growth produced by each concentration of antibiotic is calculated by comparing the rates of logarithmic growth against that exhibited by cells growing in media without antibiotic. A plot of percent inhibition against log[antibiotic concentration] allows extrapolation of an IC₅₀ value for each antibiotic.

F. Determining the Specificity of the Test Antibiotics

A comparison of the IC₅₀s generated by antibiotics of known mechanism of action under antisense induced and non-induced conditions allows the pathway in which a proliferation-required nucleic acid lies to be identified. If cells expressing an antisense nucleic acid against a proliferation-required gene are selectively sensitive to an antibiotic acting via a particular pathway, then the gene against which the antisense acts is involved in the pathway in which the antibiotic acts.

G. Identification of Pathway in which a Test Antibiotic Acts

As discussed above, the cell based assay may also be used to determine the pathway against which a test antibiotic acts. In such an analysis, the pathways against which each member of a panel of antisense nucleic acids acts are identified as described above. A panel of cells, each containing an inducible antisense vector against a gene in a known proliferation-required pathway, is contacted with a test antibiotic for which it is desired to determine the pathway on which it acts under inducing an non-inducing conditions. If heightened sensitivity is observed in induced cells expressing antisense against a gene in a particular pathway but not in induced cells expressing

antisense against genes in other pathways, then the test antibiotic acts against the pathway for which heightened sensitivity was observed.

One skilled in the art will appreciate that further optimization of the assay conditions, such as the concentration of inducer used to induce antisense expression and/or the growth conditions used for the assay (for example incubation temperature and media components) may further increase the selectivity and/or magnitude of the antibiotic sensitization exhibited.

The following example confirms the effectiveness of the methods described above.

EXAMPLE 11

Identification of the Pathway in which a Proliferation-Required Gene Lies

Antibiotics of various chemical classes and modes of action were purchased from Sigma Chemicals (St. Louis, MO). Stock solutions were prepared by dissolving each antibiotic in an appropriate aqueous solution based on information provided by the manufacturer. The final working solution of each antibiotic contained no more than 0.2% (w/v) of any organic solvent. To determine their potency against a bacterial strain engineered for expression of an antisense against a proliferation-required gene encoding 50S ribosomal protein, each antibiotic was serially diluted two or three fold in growth medium supplemented with the appropriate antibiotic for maintenance of the anti-sense construct. At least ten dilutions were prepared for each antibiotic. 25 μ L aliquots of each dilution were transferred to discrete wells of a 384-well microplate (the assay plate) using a multi-channel pipette. Quadruplicate wells were used for each dilution of an antibiotic under each treatment condition (plus and minus inducer). Each assay plate contained twenty wells for cell growth controls (growth media replacing antibiotic), ten wells for each treatment (plus and minus inducer, in this example IPTG). Assay plates were usually divided into the two treatments: half the plate containing induced cells and an appropriate concentrations of inducer (in this example IPTG) to maintain the state of induction, the other half containing non-induced cells in the absence of IPTG.

Cells for the assay were prepared as follows. Bacterial cells containing a construct, from which expression of antisense nucleic acid against *rplL* and *rplJ*, which encode proliferation-required 50S ribosomal subunit proteins, is inducible in the presence of IPTG, were grown into exponential growth (OD_{600} 0.2 to 0.3) and then diluted 1:100 into fresh media containing either 400 μ M or 0 μ M inducer (IPTG). These cultures were incubated at 37° C for 2.5 hr. After a 2.5 hr incubation, induced and non-induced cells were respectively diluted into an assay medium at a final OD_{600} value of 0.0004. The medium contained an appropriate concentration of the antibiotic for the maintenance of the anti-sense construct. In addition, the medium used to dilute induced cells was supplemented with 800 μ M IPTG so that addition to the assay plate would result in a final IPTG concentration of 400 μ M. Induced and non-induced cell suspensions were dispensed (25 μ L/well) into the appropriate wells of the assay plate as discussed previously. The plate was then loaded into

a plate reader, incubated at constant temperature, and cell growth was monitored in each well by the measurement of light scattering at 595 nm. Growth was monitored every 5 minutes until the cell culture attained a stationary growth phase. For each concentration of antibiotic, a percentage inhibition of growth was calculated at the time point corresponding to mid-exponential growth for the associated control wells (no antibiotic, plus or minus IPTG). For each antibiotic and condition (plus or minus IPTG), a plot of percent inhibition versus log of antibiotic concentration was generated and the IC_{50} determined. A comparison of the IC_{50} for each antibiotic in the presence and absence of IPTG revealed whether induction of the antisense construct sensitized the cell to the mechanism of action exhibited by the antibiotic. Cells which exhibited a significant (standard statistical analysis) numerical decrease in the IC_{50} value in the presence of inducer were considered to have an increased sensitivity to the test antibiotic.

The results are provided in the table below, which lists the classes and names of the antibiotics used in the analysis, the targets of the antibiotics, the IC_{50} in the absence of IPTG, the IC_{50} in the presence of IPTG, the concentration units for the IC_{50} s, the fold increase in IC_{50} in the presence of IPTG, and whether increased sensitivity was observed in the presence of IPTG.

TABLE IV
Effect of Expression of Antisense RNA to rplL and rplJ on Antibiotic Sensitivity

ANTIBIOTIC CLASS/Names	TARGET	IC50 (-IPTG)	IC50 (+IPTG)	Conc. Unit	Fold Increase in Sensitivity	Sensitivity Increased?
PROTEIN SYNTHESIS INHIBITOR						
ANTIBIOTICS						
AMINOGLYCOSIDES						
Gentamicin	30S ribosome function	2715	19.19	ng/ml	141	Yes
Streptomycin	30S ribosome function	11280	161	ng/ml	70	Yes
Spectinomycin	30S ribosome function	18050	<156	ng/ml		Yes
Tobramycin	30S ribosome function	3594	70.58	ng/ml	51	Yes
MACROLIDES						
Erythromycin	50S ribosome function	7467	187	ng/ml	40	Yes
AROMATIC POLYKETIDES						
Tetracycline	30S ribosome function	199.7	1.83	ng/ml	109	Yes
Minocycline	30S ribosome function	668.4	3.897	ng/ml	172	Yes
Doxycycline	30S ribosome function	413.1	27.81	ng/ml	15	Yes
OTHER PROTEIN SYNTHESIS INHIBITORS						
Fusidic acid	Elongation Factor G function	59990	641	ng/ml	94	Yes
Chloramphenicol	30S ribosome function	465.4	1.516	ng/ml	307	Yes
Lincomycin	50S ribosome function	47150	324.2	ng/ml	145	Yes

ANTIBIOTIC CLASS /Names	TARGET	IC50 (-IPTG)	IC50 (+IPTG)	Conc. Unit	Fold Increase in Sensitivity	Sensitivity Increased?
OTHER ANTIBIOTIC MECHANISMS						
B-LACTAMS						
Cefoxitin	Cell wall biosynthesis	2782	2484	ng/ml	1	No
Cefotaxime	Cell wall biosynthesis	24.3	24.16	ng/ml	1	No
DNA SYNTHESIS INHIBITORS						
Nalidixic acid	DNA Gyrase activity	6973	6025	ng/ml	1	No
Ofloxacin	DNA Gyrase activity	49.61	45.89	ng/ml	1	No
OTHER						
Bacitracin	Cell membrane function	4077	4677	mg/ml	1	No
Trimethoprim	Dihydrofolate Reductase activity	128.9	181.97	ng/ml	1	No
Vancomycin	Cell wall biosynthesis	145400	72550	ng/ml	2	No

The above results demonstrate that induction of an antisense RNA to genes encoding 50S ribosomal subunit proteins results in a selective and highly significant sensitization of cells to antibiotics that inhibit ribosomal function and protein synthesis. The above results further demonstrate that induction of an antisense construct to an essential gene sensitizes an organism to compounds that interfere with that gene products' biological role. This sensitization is restricted to compounds that interfere with pathways associated with the targeted gene and its product.

Assays utilizing antisense constructs to essential genes can be used to identify compounds that specifically interfere with the activity of multiple targets in a pathway. Such constructs can be used to simultaneously screen a sample against multiple targets in one pathway in one reaction (Combinatorial HTS).

Furthermore, as discussed above, panels of antisense construct containing cells may be used to characterize the point of intervention of any compound affecting an essential biological pathway including antibiotics with no known mechanism of action.

Another embodiment of the present invention is a method for determining the pathway against which a test antibiotic compound is active in which the activity of target proteins or nucleic acids involved in proliferation-required pathways is reduced by contacting cells with a sublethal concentration of a known antibiotic which acts against the target protein or nucleic acid. In one embodiment, the target protein or nucleic acid is a target protein or nucleic acid corresponding to a proliferation-required nucleic acid identified using the methods described above. The method is similar to those described above for determining which pathway a test antibiotic acts against except that rather than reducing the activity or level of a proliferation-required gene product using a sublethal level of antisense to a proliferation-required nucleic acid, the activity or level of the proliferation-required gene product is reduced using sublethal level of a known antibiotic which acts against the proliferation required gene product.

Interactions between drugs which affect the same biological pathway has been described in the literature. For example, Mecillinam (Amdinocillin) binds to and inactivates the penicillin binding protein 2 (PBP2, product of the *mrda* in *E. coli*). This antibiotic interacts with other antibiotics that inhibit PBP2 as well as antibiotics that inhibit other penicillin binding proteins such as PBP3 [(Gutmann, L., Vincent, S., Billot-Klein, D., Acar, J.F., Mrena, E., and Williamson, R. (1986) Involvement of penicillin-binding protein 2 with other penicillin-binding proteins in lysis of *Escherichia coli* by some beta-lactam antibiotics alone and in synergistic lytic effect of amdinocillin (mecillinam). *Antimicrobial Agents & Chemotherapy*, 30:906-912)]. Interactions between drugs could, therefore, involve two drugs that inhibit the same target protein or nucleic acid or inhibit different proteins or nucleic acids in the same pathway [(Fukuoka, T., Domon, H., Kakuta, M., Ishii, C., Hirasawa, A., Utsui, Y., Ohya, S., and Yasuda, H. (1997) Combination effect

- between panipenem and vancomycin on highly methicillin-resistant *Staphylococcus aureus*. Japan. J. Antibio. 50:411-419; Smith, C.E., Foleno, B.E., Barrett, J.F., and Frosc, M.B. (1997) Assessment of the synergistic interactions of levofloxacin and ampicillin against *Enterococcus faecium* by the checkerboard agar dilution and time-kill methods. Diagnos. Microbiol. Infect. Disease 27:85-92;
- 5 den Hollander, J.G., Horrevorts, A.M., van Goor, M.L., Verbrugh, H.A., and Mouton, J.W. (1997) Synergism between tobramycin and ceftazidime against a resistant *Pseudomonas aeruginosa* strain, tested in an in vitro pharmacokinetic model. Antimicrobial Agents & Chemotherapy. 41:95-110)].

Two drugs may interact even though they inhibit different targets. For example, the proton pump inhibitor, Omeprazole, and the antibiotic, Amoxycillin, two synergistic compounds acting

10 together, can cure *Helicobacter pylori* infection [(Gabryelewicz, A., Laszewicz, W., Dzieniszewski, J., Ciok, J., Marlicz, K., Bielecki, D., Popiela, T., Legutko, J., Knapik, Z., Poniewierka, E. (1997) Multicenter evaluation of dual-therapy (omeprazol and amoxycillin) for *Helicobacter pylori*-associated duodenal and gastric ulcer (two years of the observation). J. Physiol. Pharmacol. 48 Suppl 4:93-105)].

- 15 The growth inhibition from the sublethal concentration of the known antibiotic may be at least about 5%, at least about 8%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, or at least about 75%, or more.

Alternatively, the sublethal concentration of the known antibiotic may be determined by measuring the activity of the target proliferation-required gene product rather than by measuring

20 growth inhibition.

- Cells are contacted with a combination of each member of a panel of known antibiotics at a sublethal level and varying concentrations of the test antibiotic. As a control, the cells are contacted with varying concentrations of the test antibiotic alone. The IC_{50} of the test antibiotic in the presence and absence of the known antibiotic is determined. If the IC_{50} s in the presence and
- 25 absence of the known drug are substantially similar, then the test drug and the known drug act on different pathways. If the IC_{50} s are substantially different, then the test drug and the known drug act on the same pathway.

- Another embodiment of the present invention is a method for identifying a candidate compound for use as an antibiotic in which the activity of target proteins or nucleic acids involved
- 30 in proliferation-required pathways is reduced by contacting cells with a sublethal concentration of a known antibiotic which acts against the target protein or nucleic acid. In one embodiment, the target protein or nucleic acid is a target protein or nucleic acid corresponding to a proliferation-required nucleic acid identified using the methods described above. The method is similar to those described above for identifying candidate compounds for use as antibiotics except that rather than
- 35 reducing the activity or level of a proliferation-required gene product using a sublethal level of antisense to a proliferation-required nucleic acid, the activity or level of the proliferation-required

gene product is reduced using a sublethal level of a known antibiotic which acts against the proliferation required gene product.

The growth inhibition from the sublethal concentration of the known antibiotic may be at least about 5%, at least about 8%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, or at least about 75%, or more.

Alternatively, the sublethal concentration of the known antibiotic may be determined by measuring the activity of the target proliferation-required gene product rather than by measuring growth inhibition.

In order to characterize test compounds of interest, cells are contacted with a panel of known antibiotics at a sublethal level and one or more concentrations of the test compound. As a control, the cells are contacted with the same concentrations of the test compound alone. The IC_{50} of the test compound in the presence and absence of the known antibiotic is determined. If the IC_{50} of the test compound is substantially different in the presence and absence of the known drug then the test compound is a good candidate for use as an antibiotic. As discussed above, once a candidate compound is identified using the above methods its structure may be optimized using standard techniques such as combinatorial chemistry.

Representative known antibiotics which may be used in each of the above methods are provided in the table below. However, it will be appreciated that other antibiotics may also be used.

ANTIBIOTIC	INHIBITS/TARGET	RESISTANT MUTANTS
Inhibitors of Transcription		
Rifamycin, 1959 Rifampicin	Inhibits initiation of transcription/ β -subunit RNA polymerase, <i>rpoB</i>	<i>rpoB</i> , <i>crp</i> , <i>cyaA</i>
Rifabutin Rifaximin	Accelerates transcription chain termination/ β -subunit RNA polymerase	<i>rpoB</i>
Streptolydigin	an acyclic ansamycin, inhibits RNA polymerase	<i>rpoB</i>
Streptovaricin	Intercalates between 2 successive G-C pairs, <i>rpoB</i> , inhibits RNA synthesis	<i>pldA</i>
Actinomycin D+EDTA		
Inhibitors of Nucleic Acid Metabolism		
Quinolones, 1962 Nalidixic acid Oxolinic acid	α subunit gyrase and/or topoisomerase IV, <i>gyrA</i>	<i>gyrA</i> or <i>B</i> , <i>icd</i> , <i>sloB</i>
Fluoroquinolones	α subunit gyrase, <i>gyrA</i> and/or topoisomerase IV (probable target in Staph)	<i>gyrA</i>
Ciprofloxacin, 1983 Norfloxacin		<i>norA</i> (efflux in Staph)
Coumerins Novobiocin	Inhibits ATPase activity of β -subunit gyrase, <i>gyrB</i>	<i>hipQ</i>
		<i>gyrB</i> , <i>cysB</i> , <i>cysE</i> , <i>nov</i> , <i>ompA</i>
Coumermycin	Inhibits ATPase activity of β -subunit gyrase, <i>gyrB</i>	<i>gyrB</i> , <i>hisW</i>
Albicidin	DNA synthesis	<i>tsx</i> (nucleoside channel)
Metronidazole	Causes single-strand breaks in DNA	<i>nar</i>

Inhibitors of Metabolic Pathways

Sulfonamides, 1932	blocks synthesis of dihydrofolate, dihydro- pteroate synthesis, <i>folP</i>	<i>folP</i> , <i>gpt</i> , <i>pabA</i> , <i>pabB</i> , <i>pabC</i>
Sulfanilamide		
Trimethoprim, 1962	Inhibits dihydrofolate reductase, <i>folA</i>	<i>folA</i> , <i>thyA</i>
Showdomycin	Nucleoside analogue capable of alkylating sulfhydryl groups, inhibitor of thymidylate synthetase	<i>nupC</i> , <i>pnp</i>
Thiolactomycin	type II fatty acid synthase inhibitor	<i>emrB</i> <i>fadB</i> , <i>emrB</i> due to gene dosage
Psicofuranine	Adenosine glycoside antibiotic, target is GMP synthetase	<i>guaA</i> , <i>B</i>
Triclosan	Inhibits fatty acid synthesis	<i>fabI</i> (<i>envM</i>)
Diazaborines Isoniazid, Ethionamide	heterocyclic, contains boron, inhibit fatty acid synthesis, enoyl-ACP reductase, <i>fabI</i>	<i>fabI</i> (<i>envM</i>)

Inhibitors of Translation

Phenylpropanoids		
Chloramphenicol, 1947	Binds to ribosomal peptidyl transfer center preventing peptide translocation/ binds to S6, L3, L6, L14, L16, L25, L26, L27, but preferentially to L16	<i>rrn</i> , <i>cmlA</i> , <i>marA</i> , <i>ompF</i> , <i>ompR</i>
Tetracyclines, 1948, type II polyketides	Binding to 30S ribosomal subunit, "A" site on 30S subunit, blocks peptide elongation, strongest binding to S7	<i>clmA</i> (<i>cmr</i>), <i>mar</i> , <i>ompF</i>
Minocycline		
Doxycycline		
Macrolides (type I polyketides)		
Erythromycin, 1950	Binding to 50 S ribosomal subunit, 23S rRNA, blocks peptide translocation, L15, L4, L12	<i>rrn</i> , <i>rplC</i> , <i>rplD</i> , <i>rplV</i> , <i>mac</i>
Carbomycin, Spiramycin		
etc		
Aminoglycosides Streptomycin, 1944	Irreversible binding to 30S ribosomal subunit, prevents translation or causes mistranslation of mRNA/16S rRNA	<i>rpsL</i> , <i>strC</i> , <i>M</i> , <i>ubiF</i> <i>atpA-E</i> , <i>ecfB</i> , <i>hemAC</i> , <i>D</i> , <i>E</i> , <i>G</i> , <i>topA</i> , <i>rpsC</i> , <i>D</i> , <i>E</i> , <i>rrn</i> , <i>spcB</i> <i>atpA-atpE</i> , <i>cpxA</i> , <i>ecfB</i> , <i>hemA</i> , <i>B</i> , <i>L</i> , <i>topA</i> <i>ksgA</i> , <i>B</i> , <i>C</i> , <i>D</i> , <i>rplB</i> , <i>K</i> , <i>rpsL</i> , <i>N</i> , <i>M</i> , <i>R</i> <i>rplF</i> , <i>ubiF</i> <i>cpxA</i> <i>rpsL</i>
Neomycin		
Spectinomycin		
Kanamycin		
Kasugamycin		
Gentamicin, 1963		
Amikacin		
Paromycin		
Lincosamides		
Lincomycin, 1955	Binding to 50 S ribosomal subunit, blocks peptide translocation	<i>linB</i> , <i>rplN</i> , <i>O</i> , <i>rpsG</i>
Clindamycin		
Streptogramins Virginiamycin, 1955 Pristinamycin	2 components, Streptogramins A&B, bind to the 50S ribosomal subunit blocking peptide translocation and peptide bond formation	
Synercid: quinupristin /dalbopristin		
Fusidanes	Inhibition of elongation factor G (EF-G) prevents peptide translocation	<i>fusA</i>
Fusidic Acid		
Kirromycin (Mocimycin)	Inhibition of elongation factor TU (EF-Tu), prevents peptide bond formation	<i>tufA</i> , <i>B</i>
Pulvomycin	Binds to and inhibits EF-TU	
Thiopeptin	Sulfur-containing antibiotic, inhibits protein synthesis, EF-G	<i>rplE</i>

Tiamulin	Inhibits protein synthesis	<i>rplC, rplD</i>
Negamycin	Inhibits termination process of protein synthesis	<i>prfB</i>
Oxazolidinones Linezolid	23S rRNA	
Isoniazid		
Nitrofurantoin	Inhibits protein synthesis, nitroreductases convert nitrofurantoin to highly reactive electrophilic intermediates which attack bacterial ribosomal proteins non-specifically	<i>pdx</i> <i>nfnA, B</i>
Pseudomonic Acids Mupirocin (Bactroban)	Inhibition of isoleucyl tRNA synthetase-used for Staph, topical cream, nasal spray	<i>ileS</i>
Indolmycin	Inhibits tryptophanyl-tRNA synthetase	<i>trpS</i>
Viomycin		<i>rrmA</i> (23S rRNA methyltransferase; mutant has slow growth rate, slow chain elongation rate, and viomycin resistance)
Thiopeptides	Binds to L11-23S RNA complex	
Thiostrepton	Inhibits GTP hydrolysis by EF-G	
Micrococcin	Stimulates GTP hydrolysis by EF-G	

Inhibitors of Cell Walls/Membranes

β-lactams	Inhibition of one or more cell wall	
Penicillin, 1929 Ampicillin	transpeptidases, endopeptidases, and	
Methicillin, 1960	glycosidases (PBPs), of the 12 PBPs only 2 are essential: <i>mrda</i> (PBP2) and <i>fisI</i> (<i>pbpB</i> , PBP3)	<i>ampC, ampD, ampE, envZ, galU, hipA, hipQ, ompC, ompF, ompR, ptsI, rfa, tolD, tolE</i>
Cephalosporins, 1962		<i>tonB</i>
Mecillinam (amdinocillin)	Binds to and inactivates PBP2 (<i>mrda</i>) Inactivates PBP3 (<i>fisI</i>)	<i>alaS, argS, crp, cyaA, envB, mrda, B, mreB, C, D</i>
Aztreonam (Furazlocillin)		
Bacilysin, Tetaine	Dipeptide, inhib glucosamine synthase	<i>dppA</i>
Glycopeptides Vancomycin, 1955	Inhib G+ cell wall syn, binds to terminal D-ala-D-ala of pentapeptide,	
Polypeptides Bacitracin	Prevents dephosphorylation and regeneration of lipid carrier	<i>rfa</i>
Cyclic lipopeptide Daptomycin, 1980	Disrupts multiple aspects of membrane function, including peptidoglycan synthesis, lipoteichoic acid synthesis, and the bacterial membrane potential	
Cyclic polypeptides Polymixin, 1939	Surfactant action disrupts cell membrane lipids, binds lipid A moiety of LPS	<i>pmrA</i>
Fosfomycin, 1969	Analogue of P-enolpyruvate, inhibits 1 st step in peptidoglycan synthesis - UDP-N-acetylglucosamine enolpyruvyl transferase, <i>murA</i> . Also acts as Immunosuppressant	<i>murA, crp, cyaA glpT, hipA, ptsI, uhpT</i>
Cycloserine	Prevents formation of D-ala dimer, inhibits D-ala ligase, <i>ddlA, B</i>	<i>hipA, cycA</i>

Alafosfalin	phosphonodipeptide, cell wall synthesis inhibitor, potentiator of β -lactams	<i>pepA</i> , <i>tpp</i>
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Inhibitors of Protein Processing/Transport

Globomycin	Inhibits signal peptidase II (cleaves prolipoproteins subsequent to lipid modification, <i>lspA</i>)	<i>lpp</i> , <i>dnaE</i>
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EXAMPLE 12**Transfer of Exogenous Nucleic Acid Sequences to other Bacterial Species Using the *E. coli* Expression****Vectors or Expression Vectors Functional in Bacterial Species other than *E. coli*.**

5 Molecule No. EcXA059, encoding a portion of the *ypjA* gene of *Escherichia coli*, was either transformed directly into *Enterobacter cloacae*, *Salmonella typhimurium* and/or *Klebsiella pneumoniae* or subcloned into an expression vector functional in these species and the subclones transformed into these organisms. Suitable expression vectors are well known in the art. These expression vectors were introduced into *Enterobacter cloacae*, *Salmonella typhimurium* and/or

10 *Klebsiella pneumoniae* cells that were then assayed for growth inhibition according to the method of Example 1. After growth in liquid culture, cells were plated at various serial dilutions and a score determined by calculating the log difference in growth for INDUCED vs. UNINDUCED antisense RNA expression as determined by the maximum 10 fold dilution at which a colony was observed. If there was no effect of antisense RNA expression in one organism, the clone is given a

15 score of zero "0" in that organism. In contrast, a score of "8" means that 10^8 times more cells were required to observe a colony formed on the induced state than in the non-induced state under the conditions used and in that organism.

Expression vectors containing Molecule No. EcXA059 were found to inhibit bacterial growth in all four organisms when expression of the antisense RNA was induced with IPTG. A

20 score of 8 was assigned for *Escherichia coli*, *Enterobacter cloacae*, and *Salmonella typhimurium* and in *Klebsiella pneumoniae* the score was >7. The protein encoded by this sequence is used as a target sequence to screen candidate compound libraries as described above.

In addition, the above methods were validated using other antisense nucleic acids which inhibit the growth of *E. coli* which were identified using methods similar to those described above.

25 Expression vectors which inhibited growth of *E. coli* upon induction of antisense RNA expression with IPTG were transformed directly into *Enterobacter cloacae*, *Klebsiella pneumonia* or *Salmonella typhimurium*. The transformed cells were then assayed for growth inhibition according to the method of Example 1. After growth in liquid culture, cells were plated at various serial dilutions and a score determined by calculating the log difference in growth for INDUCED vs.

30 UNINDUCED antisense RNA expression as determined by the maximum 10 fold dilution at which a colony was observed. The results of these experiments are listed in Table V below. If there was no effect of antisense RNA expression in a microorganism, the clone is minus in Table V below. In

contrast, a positive in Table V below means that at least 10 fold more cells were required to observe a colony on the induced plate than on the non-induced plate under the conditions used and in that microorganism.

- 5 Sixteen of the constructs were found to inhibit growth in all the microorganisms tested upon induction of antisense RNA expression with IPTG.

TABLE V

Sensitivity of Other Microorganisms to Antisense Nucleic Acids That Inhibit Proliferation in *E. coli*

Mol. No.	<i>S. typhimurium</i>	<i>E. cloacae</i>	<i>K. pneumoniae</i>
EcXA001	+	+	-
EcXA004	+	-	-
EcXA005	+	+	+
EcXA006	-	-	-
EcXA007	-	+	-
EcXA008	+	-	+
EcXA009	-	-	-
EcXA010	+	+	+
EcXA011	-	+	-
EcXA012	-	+	-
EcXA013	+	+	+
EcXA014	+	+	-
EcXA015	+	+	+
EcXA016	+	+	+
EcXA017	+	+	+
EcXA018	+	+	+
EcXA019	+	+	+
EcXA020	+	+	+
EcXA021	+	+	+
EcXA023	+	+	+
EcXA024	+	-	+
EcXA025	-	-	-
EcXA026	+	+	-
EcXA027	+	+	-
EcXA028	+	-	-
EcXA029	-	-	-
EcXA030	+	+	+
EcXA031	+	-	-
EcXA032	+	+	-
EcXA033	+	+	+
EcXA034	+	+	+
EcXA035	-	-	-
EcXA036	+	-	+
EcXA037	+	+	-
EcXA038	+	+	+
EcXA039	+	-	-
EcXA041	+	+	+
EcXA042	-	+	+

Mol. No.	<i>S. typhimurium</i>	<i>E. cloacae</i>	<i>K. pneumoniae</i>
EcXA043	-	-	-
EcXA044	-	-	-
EcXA045	+	+	+
EcXA046	-	-	-
EcXA047	+	+	-
EcXA048	-	-	-
EcXA049	+	-	-
EcXA050	-	-	-
EcXA051	+	-	-
EcXA052	+	-	-
EcXA053	+	+	+
EcXA054	-	-	+
EcXA055	+	-	-
EcXA056	+	-	+
EcXA057	+	+	-
EcXA058	-	-	-
EcXA059	+	+	+
EcXA060	-	-	-
EcXA061	-	-	-
EcXA062	-	-	-
EcXA063	+	+	-
EcXA064	-	-	-
EcXA065	+	+	-
EcXA066	-	-	-
EcXA067	-	+	-
EcXA068	-	-	-
EcXA069	-	+	-
EcXA070	-	-	-
EcXA071	+	-	-
EcXA072	+	-	+
EcXA073	+	+	+
EcXA074	+	+	+
EcXA075	+	-	-
EcXA076	-	+	-
EcXA077	+	+	-
EcXA079	+	+	+
EcXA080	+	-	-
EcXA082	-	+	-
EcXA083	-	-	-
EcXA084	-	+	-
EcXA086	-	-	-
EcXA087	-	-	-
EcXA088	-	-	-
EcXA089	-	-	-
EcXA090	-	-	-
EcXA091	-	-	-
EcXA092	-	-	-
EcXA093	-	-	-

Mol. No.	<i>S. typhimurium</i>	<i>E. cloacae</i>	<i>K. pneumoniae</i>
EcXA094	+	+	+
EcXA095	+	+	-
EcXA096	-	-	-
EcXA097	+	-	-
EcXA098	+	-	-
EcXA099	-	-	-
EcXA100	-	-	-
EcXA101	-	-	-
EcXA102	-	-	-
EcXA103	-	+	-
EcXA104	+	+	+
EcXA106	+	+	-
EcXA107	-	-	-
EcXA108	-	-	-
EcXA109	-	-	-
EcXA110	+	+	-
EcXA111	-	-	-
EcXA112	-	+	-
EcXA113	+	+	+
EcXA114	-	+	-
EcXA115	-	+	-
EcXA116	+	+	-
EcXA117	+	-	-
EcXA118	-	-	-
EcXA119	+	+	-
EcXA120	-	-	-
EcXA121	-	-	-
EcXA122	+	-	+
EcXA123	+	-	-
EcXA124	-	-	-
EcXA125	-	-	-
EcXA126	-	-	-
EcXA127	+	+	-
EcXA128	-	-	-
EcXA129	-	+	-
EcXA130	+	+	-
EcXA132	-	-	-
EcXA133	-	-	-
EcXA136	-	-	-
EcXA137	-	-	-
EcXA138	+	-	-
EcXA139	-	-	-
EcXA140	+	-	-
EcXA141	+	-	-
EcXA142	-	-	-
EcXA143	-	+	-
EcXA144	+	+	-
EcXA145	-	-	-

Mol No.	<i>S. typhimurium</i>	<i>E. cloacae</i>	<i>K. pneumoniae</i>
EcXA146	-	-	-
EcXA147	-	-	-
EcXA148	-	-	-
EcXA149	+	+	+
EcXA150	-	-	-
EcXA151	+	-	-
EcXA152	-	-	-
EcXA153	+	+	-
EcXA154	-	-	-
EcXA155	-	-	ND
EcXA156	-	+	-
EcXA157	-	-	-
EcXA158	-	-	-
EcXA159	+	-	-
EcXA160	+	-	-
EcXA162	-	-	-
EcXA163	-	-	-
EcXA164	-	-	-
EcXA165	-	-	-
EcXA166	-	-	-
EcXA167	-	-	-
EcXA168	-	-	-
EcXA169	-	+	-
EcXA171	-	-	-
EcXA172	-	-	-
EcXA173	-	-	-
EcXA174	-	-	-
EcXA175	-	-	-
EcXA176	-	-	-
EcXA178	-	-	-
EcXA179	-	-	-
EcXA180	+	-	-
EcXA181	-	-	-
EcXA182	-	-	-
EcXA183	-	-	-
EcXA184	-	-	-
EcXA185	-	-	-
EcXA186	-	-	-
EcXA187	+	+	+
EcXA189	+	-	-
EcXA190	+	+	+
EcXA191	+	+	-
EcXA192	-	+	-

Thus, the ability of an antisense nucleic acid which inhibits the proliferation of *E. coli* to inhibit the growth of other organisms may be evaluated by either transforming the antisense nucleic acid directly into other *Escherichia* species or inserting the antisense nucleic acid into expression

vectors that are functional in other Gram negative species such as *Enterobacter cloacae*, *Salmonella typhimurium*, and/or *Klebsiella pneumoniae*. Similarly, the antisense nucleic acid can be inserted in expression vectors that are functional in Gram-positive species such as *Staphylococcus aureus*, *Enterococcus faecalis* and *Streptococcus pneumoniae* or other species.

5 Those skilled in the art will appreciate that a negative result in a heterologous microorganism does not mean that that microorganism is missing that gene nor does it mean that the gene is unessential. However, a positive result means that the heterologous microorganism contains a homologous gene which is required for proliferation of that microorganism. The homologous gene may be obtained using the methods described herein. Those cells that are inhibited by antisense may
10 be used in cell based assays as described herein for the identification and characterization of compounds in order to develop antibiotics effective in these microorganisms. Those skilled in the art will appreciate that an antisense molecule which works in the microorganism from which it was obtained will not always work in a heterologous microorganism.

EXAMPLE 13

15 Use of Identified Exogenous Nucleic Acid Sequences as Probes

The identified sequence of the present invention can be used as probes to obtain the sequence of additional genes of interest from a second organism. For example, probes to potential bacterial target proteins may be hybridized to nucleic acids from other organisms including other bacteria and higher organisms, to identify homologous sequences. Such hybridization might
20 indicate that the protein encoded by the gene to which the probe corresponds is found in humans and therefore not necessarily a good drug target. Alternatively, the gene can be conserved only in bacteria and therefore would be a good drug target for a broad spectrum antibiotic or antimicrobial.

Probes derived from the identified nucleic acid sequences of interest or portions thereof can be labeled with detectable labels familiar to those skilled in the art, including radioisotopes and non-
25 radioactive labels, to provide a detectable probe. The detectable probe can be single stranded or double stranded and can be made using techniques known in the art, including *in vitro* transcription, nick translation, or kinase reactions. A nucleic acid sample containing a sequence capable of hybridizing to the labeled probe is contacted with the labeled probe. If the nucleic acid in the sample is double stranded, it can be denatured prior to contacting the probe. In some applications, the nucleic acid
30 sample can be immobilized on a surface such as a nitrocellulose or nylon membrane. The nucleic acid sample can comprise nucleic acids obtained from a variety of sources, including genomic DNA, cDNA libraries, RNA, or tissue samples.

Procedures used to detect the presence of nucleic acids capable of hybridizing to the detectable probe include well known techniques such as Southern blotting, Northern blotting, dot blotting, colony
35 hybridization, and plaque hybridization. In some applications, the nucleic acid capable of hybridizing to the labeled probe can be cloned into vectors such as expression vectors, sequencing vectors, or in

vitro transcription vectors to facilitate the characterization and expression of the hybridizing nucleic acids in the sample. For example, such techniques can be used to isolate, purify and clone sequences from a genomic library, made from a variety of bacterial species, which are capable of hybridizing to probes made from the sequences identified in Examples 5 and 6.

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EXAMPLE 14

Preparation of PCR Primers and Amplification of DNA

The identified *E. coli* genes corresponding directly to or located within the operon of nucleic acid sequences required for proliferation or portions thereof can be used to prepare PCR primers for a variety of applications, including the identification or isolation of homologous sequences from other species, for example *S. typhimurium*, *E. cloacae*, and *Klebsiella pneumoniae*, which contain part or all of the homologous genes. Because homologous genes are related but not identical in sequence, those skilled in the art will often employ degenerate sequence PCR primers. Such degenerate sequence primers are designed based on conserved sequence regions, either known or suspected, such as conserved coding regions. The successful production of a PCR product using degenerate probes generated from the sequences identified herein would indicate the presence of a homologous gene sequence in the species being screened. The PCR primers are at least 10 bases, and preferably at least 20 bases in length. More preferably, the PCR primers are at least 20-30 bases in length. In some embodiments, the PCR primers can be more than 30 bases in length. It is preferred that the primer pairs have approximately the same G/C ratio, so that melting temperatures are approximately the same. A variety of PCR techniques are familiar to those skilled in the art. For a review of PCR technology, see Molecular Cloning to Genetic Engineering White, B.A. Ed. in **Methods in Molecular Biology** 67: Humana Press, Totowa 1997. When the entire coding sequence of the target gene is known, the 5' and 3' regions of the target gene can be used as the sequence source for PCR probe generation. In each of these PCR procedures, PCR primers on either side of the nucleic acid sequences to be amplified are added to a suitably prepared nucleic acid sample along with dNTPs and a thermostable polymerase such as Taq polymerase, Pfu polymerase, or Vent polymerase. The nucleic acid in the sample is denatured and the PCR primers are specifically hybridized to complementary nucleic acid sequences in the sample. The hybridized primers are extended. Thereafter, another cycle of denaturation, hybridization, and extension is initiated. The cycles are repeated multiple times to produce an amplified fragment containing the nucleic acid sequence between the primer sites.

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EXAMPLE 15

Inverse PCR

The technique of inverse polymerase chain reaction can be used to extend the known nucleic acid sequence identified in Examples 5 and 6. The inverse PCR reaction is described generally by Ochman et al., in Ch. 10 of **PCR Technology: Principles and Applications for DNA Amplification**, (Henry A. Erlich, Ed.) W.H. Freeman and Co. (1992). Traditional PCR requires two primers that are

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used to prime the synthesis of complementary strands of DNA. In inverse PCR, only a core sequence need be known.

Using the sequences identified as relevant from the techniques taught in Examples 5 and 6 and applied to other species of bacteria, a subset of exogenous nucleic sequences are identified that correspond to genes or operons that are required for bacterial proliferation. In species for which a genome sequence is not known, the technique of inverse PCR provides a method for obtaining the gene in order to determine the sequence or to place the probe sequences in full context to the target sequence to which the identified exogenous nucleic acid sequence binds.

To practice this technique, the genome of the target organism is digested with an appropriate restriction enzyme so as to create fragments of nucleic acid that contain the identified sequence as well as unknown sequences that flank the identified sequence. These fragments are then circularized and become the template for the PCR reaction. PCR primers are designed in accordance with the teachings of Example 15 and directed to the ends of the identified sequence are synthesized. The primers direct nucleic acid synthesis away from the known sequence and toward the unknown sequence contained within the circularized template. After the PCR reaction is complete, the resulting PCR products can be sequenced so as to extend the sequence of the identified gene past the core sequence of the identified exogenous nucleic acid sequence identified. In this manner, the full sequence of each novel gene can be identified. Additionally the sequences of adjacent coding and noncoding regions can be identified.

EXAMPLE 16

Identification of Genes Required for *Staphylococcus aureus* Proliferation

Genes required for proliferation in *Staphylococcus aureus* are identified according to the methods described above.

EXAMPLE 17

Identification of Genes Required for *Neisseria gonorrhoeae* Proliferation

Genes required for proliferation in *Neisseria gonorrhoeae* are identified according to the methods described above.

EXAMPLE 18

Identification of Genes Required for *Pseudomonas aeruginosa* Proliferation

Genes required for proliferation in *Pseudomonas aeruginosa* are identified according to the methods described above.

EXAMPLE 19

Identification of Genes Required for *Enterococcus faecalis* Proliferation

Genes required for proliferation in *Enterococcus faecalis* are identified according to the methods described above.

EXAMPLE 20**Identification of Genes Required for *Haemophilus influenzae* Proliferation**

Genes required for proliferation in *Haemophilus influenzae* are identified according to the methods described above.

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EXAMPLE 21**Identification of Genes Required for *Salmonella typhimurium* Proliferation**

Genes required for proliferation in *Salmonella typhimurium* are identified according to the methods described above.

EXAMPLE 22

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Identification of Genes Required for *Helicobacter pylori* Proliferation

Genes required for proliferation in *Helicobacter pylori* are identified according to the methods described above.

EXAMPLE 23**Identification of Genes Required for *Mycoplasma pneumoniae* Proliferation**

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Genes required for proliferation in *Mycoplasma pneumoniae* are identified according to the methods described above.

EXAMPLE 24**Identification of Genes Required for *Plasmodium ovale* Proliferation**

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Genes required for proliferation in *Plasmodium ovale* are identified according to the methods described above.

EXAMPLE 25**Identification of Genes Required for *Saccharomyces cerevisiae* Proliferation**

Genes required for proliferation in *Saccharomyces cerevisiae* are identified according to the methods described above.

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EXAMPLE 26**Identification of Genes Required for *Entamoeba histolytica* Proliferation**

Genes required for proliferation in *Entamoeba histolytica* are identified according to the methods described above.

EXAMPLE 27

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Identification of Genes Required for *Candida albicans* Proliferation

Genes required for proliferation in *Candida albicans* are identified according to the methods described above.

EXAMPLE 28**Identification of Genes Required for *Klebsiella pneumoniae* Proliferation**

Genes required for proliferation in *Klebsiella pneumoniae* are identified according to the methods described above.

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EXAMPLE 29**Identification of Genes Required for *Salmonella typhi* Proliferation**

Genes required for proliferation in *Salmonella typhi* are identified according to the methods described above.

EXAMPLE 30

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Identification of Genes Required for *Salmonella paratyphi* Proliferation

Genes required for proliferation in *Salmonella paratyphi* are identified according to the methods described above.

EXAMPLE 31**Identification of Genes Required for *Salmonella choleraesuis* Proliferation**

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Genes required for proliferation in *Salmonella choleraesuis* are identified according to the methods described above.

EXAMPLE 32**Identification of Genes Required for *Staphylococcus epidermis* Proliferation**

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Genes required for proliferation in *Staphylococcus epidermis* are identified according to the methods described above.

EXAMPLE 33**Identification of Genes Required for *Mycobacterium tuberculosis* Proliferation**

Genes required for proliferation in *Mycobacterium tuberculosis* are identified according to the methods described above.

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EXAMPLE 34**Identification of Genes Required for *Mycobacterium leprae* Proliferation**

Genes required for proliferation in *Mycobacterium leprae* are identified according to the methods described above.

EXAMPLE 35

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Identification of Genes Required for *Treponema pallidum* Proliferation

Genes required for proliferation in *Treponema pallidum* are identified according to the methods described above.

EXAMPLE 36**Identification of Genes Required for *Bacillus anthracis* Proliferation**

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Genes required for proliferation in *Bacillus anthracis* are identified according to the methods described above.

EXAMPLE 37**Identification of Genes Required for *Yersinia pestis* Proliferation**

Genes required for proliferation in *Yersinia pestis* are identified according to the methods described above.

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EXAMPLE 38**Identification of Genes Required for *Clostridium botulinum* Proliferation**

Genes required for proliferation in *Clostridium botulinum* are identified according to the methods described above.

EXAMPLE 39

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Identification of Genes Required for *Campylobacter jejuni* Proliferation

Genes required for proliferation in *Campylobacter jejuni* are identified according to the methods described above.

EXAMPLE 40**Identification of Genes Required for *Chlamydia trachomatis* Proliferation**

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Genes required for proliferation in *Chlamydia trachomatis* are identified according to the methods described above.

Use of Isolated Exogenous Nucleic Acid Fragments as Antisense Antibiotics

In addition to using the identified sequences to enable screening of molecule libraries to identify compounds useful to identify antibiotics, the sequences themselves can be used as therapeutic agents. Specifically, the identified exogenous sequences in an antisense orientation can be provided to an individual to inhibit the translation of a bacterial target gene.

Generation of Antisense Therapeutics from Identified Exogenous Sequences

The sequences of the present invention can be used as antisense therapeutics for the treatment of bacterial infections or simply for inhibition of bacterial growth *in vitro* or *in vivo*. The therapy exploits the biological process in cells where genes are transcribed into messenger RNA (mRNA) that is then translated into proteins. Antisense RNA technology contemplates the use of antisense oligonucleotides directed against a target gene that will bind to its target and decrease or inhibit the translation of the target mRNA. In one embodiment, antisense oligonucleotides can be used to treat and control a bacterial infection of a cell culture containing a population of desired cells contaminated with bacteria. In another embodiment, the antisense oligonucleotides can be used to treat an organism with a bacterial infection.

Antisense oligonucleotides can be synthesized from any of the sequences of the present invention using methods well known in the art. In a preferred embodiment, antisense oligonucleotides are synthesized using artificial means. Uhlmann & Peymann, Chemical Rev. 90:543-584 (1990) review antisense oligonucleotide technology in detail. Modified or unmodified

antisense oligonucleotides can be used as therapeutic agents. Modified antisense oligonucleotides are preferred since it is well known that antisense oligonucleotides are extremely unstable. Modification of the phosphate backbones of the antisense oligonucleotides can be achieved by substituting the internucleotide phosphate residues with methylphosphonates, phosphorothioates, 5 phosphoramidates, and phosphate esters. Nonphosphate internucleotide analogs such as siloxane bridges, carbonate bridges, thioester bridges, as well as many others known in the art. The preparation of certain antisense oligonucleotides with modified internucleotide linkages is described in U.S. Patent No. 5,142,047.

10 Modifications to the nucleoside units of the antisense oligonucleotides are also contemplated. These modifications can increase the half-life and increase cellular rates of uptake for the oligonucleotides *in vivo*. For example, α -anomeric nucleotide units and modified bases such as 1,2-dideoxy-d-ribofuranose, 1,2-dideoxy-1-phenylribofuranose, and N^4 , N^4 -ethano-5-methyl-cytosine are contemplated for use in the present invention.

An additional form of modified antisense molecules is found in peptide nucleic acids. 15 Peptide nucleic acids (PNA) have been developed to hybridize to single and double stranded nucleic acids. PNA are nucleic acid analogs in which the entire deoxyribose-phosphate backbone has been exchanged with a chemically completely different, but structurally homologous, polyamide (peptide) backbone containing 2-aminoethyl glycine units. Unlike DNA, which is highly negatively charged, the PNA backbone is neutral. Therefore, there is much less repulsive energy between complementary 20 strands in a PNA-DNA hybrid than in the comparable DNA-DNA hybrid, and consequently they are much more stable. PNA can hybridize to DNA in either a Watson/Crick or Hoogsteen fashion (Demidov et al., *Proc. Natl. Acad. Sci. U.S.A.* 92:2637-2641, 1995; Egholm, *Nature* 365:566-568, 1993; Nielsen et al., *Science* 254:1497-1500, 1991; Dueholm et al., *New J. Chem.* 21:19-31, 1997).

Molecules called PNA "clamps" have been synthesized which have two identical PNA 25 sequences joined by a flexible hairpin linker containing three 8-amino-3,6-dioxaoctanoic acid units. When a PNA clamp is mixed with a complementary homopurine or homopyrimidine DNA target sequence, a PNA-DNA-PNA triplex hybrid can form which has been shown to be extremely stable (Bentin et al., *Biochemistry* 35:8863-8869, 1996; Egholm et al., *Nucleic Acids Res.* 23:217-222, 1995; Griffith et al., *J. Am. Chem. Soc.* 117:831-832, 1995).

30 The sequence-specific and high affinity duplex and triplex binding of PNA have been extensively described (Nielsen et al., *Science* 254:1497-1500, 1991; Egholm et al., *J. Am. Chem. Soc.* 114:9677-9678, 1992; Egholm et al., *Nature* 365:566-568, 1993; Almarsson et al., *Proc. Natl. Acad. Sci. U.S.A.* 90:9542-9546, 1993; Demidov et al., *Proc. Natl. Acad. Sci. U.S.A.* 92:2637-2641, 1995). They have also been shown to be resistant to nuclease and protease digestion (Demidov et al., 35 *Biochem. Pharm.* 48:1010-1313, 1994). PNA has been used to inhibit gene expression (Hanvey et al., *Science* 258:1481-1485, 1992; Nielsen et al., *Nucl. Acids. Res.*, 21:197-200, 1993; Nielsen et al., *Gene*

149:139-145, 1994; Good & Nielsen, *Science*, 95: 2073-2076, 1998), to block restriction enzyme activity (Nielsen et al., *supra*, 1993), to act as an artificial transcription promoter (Mollegaard, *Proc. Natl. Acad. Sci. U.S.A.* 91:3892-3895, 1994) and as a pseudo restriction endonuclease (Demidov et al., *Nucl. Acids. Res.* 21:2103-2107, 1993). Recently, PNA has also been shown to have antiviral and antitumoral activity mediated through an antisense mechanism (Norton, *Nature Biotechnol.*, 14:615-619, 1996; Hirschman et al., *J. Investig. Med.* 44:347-351, 1996). PNAs have been linked to various peptides in order to promote PNA entry into cells (Basu et al., *Bioconj. Chem.* 8:481-488, 1997; Pardridge et al., *Proc. Natl. Acad. Sci. U.S.A.* 92:5592-5596, 1995).

The antisense oligonucleotides contemplated by the present invention can be administered by direct application of oligonucleotides to a target using standard techniques well known in the art. The antisense oligonucleotides can be generated within the target using a plasmid, or a phage. Alternatively, the antisense nucleic acid may be expressed from a sequence in the chromosome of the target cell. It is further contemplated that the antisense oligonucleotide contemplated are incorporated in a ribozyme sequence to enable the antisense to specifically bind and cleave its target mRNA. For technical applications of ribozyme and antisense oligonucleotides see Rossi et al., *Pharmacol. Ther.* 50(2):245-254, (1991). The present invention also contemplates using a retron to introduce an antisense oligonucleotide to a cell. Retron technology is exemplified by U.S. Patent No. 5,405,775. Antisense oligonucleotides can also be delivered using liposomes or by electroporation techniques which are well known in the art.

The antisense nucleic acids of the present invention can also be used to design antibiotic compounds comprising nucleic acids which function by intracellular triple helix formation. Triple helix oligonucleotides are used to inhibit transcription from a genome. The sequences identified as required for proliferation in the present invention, or portions thereof, can be used as templates to inhibit microorganism gene expression in individuals infected with such organisms. Traditionally, homopurine sequences were considered the most useful for triple helix strategies. However, homopyrimidine sequences can also inhibit gene expression. Such homopyrimidine oligonucleotides bind to the major groove at homopurine:homopyrimidine sequences. Thus, both types of sequences based on the sequences of the present invention that are required for proliferation are contemplated for use as antibiotic compound templates.

The antisense oligonucleotides of this example employ the identified sequences of the present invention to induce bacterial cell death or at least bacterial stasis by inhibiting target gene translation. Antisense oligonucleotides containing from about 8 to 40 bases of the sequences of the present invention have sufficient complementarity to form a duplex with the target sequence under physiological conditions.

To kill bacterial cells or inhibit their growth, the antisense oligonucleotides are applied to the bacteria or to the target cells under conditions that facilitate their uptake. These conditions

include sufficient incubation times of cells and oligonucleotides so that the antisense oligonucleotides are taken up by the cells. In one embodiment, an incubation period of 7-10 days is sufficient to kill bacteria in a sample. An optimum concentration of antisense oligonucleotides is selected for use.

5 The concentration of antisense oligonucleotides to be used can vary depending on the type of bacteria sought to be controlled, the nature of the antisense oligonucleotide to be used, and the relative toxicity of the antisense oligonucleotide to the desired cells in the treated culture. Antisense oligonucleotides can be introduced to cell samples at a number of different concentrations preferably between $1 \times 10^{-10} \text{M}$ to $1 \times 10^{-4} \text{M}$. Once the minimum concentration that can adequately
10 control gene expression is identified, the optimized dose is translated into a dosage suitable for use *in vivo*. For example, an inhibiting concentration in culture of 1×10^{-7} translates into a dose of approximately 0.6 mg/kg body weight. Levels of oligonucleotide approaching 100 mg/kg body weight or higher may be possible after testing the toxicity of the oligonucleotide in laboratory animals. It is additionally contemplated that cells from the subject are removed, treated with the antisense
15 oligonucleotide, and reintroduced into the subject. This range is merely illustrative and one of skill in the art are able to determine the optimal concentration to be used in a given case.

After the bacterial cells have been killed or controlled in a desired culture, the desired cell population may be used for other purposes.

EXAMPLE 41

20 The following example demonstrates the ability of an *E. coli* antisense oligonucleotide to act as a bactericidal or bacteriostatic agent to treat a contaminated cell culture system. The application of the antisense oligonucleotides of the present invention are thought to inhibit the translation of bacterial gene products required for proliferation.

 The antisense oligonucleotide of this example corresponds to a 30 base phosphorothioate
25 modified oligodeoxynucleotide complementary to a nucleic acid involved in proliferation, such as Molecule Number EcXA056 (SEQ ID NO: 1). A sense oligodeoxynucleotide complementary to the antisense sequence is synthesized and used as a control. The oligonucleotides are synthesized and purified according to the procedures of Matsukura, et al., Gene 72:343 (1988). The test oligonucleotides are dissolved in a small volume of autoclaved water and added to culture medium
30 to make a 100 micromolar stock solution.

Human bone marrow cells are obtained from the peripheral blood of two patients and cultured according standard procedures well known in the art. The culture is contaminated with the K-12 strain of *E. coli* and incubated at 37°C overnight to establish bacterial infection.

 The control and antisense oligonucleotide containing solutions are added to the
35 contaminated cultures and monitored for bacterial growth. After a 10 hour incubation of culture and oligonucleotides, samples from the control and experimental cultures are drawn and analyzed

for the translation of the target bacterial gene using standard microbiological techniques well known in the art. The target *E. coli* gene is found to be translated in the control culture treated with the control oligonucleotide, however, translation of the target gene in the experimental culture treated with the antisense oligonucleotide of the present invention is not detected or reduced.

5

EXAMPLE 42

A subject suffering from an *E. coli* infection is treated with the antisense oligonucleotide preparation of Example 39. The antisense oligonucleotide is provided in a pharmaceutically acceptable carrier at a concentration effective to inhibit the translation of the target gene. The present subject is treated with a concentration of antisense oligonucleotide sufficient to achieve a blood concentration of about 100 micromolar. The patient receives daily injections of antisense oligonucleotide to maintain this concentration for a period of 1 week. At the end of the week a blood sample is drawn and analyzed for the presence or absence using standard techniques well known in the art. There is no detectable evidence of *E. coli* and the treatment is terminated.

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EXAMPLE 43

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Preparation and use of Triple Helix Probes

The sequences of microorganism genes required for proliferation of the present invention are scanned to identify 10-mer to 20-mer homopyrimidine or homopurine stretches that could be used in triple-helix based strategies for inhibiting gene expression. Following identification of candidate homopyrimidine or homopurine stretches, their efficiency in inhibiting gene expression is assessed by introducing varying amounts of oligonucleotides containing the candidate sequences into a population of bacterial cells that normally express the target gene. The oligonucleotides may be prepared on an oligonucleotide synthesizer or they may be purchased commercially from a company specializing in custom oligonucleotide synthesis, such as GENSET, Paris, France.

20

The oligonucleotides can be introduced into the cells using a variety of methods known to those skilled in the art, including but not limited to calcium phosphate precipitation, DEAE-Dextran, electroporation, liposome-mediated transfection or native uptake.

25

Treated cells are monitored for a reduction in proliferation using techniques such as monitoring growth levels as compared to untreated cells using optical density measurements. The oligonucleotides that are effective in inhibiting gene expression in cultured cells can then be introduced *in vivo* using the techniques well known in that art at a dosage level shown to be effective.

30

In some embodiments, the natural (beta) anomers of the oligonucleotide units can be replaced with alpha anomers to render the oligonucleotide more resistant to nucleases. Further, an intercalating agent such as ethidium bromide, or the like, can be attached to the 3' end of the alpha oligonucleotide to stabilize the triple helix. For information on the generation of oligonucleotides suitable for triple helix formation see Griffin et al. (*Science* 245:967-971 (1989)).

35

EXAMPLE 44**Identification of Bacterial Strains from Isolated Specimens by PCR**

Classical bacteriological methods for the detection of various bacterial species are time consuming and costly. These methods include growing the bacteria isolated from a subject in specialized media, cultivation on selective agar media, followed by a set of confirmation assays that can take from 8 to 10 days or longer to complete. Use of the identified sequences of the present invention provides a method to dramatically reduce the time necessary to detect and identify specific bacterial species present in a sample.

In one exemplary method, bacteria are grown in enriched media and DNA samples are isolated from specimens of, for example, blood, urine, stool, saliva or central nervous system fluid by conventional methods. A panel of PCR primers based on identified sequences unique to various species of microorganisms are then utilized in accordance with Example 12 to amplify DNA of approximately 100-200 bases in length from the specimen. A separate PCR reaction is set up for each pair of PCR primers and after the PCR reaction is complete, the reaction mixtures are assayed for the presence of PCR product. The presence or absence of bacteria from the species to which the PCR primer pairs belong is determined by the presence or absence of a PCR product in the various test PCR reaction tubes.

Although the PCR reaction is used to assay the isolated sample for the presence of various bacterial species, other assays such as the Southern blot hybridization are also contemplated.

20

WHAT IS CLAIMED IS:

1. A purified or isolated nucleic acid sequence consisting essentially of one of SEQ ID NOs: 1-127, wherein expression of said nucleic acid inhibits proliferation of a microorganism.
2. The nucleic acid sequence of Claim 1, wherein said nucleic acid sequence is complementary to at least a portion of a coding sequence of a gene whose expression is required for proliferation of a microorganism.
3. The nucleic acid of Claim 1, wherein said nucleic acid sequence is complementary to at least a portion of an RNA required for proliferation of a microorganism.
4. The nucleic acid of Claim 3, wherein said RNA is an RNA encoding more than one gene product.
5. A nucleic acid comprising a fragment of one of SEQ ID NOs: 1-127, said fragment selected from the group consisting of fragments comprising at least 10, at least 20, at least 25, at least 30, at least 50 and more than 50 consecutive bases of one of SEQ ID NOs: 1-127.
6. A vector comprising a promoter operably linked to the nucleic acid sequence of Claims 1,2,3,4, or 5.
7. The vector of Claim 6, wherein said promoter is active in a microorganism selected from the group consisting of *Aspergillus fumigatus*, *Bacillus anthracis*, *Campylobacter jejuni*, *Candida albicans*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Pseudomonas aeruginosa*, *Saccharomyces cerevisiae*, *Salmonella choleraesuis*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Treponema pallidum*, and *Yersinia pestis* or any species falling within the genera of any of the above species.
8. A host cell containing the vector of Claim 6 or Claim 7.
9. A purified or isolated nucleic acid consisting essentially of the coding sequence of one of SEQ ID NOs: 128-298.
10. A fragment of the nucleic acid of Claim 8, said fragment comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive bases of one of SEQ ID NOs: 128-298.
11. A vector comprising a promoter operably linked to the nucleic acid of Claim 9 or Claim 10.
12. A purified or isolated antisense nucleic acid comprising a nucleic acid sequence complementary to at least a portion of an intragenic sequence, intergenic sequence, sequences spanning at least a portion of two or more genes, 5' noncoding region, or 3' noncoding region

within an operon comprising a proliferation-required gene whose activity or expression is inhibited by an antisense nucleic acid comprising one of SEQ ID NOs.: 1-127.

13. A purified or isolated nucleic acid comprising a nucleic acid having at least 70% identity to a sequence selected from the group consisting of SEQ ID NOs.: 1-127, fragments comprising at least 25 consecutive nucleotides of SEQ ID NOs.: 1-127, the sequences complementary to SEQ ID NOs.: 1-127 and the sequences complementary to fragments comprising at least 25 consecutive nucleotides of SEQ ID NOs.: 1-127 as determined using BLASTN version 2.0 with the default parameters.

14. The nucleic acid of Claim 13, wherein said nucleic acid is from an organism selected from the group consisting of *Aspergillus fumigatus*, *Bacillus anthracis*, *Campylobacter jejuni*, *Candida albicans*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Staphylococcus aureus*, *Haemophilus influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Pseudomonas aeruginosa*, *Saccharomyces cerevisiae*, *Salmonella choleraesuis*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Treponema pallidum*, and *Yersinia pestis* or any species falling within the genera of any of the above species.

15. A vector comprising a promoter operably linked to a nucleic acid encoding a polypeptide whose expression is inhibited by an antisense nucleic acid comprising one of SEQ ID NOs.: 1-127.

16. A host cell containing the vector of Claim 16.

17. The vector of Claim 15, wherein said polypeptide comprises a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs: 299-469.

18. A purified or isolated polypeptide comprising a polypeptide whose expression is inhibited by an antisense nucleic acid comprising one of SEQ ID NOs.: 1-127, or a fragment selected from the group consisting of fragments comprising at least 5, at least 10, at least 20, at least 30, at least 40, at least 50, at least 60 or more than 60 consecutive amino acids of one of the said polypeptides.

19. The polypeptide of Claim 18, wherein said polypeptide comprises a polypeptide comprising one of SEQ ID NOs.: 299-469 or a fragment comprising at least 5, at least 10, at least 20, at least 30, at least 40, at least 50, at least 60 or more than 60 consecutive amino acids of a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 299-469.

20. A purified or isolated polypeptide comprising a polypeptide having at least 25% identity to a polypeptide whose expression is inhibited by a sequence selected from the group consisting of SEQ ID NOs.: 1-127, or at least 25% identity to a fragment comprising at least 5, at

least 10, at least 20, at least 30, at least 40, at least 50, at least 60 or more than 60 consecutive amino acids of a polypeptide whose expression is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-127 as determined using FASTA version 3.0t78 with the default parameters.

5 21. The polypeptide of Claim 20, wherein said polypeptide has at least 25% identity to a polypeptide comprising one of SEQ ID NOs.: 299-469 or at least 25% identity to a fragment comprising at least 5, at least 10, at least 20, at least 30, at least 40, at least 50, at least 60 or more than 60 consecutive amino acids of a polypeptide comprising one of SEQ ID NOs.: 299-469 as determined using FASTA version 3.0t78 with the default parameters.

10 22. An antibody capable of specifically binding the polypeptide of one of Claims 18-21.

 23. A method of producing a polypeptide, comprising introducing a vector comprising a promoter operably linked to a nucleic acid encoding a polypeptide whose expression is inhibited by an antisense nucleic acid comprising one of SEQ ID NOs.: 1-127 into a cell.

15 24. The method of Claim 23, further comprising the step of isolating said polypeptide.

 25. The method of Claim 23, wherein said polypeptide comprises a sequence selected from the group consisting of SEQ ID NOs.: 299-469.

 26. A method of inhibiting proliferation of a microorganism comprising inhibiting the activity or reducing the amount of a gene product whose expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-127 or inhibiting the activity or reducing the amount of a nucleic acid encoding said gene product.

 27. The method of Claim 26, wherein said gene product comprises a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 299-469.

 28. A method for identifying a compound which influences the activity of a gene product required for proliferation, said gene product comprising a gene product whose expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-127, said method comprising:

 contacting said gene product with a candidate compound; and

 determining whether said compound influences the activity of said gene product.

30 29. The method of Claim 28, wherein said gene product is a polypeptide and said activity is an enzymatic activity.

 30. The method of Claim 28, wherein said gene product is a polypeptide and said activity is a carbon compound catabolism activity.

 31. The method of Claim 28, wherein said gene product is a polypeptide and said activity is a biosynthetic activity.

32. The method of Claim 28, wherein said gene product is a polypeptide and said activity is a transporter activity.

33. The method of Claim 28, wherein said gene product is a polypeptide and said activity is a transcriptional activity.

5 34. The method of Claim 28, wherein said gene product is a polypeptide and said activity is a DNA replication activity.

35. The method of Claim 28, wherein said gene product is a polypeptide and said activity is a cell division activity.

36. A compound identified using the method of Claim 28.

10 37. The method of Claim 28, wherein said gene product is a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 299-469.

38. A method for identifying a compound or nucleic acid having the ability to reduce the activity or level of a gene product required for proliferation, said gene product comprising a gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-127, said method comprising:

(a) providing a target that is a gene or RNA, wherein said target comprises a nucleic acid encoding said gene product;

(b) contacting said target with a candidate compound or nucleic acid; and

(c) measuring an activity of said target.

20 39. The method of Claim 38, wherein said target is a messenger RNA molecule and said activity is translation of said messenger RNA.

40. The method of Claim 38, wherein said target is a messenger RNA molecule and said activity is transcription of a gene encoding said messenger RNA.

25 41. The method of Claim 38, wherein said target is a gene and said activity is transcription of said gene.

42. The method of Claim 38, wherein said target is a nontranslated RNA and said activity is processing or folding of said nontranslated RNA or assembly of said nontranslated RNA into a protein/RNA complex.

30 43. The method of Claim 38, wherein said target gene or RNA encodes a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 299-469.

44. A compound or nucleic acid identified using the method of Claim 38.

35 45. A method for identifying a compound which reduces the activity or level of a gene product required for proliferation of a microorganism, wherein the activity or expression of said gene product is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-127, said method comprising the steps of:

(a) expressing a sublethal level of an antisense nucleic acid complementary to a nucleic acid encoding said gene product in a cell to reduce the activity or amount of said gene product in said cell, thereby producing a sensitized cell;

(b) contacting said sensitized cell with a compound; and

5 (c) determining whether said compound inhibits the growth of said sensitized cell.

46. The method of Claim 45, wherein said determining step comprises determining whether said compound inhibits the growth of said sensitized cell to a greater extent than said compound inhibits the growth of a nonsensitized cell.

10 47. The method of Claim 45, wherein said cell is selected from the group consisting of bacterial cells, fungal cells, plant cells, and animal cells.

48. The method of Claim 45, wherein said cell is a Gram negative bacterium.

49. The method of Claim 45, wherein said cell is an *E. coli* cell.

15 50. The method of Claim 45, wherein said cell is from an organism selected from the group consisting of *Aspergillus fumigatus*, *Bacillus anthracis*, *Campylobacter jejuni*, *Candida albicans*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Haemophilus influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Pseudomonas aeruginosa*, *Saccharomyces cerevisiae*, *Salmonella choleraesuis*,
20 *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Treponema pallidum*, and *Yersinia pestis* or any species falling within the genera of any of the above species.

51. The method of Claim 45, wherein said antisense nucleic acid is transcribed from an inducible promoter.

25 52. The method of Claim 51, further comprising the step of contacting said cell with a concentration of inducer which induces said antisense nucleic acid to a sublethal level.

53. The method of Claim 45, wherein growth inhibition is measured by monitoring optical density of a culture growth solution.

54. The method of Claim 45, wherein said gene product is a polypeptide.

30 55. The method of Claim 54, wherein said polypeptide comprises a sequence selected from the group consisting of SEQ ID NOs.: 299-469.

56. The method of Claim 45, wherein said gene product is an RNA.

57. A compound identified using the method of Claim 45.

35 58. A method for inhibiting cellular proliferation comprising introducing a compound with activity against a gene whose activity or expression is inhibited by an antisense nucleic acid

comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-127 or a compound with activity against the product of said gene into a population of cells expressing said gene.

5 59. The method of Claim 58, wherein said compound is an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-127, or a proliferation-inhibiting portion thereof.

60. The method of Claim 59, wherein said proliferation inhibiting portion of one of SEQ ID NOs.: 1-127 is a fragment comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 51 consecutive bases of one of SEQ ID NOs.: 1-127.

10 61. The method of Claim 58, wherein said population is a population selected from the group consisting of bacterial cells, fungal cells, plant cells, and animal cells.

62. The method of Claim 58, wherein said population is a population of Gram negative bacteria.

63. The method of Claim 58, wherein said population is a population of *E. coli* cells.

15 64. The method of Claim 58, wherein said population is a population selected from the group consisting of *Aspergillus fumigatus*, *Bacillus anthracis*, *Campylobacter jejuni*, *Candida albicans*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Haemophilus influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Pseudomonas aeruginosa*, *Saccharomyces cerevisiae*, *Salmonella choleraesuis*,
20 *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Treponema pallidum*, and *Yersinia pestis* cells or cells from any species falling within the genera of any of the above species.

65. The method of Claim 58, wherein said gene encodes a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 299-469.

25 66. A preparation comprising an effective concentration of an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-127, or a proliferation-inhibiting portion thereof in a pharmaceutically acceptable carrier.

67. The preparation of Claim 66, wherein said proliferation-inhibiting portion of one of SEQ ID NOs.: 1-127 comprises at least 10, at least 20, at least 25, at least 30, at least 50 or more
30 than 50 consecutive bases of one of SEQ ID NOs.: 1-127.

68. A method for inhibiting the activity or expression of a gene in an operon required for proliferation wherein the activity or expression of at least one gene in said operon is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-127, said method comprising contacting a cell in a cell population with an antisense nucleic
35 acid comprising at least a proliferation-inhibiting portion of said operon.

69. The method of Claim 68, wherein said antisense nucleic acid comprises a sequence selected from the group consisting of SEQ ID NOs.: 1-127 or a proliferation inhibiting portion thereof.

70. The method of Claim 68, wherein said cell is contacted with said antisense nucleic acid by introducing a plasmid which expresses said antisense nucleic acid into said cell population.

71. The method of Claim 68, wherein said cell is contacted with said antisense nucleic acid by introducing a phage which expresses said antisense nucleic acid into said cell population.

72. The method of Claim 68, wherein said cell is contacted with said antisense nucleic acid by expressing said antisense nucleic acid from the chromosome of cells in said cell population.

73. The method of Claim 68, wherein said cell is contacted with said antisense nucleic acid by introducing a promoter adjacent to a chromosomal copy of said antisense nucleic acid such that said promoter directs the synthesis of said antisense nucleic acid.

74. The method of Claim 68, wherein said cell is contacted with said antisense nucleic acid by introducing a retron which expresses said antisense nucleic acid into said cell population.

75. The method of Claim 68, wherein said cell is contacted with said antisense nucleic acid by introducing a ribozyme into said cell-population, wherein a binding portion of said ribozyme is complementary to said antisense oligonucleotide.

76. The method of Claim 68, wherein said cell is contacted with said antisense nucleic acid by introducing a liposome comprising said antisense oligonucleotide into said cell.

77. The method of Claim 68, wherein said cell is contacted with said antisense nucleic acid by electroporation of said antisense nucleic acid.

78. The method of Claim 68, wherein said antisense nucleic acid is a fragment comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive bases of one of SEQ ID NOs.: 1-127.

79. The method of Claim 68 wherein said antisense nucleic acid is an oligonucleotide.

80. A method for identifying a gene which is required for proliferation of a microorganism comprising:

(a) contacting a microorganism other than *E. coli* with a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-127;

(b) determining whether said nucleic acid inhibits proliferation of said microorganism; and

(c) identifying the gene in said microorganism which is inhibited by said nucleic acid.

81. The method of Claim 80, wherein said microorganism is a Gram negative bacterium.

82. The method of Claim 80 wherein said microorganism is selected from the group consisting of *Aspergillus fumigatus*, *Bacillus anthracis*, *Campylobacter jejuni*, *Candida albicans*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Haemophilus influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Pseudomonas aeruginosa*, *Saccharomyces cerevisiae*, *Salmonella choleraesuis*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Treponema pallidum*, and *Yersinia pestis* or any species falling within the genera of any of the above species.

83. The method of Claim 80, further comprising introducing said nucleic acid into a vector functional in said microorganism prior to introducing said inhibitory nucleic acid into said microorganism.

84. A method for identifying a compound having the ability to inhibit proliferation of a microorganism comprising:

(a) identifying in a first microorganism a homolog of a gene or gene product present in a second microorganism which is different than said first microorganism, wherein the activity or level of said gene or gene product is inhibited by a nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs. 1-127 ;

(b) identifying an inhibitory nucleic acid sequence which inhibits the activity of said homolog in said first microorganism;

(c) contacting said first microorganism with a sublethal level of said inhibitory nucleic acid, thus sensitizing said first microorganism;

(d) contacting the sensitized microorganism of step (c) with a compound; and

(e) determining whether said compound inhibits proliferation of said sensitized microorganism.

85. The method of Claim 84, wherein said determining step comprises determining whether said compound inhibits proliferation of said sensitized microorganism to a greater extent than said compound inhibits proliferation of a nonsensitized microorganism.

86. The method of Claim 84 wherein step (a) comprises identifying a homologous nucleic acid to a gene or gene product whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs. 1-127 or a nucleic acid encoding a homologous polypeptide to a polypeptide whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs. 1-127 by using an algorithm selected from the group consisting of BLASTN version 2.0 with the default parameters and FASTA version 3.0t78 algorithm with the default parameters to identify said homologous nucleic acid or said nucleic acid encoding a homologous polypeptide in a database.

87. The method of Claim 84 wherein said step (a) comprises identifying a homologous nucleic acid or a nucleic acid encoding a homologous polypeptide by identifying nucleic acids which hybridize to said first gene.

88. The method of Claim 84 wherein the step (a) comprises expressing a nucleic acid
5 selected from the group consisting of SEQ ID NOs. 1-127 in said microorganism.

89. The method of Claim 84, wherein said inhibitory nucleic acid is an antisense nucleic acid.

90. The method of Claim 84, wherein said inhibitory nucleic acid comprises an antisense nucleic acid to a portion of said homolog.

10 91. The method of Claim 84, wherein said inhibitory nucleic acid comprises an antisense nucleic acid to a portion of the operon encoding said homolog.

92. The method of Claim 84, wherein the step of contacting the first microorganism with a sublethal level of said inhibitory nucleic acid comprises directly contacting said microorganism with said inhibitory nucleic acid.

15 93. The method of Claim 84, wherein the step of contacting the first microorganism with a sublethal level of said inhibitory nucleic acid comprises expressing an antisense nucleic acid to said homolog in said microorganism.

94. The method of Claim 84, wherein said gene product comprises a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 299-469.

20 95. A compound identified using the method of Claim 84.

96. A method of identifying a compound having the ability to inhibit proliferation comprising:

25 (a) contacting a microorganism other than *E. coli* with a sublethal level of a nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs. 1-127 or a portion thereof which inhibits the proliferation of *E. coli*, thus sensitizing said microorganism;

(b) contacting the sensitized microorganism of step (a) with a compound; and

(c) determining whether said compound inhibits proliferation of said sensitized microorganism.

30 97. The method of Claim 96, wherein said determining step comprises determining whether said compound inhibits proliferation of said sensitized microorganism to a greater extent than said compound inhibits proliferation of a nonsensitized microorganism.

98. A compound identified using the method of Claim 96.

35 99. A method for identifying a compound having activity against a biological pathway required for proliferation comprising:

(a) sensitizing a cell by expressing a sublethal level of an antisense nucleic acid complementary to a nucleic acid encoding a gene product required for proliferation, wherein the activity or expression of said gene product is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-127, in said cell to reduce the activity or amount of said gene product;

(b) contacting the sensitized cell with a compound; and

(c) determining whether said compound inhibits the growth of said sensitized cell.

100. The method of Claim 99, wherein said determining step comprises determining whether said compound inhibits the growth of said sensitized cell to a greater extent than said compound inhibits the growth of a nonsensitized cell.

101. The method of Claim 99, wherein said cell is selected from the group consisting of bacterial cells, fungal cells, plant cells, and animal cells.

102. The method of Claim 99, wherein said cell is a Gram negative bacterium.

103. The method of Claim 99, wherein said Gram negative bacterium is *E. coli*.

104. The method of Claim 99, wherein said cell is selected from the group consisting of *Aspergillus fumigatus*, *Bacillus anthracis*, *Campylobacter jejuni*, *Candida albicans*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Haemophilus influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Pseudomonas aeruginosa*, *Saccharomyces cerevisiae*, *Salmonella choleraesuis*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Treponema pallidum*, and *Yersinia pestis* or any species falling within the genera of any of the above species.

105. The method of Claim 99, wherein said antisense nucleic acid is transcribed from an inducible promoter.

106. The method of Claim 99, further comprising contacting the cell with an agent which induces expression of said antisense nucleic acid from said inducible promoter, wherein said antisense nucleic acid is expressed at a sublethal level.

107. The method of Claim 99, wherein inhibition of proliferation is measured by monitoring the optical density of a liquid culture.

108. The method of Claim 99, wherein said gene product comprises a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 299-469

109. A compound identified using the method of Claim 99.

110. A method for identifying a compound having the ability to inhibit cellular proliferation comprising:

(a) contacting a cell with an agent which reduces the activity or level of a gene product required for proliferation of said cell, wherein said gene product is a gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-127;

5 (b) contacting said cell with a compound; and

(c) determining whether said compound reduces proliferation of said contacted cell.

111. The method of Claim 110, wherein said determining step comprises determining whether said compound reduces proliferation of said contacted cell to a greater extent than said
10 compound reduces proliferation of cells which have not been contacted with said agent.

112. The method of Claim 110, wherein said agent which reduces the activity or level of a gene product required for proliferation of said cell comprises an antisense nucleic acid to a gene or operon required for proliferation.

113. The method of Claim 110, wherein said agent which reduces the activity or level of
15 a gene product required for proliferation of said cell comprises a compound known to inhibit growth or proliferation of a microorganism.

114. The method of Claim 110, wherein said cell contains a mutation which reduces the activity or level of said gene product required for proliferation of said cell.

115. The method of Claim 114, wherein said mutation is a temperature sensitive
20 mutation.

116. The method of Claim 110, wherein said gene product comprises a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 299-469

117. A compound identified using the method of Claim 110.

118. A method for identifying the biological pathway in which a proliferation-required
25 gene or its gene product lies, wherein said gene or gene product comprises a gene or gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-127, said method comprising:

(a) expressing a sublethal level of an antisense nucleic acid which inhibits the activity of said proliferation-required gene or gene product in a cell;

30 (b) contacting said cell with a compound known to inhibit growth or proliferation of a microorganism, wherein the biological pathway on which said compound acts is known; and

(c) determining whether said cell is sensitive to said compound.

119. The method of Claim 118, wherein said determining step comprises determining
35 whether said cell has a substantially greater sensitivity to said compound than a cell which does not express said sublethal level of said antisense nucleic acid and wherein said gene or gene product

lies in the same pathway on which said compound acts if said cell expressing said sublethal level of said antisense nucleic acid has a substantially greater sensitivity to said compound than said cell which does not express said sublethal level of said antisense nucleic acid.

120. The method of Claim 118, wherein said gene product comprises a polypeptide
5 comprising a sequence selected from the group consisting of SEQ ID NOs.: 299-469

121. A method for determining the biological pathway on which a test compound acts comprising:

(a) expressing a sublethal level of an antisense nucleic acid complementary to a proliferation-required nucleic acid in a cell, wherein the activity or expression of said proliferation-required nucleic acid is inhibited by an antisense nucleic acid comprising a
10 sequence selected from the group consisting of SEQ ID NOs.: 1-127 and wherein the biological pathway in which said proliferation-required nucleic acid or a protein encoded by said proliferation-required polypeptide lies is known,

(b) contacting said cell with said test compound; and

15 (c) determining whether said cell is sensitive to said test compound.

122. The method of Claim 121, wherein said determining step comprises determining whether said cell has a substantially greater sensitivity to said test compound than a cell which does not express said sublethal level of said antisense nucleic acid.

123. The method of Claim 121, further comprising:

20 (d) expressing a sublethal level of a second antisense nucleic acid complementary to a second proliferation-required nucleic acid in a second cell, wherein said second proliferation-required nucleic acid is in a different biological pathway than said proliferation-required nucleic acid in step (a); and

(e) determining whether said second cell does not have a substantially greater
25 sensitivity to said test compound than a cell which does not express said sublethal level of said second antisense nucleic acid, wherein said test compound is specific for the biological pathway against which the antisense nucleic acid of step (a) acts if said second cell does not have substantially greater sensitivity to said test compound.

124. A purified or isolated nucleic acid comprising a sequence selected from the group
30 consisting of SEQ ID NOs.: 1-127.

125. A compound which interacts with a gene or gene product whose activity or expression is inhibited by an antisense nucleic acid comprising one of SEQ ID NOs.: 1-127 to inhibit proliferation.

126. A compound which interacts with a polypeptide whose expression is inhibited by
35 an antisense nucleic acid comprising one of SEQ ID NOs.: 1-127 to inhibit proliferation.

127. A method for manufacturing an antibiotic comprising the steps of:

screening one or more candidate compounds to identify a compound that reduces the activity or level of a gene product required for proliferation, said gene product comprising a gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-127; and

5 manufacturing the compound so identified.

128. The method of Claim 127, wherein said screening step comprises performing any one of the methods of Claims 28, 38, 45, 96, 99 and 110.

129. A method for inhibiting proliferation of a microorganism in a subject comprising administering a compound that reduces the activity or level of a gene product required for proliferation of said microorganism, said gene product comprising a gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-127 to said subject.

130. The method of Claim 129 wherein said subject is selected from the group consisting of vertebrates, mammals, avians, and human beings.

15 131. The method of Claim 129, wherein said gene product comprises a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 299-469.

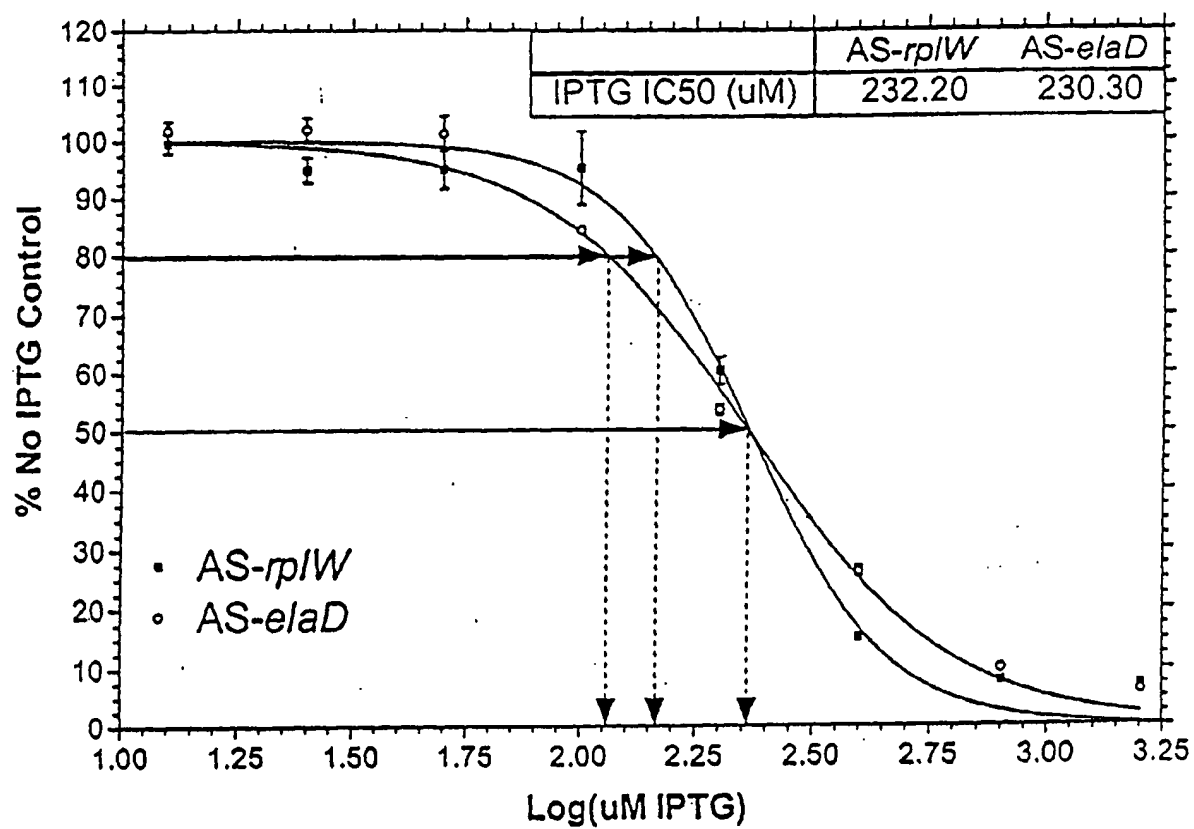
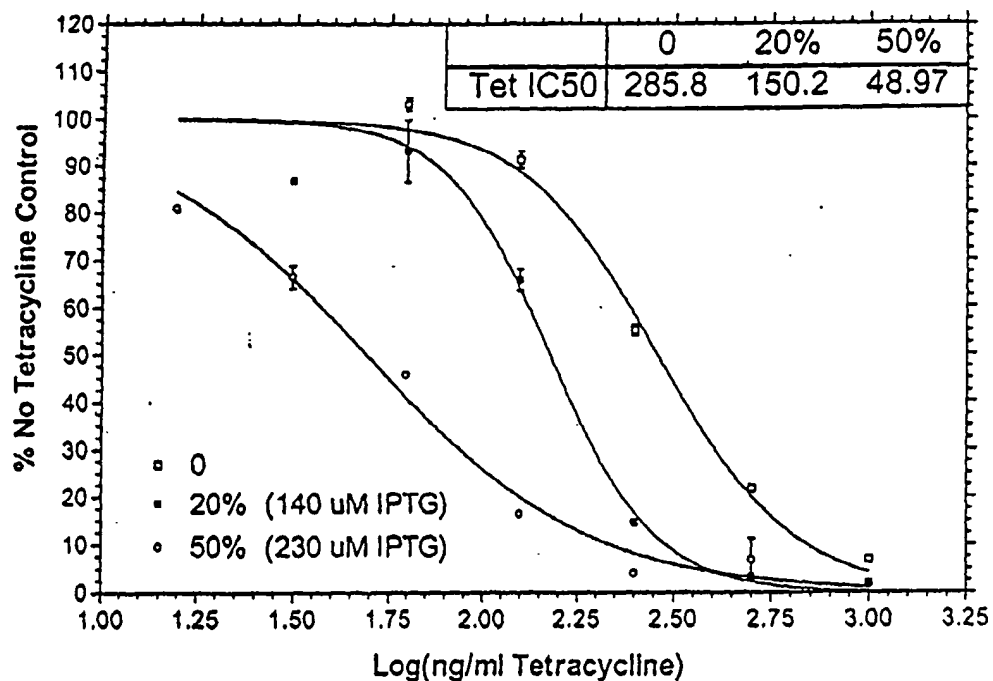
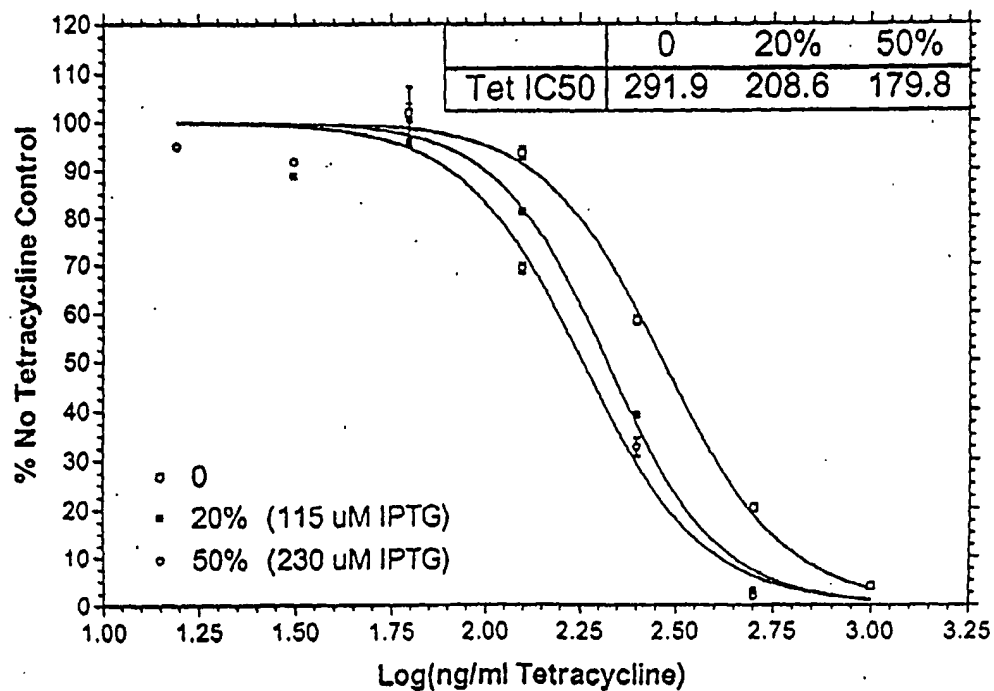


Figure . 1

AS-rplW**Figure 1A****AS-elaD****Figure 1B**

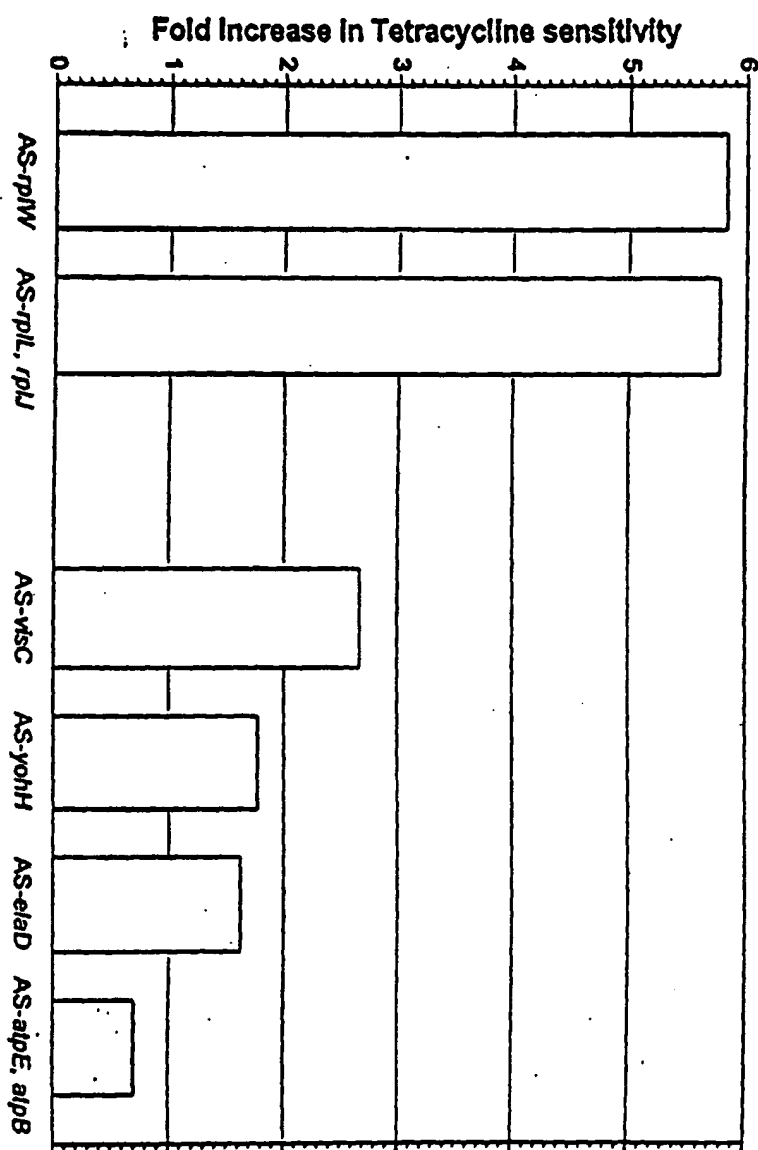


Figure 3

SEQUENCE LISTING

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 FORSYTH, R. Allyn
 OHLSEN, Kari
 ZYSKIND, Judith

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<212> DNA

<213> Escherichia coli

<220>

<221> misc_feature

<222> (1)...(246)

<223> n = A,T,C or G

<400> 17

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cttcctgggc tgccatgcac acaaatgcac cgcaactttg gcttaagtat tgctgaagat      60
cggcatgtaa aaatattatc tctggttcat ttaaataaac ttttatatta ttattcgaca      120
tttctcccat gagttcagaa ttaaaactat taatgacacg cttaagtga ttttctttat      180
catagcctag tgacgcnnnt nnnttgaata tgacgcattt tatttgtagn tnattattnt      240
ttttat

```

<210> 18

<211> 208

<212> DNA

<213> Escherichia coli

<400> 18

```

aatgacacgc ttaagtgaat tttctttatc atagcctagt gcacgcaatg agttgaatat      60
gacgcatttt attttagtatt tattattttt tttatttact attttctgta gcgaaactaa      120
tatccagtgt ccgccagtat ttatggggaa taactggact tcattcggcc atgatggatc      180
gctcttaata ttttcattga gagcgtct

```

<210> 19

<211> 159

<212> DNA

<213> Escherichia coli

<400> 19

```

tatgtaagcg gcaaacgaat ggggtaaaca tgccgatttt ttagtaaata tttcgagagg      60
gatatgtttc taatgctaag aaaaaagggt ccgtagcacc tttttaatag agagggtttg      120
ttaccacaca gcagccagca gcgtatgcga gtccggtac

```

<210> 20
 <211> 294
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(294)
 <223> n = A,T,C or G

<400> 20
 cggtttcaat tttcaggaac atccacgggg ganggtaaac gaatacgtgg gnaattttgg 60
 tggattttca tttgcacttg nctcttcgat cgccttaaca aaatgctgct tgccttgctt 120
 gcgcccgtgc gcttctacng gattgnccgg cgcgatacaa aatcgcttgc ctaagcccgn 180
 cccctgcaca acctggggtn tattcacttg cgcaggtttt tcttgggcgt cagccccgc 240
 aaccggcaaa agactggcga tgtcccgatg gcaatacccg cttttaacgc tttt 294

<210> 21
 <211> 129
 <212> DNA
 <213> Escherichia coli

<400> 21
 tcgggttcaa ttttcaagga acatccagcg gggaggtaaa cgatacgtgg taattttggt 60
 gattttcatt gcactgcctc tcgatacgcc ttaacaaatg ctgctgcctg ctgcgcggtg 120
 cgctctacg 129

<210> 22
 <211> 151
 <212> DNA
 <213> Escherichia coli

<400> 22
 ctctgtatc tatattctaa ttaaaaagtt aaaaacgtta acggcttatg cgtaccgcag 60
 gcacgcgatt accaggccca gatcgctttt ggaaaccatg gctttcggac gcaggtgacg 120
 tttacgtttg gtcgcttttt tggtcagaat g 151

<210> 23
 <211> 579
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(579)
 <223> n = A,T,C or G

<400> 23
 ccaggatctt acggtcgatt tcaacagagg cttttttcag gccattgatg aatttgctgt 60
 aagaaatacc gttctgacgt gctgctgcgt tgatacgcgc aatccacagt tgacggaact 120
 gacgcttacg ttgacgacgg tcacggtaag catactgacc agctttgata acagcctgga 180
 aggcaacgcg gtatacgcga gaacgcgcac cgtagtagcc tttagcttgt ttcaaaat 240
 tcttgtgacg tgcacgtgca ataacaccac gttttacgag agccatatgt gctctcctgt 300
 atctatatc taattgaaaa gttaaaaacg ttaacggctt atgcgtacgg caggcacgcg 360
 attaccaggc ccagatcgcc tttgaaacc atggctttcg gacgcaggtg acgtttacgt 420
 ttggtcgctt ttttggtcag aatgtgacgc aggttagcgt gcttgtgctt aaaaccacct 480
 ttaccgggtt ttttgaagcg cttagcagca ccgcgtacgg tcttaatttt tggcatttta 540
 ataacttnca cttcgcatg gtaataaacg aaacaaagg 579

<210> 24
 <211> 222
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(222)
 <223> n = A,T,C or G

<400> 24
 gaggggtgcaa caggggtgag tagaatgggt ctttattttc atgggtgtang gcctttctgtn 60
 gttngaggac agttttaata aagttacaat caccgcgata aacgtaacca attttttagca 120
 actaaacagg ggaaaacaat tacagatttt tatctttcga ttacgatttt tgggtttattt 180
 cttgatttat gaccgagatc ttacttttgt tgcgcaattg ta 222

<210> 25
 <211> 278
 <212> DNA
 <213> Escherichia coli

<400> 25
 ggagagtttg cagtcattta aaaggttaaca tgacaatgca tgatgaatat aacaacatat 60
 gatgttatgt aatgtgggag gaaagatcac aaaatttcgc acaggatcgc gctgtggcta 120
 atggatgtag ttatcaaatt gaatttaaag tgaaaatatt ttacggggcg ggggcaagaa 180
 ggacatataa acaaatacgc cctcggaaaa tccagagggc gtcgggcaat taaaccgggtg 240
 ttagccgatt tctgtcagag acttactgtg cagtagga 278

<210> 26
 <211> 156
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(156)
 <223> n = A,T,C or G

<400> 26
 tgaaatncga ccgaaggtag ttctcgaaac agtcagcgcg ctctgcgcgt ctttcaatac 60
 taattccatt gctatctcct tacgccttca cagctggttt aacgatcagg tcgctaccgg 120
 ttgcacccgg gacagcacct ttaaccagca gcaggt 156

<210> 27
 <211> 143
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(143)
 <223> n = A,T,C or G

<400> 27
 gcgcgtcttt caatactaatt tccattgcta tctccttacg ccttcacagc tggtttaacg 60
 atcaggtcgc tccgngtgcc ccgggacagc accttaacc agcagcaggt tgcgctcagc 120
 gtcaacgcgt actacgtcaa ggc 143

<210> 28
 <211> 266

<212> DNA

<213> Escherichia coli

<400> 28

gcttcggttga aatcacgacc gaaggtagtt tcggaacag tcagcgcgct ctgcgcgctct	60
ttcaatacta attccattgc tatctcctta cgccttcaca gctgggtttaa cgatcaggtc	120
gctaccggtt gcacccggga cagcaccttt aaccagcagc aggttgcgct cagcgtcaac	180
gcgtactacg tcaaggctct gaacggttac acgttcgcta cccatctgac ctgccatttt	240
cttgcccttg aacactttgc ccggag	266

<210> 29

<211> 535

<212> DNA

<213> Escherichia coli

<400> 29

gcataagcaa caacaacctg gtgaaccagc gcttcggttga aatcacgacc gaaggtagtt	60
tcggaacag tcagcgcgct ctgcgcgctt ttcaatacta attccattgc tatctcctta	120
cgccttcaca gctgggtttaa cgatcaggtc gctaccggtt gcacccggga cagcaccttt	180
aaccagcagc aggttgcgct cagcgtcaac gcgtactacg tcaaggctct gaacggttac	240
acgttcgcta cccatctgac ctgccatttt cttgcccttg aacactttgc ccggagtctg	300
gttctgaccg atagaacctg gaacgcggtg agacaaggag ttaccgtgag tagcgtcctg	360
ggtacgggaag ttccagcgct taacggtacc tgcgaaacct ttacctttag aggtgccagt	420
tacgtcaact tttttaacgt cagcaaacag ttcaacgcta atgctctgac ctacagtga	480
ctcttcgcct tcagccaggc ggaattccca cagaccagg ccagcttcta cgcca	535

<210> 30

<211> 223

<212> DNA

<213> Escherichia coli

<400> 30

ttcaacgcta atgctctgac ctacagtga ctcttcgcct tcagccaggc ggaattccca	60
cagaccagg ccagcttcta cgccagcttt agcgaagtgg ccagcttcag gcttggtcac	120
acggttagct tttttagcac cggtaggtcac ctgaatagca cggtagccat cgtagccag	180
gtctttaacc tgagtaacgc ggtttgcttc aacttcgatt acg	223

<210> 31

<211> 225

<212> DNA

<213> Escherichia coli

<220>

<221> misc_feature

<222> (1)...(225)

<223> n = A,T,C or G

<400> 31

cgctctgcgc gtctttcaat actaattcca ttgctatctc cttacgcctt cacagctggt	60
ttaacgatca ggctgctacc ggntgcaccc gggacagcac ctttaaccaa cagcangntg	120
cgctcaacgt caacgcgtac tacgtcaagg ctctgaacgg gtacacgttc gttacccatn	180
tgacctgnca ttttcttgcc tttgaacact ttgcccgag tctgg	225

<210> 32

<211> 341

<212> DNA

<213> Escherichia coli

<400> 32

tgctatctcc ttacgccttc acagctggtt taacgatcag gtcgctaccg gttgcacccg	60
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ggacagcacc ttttaaccagc agcaggttgc gctcagcgtc aacgcgtact acgtcaaggc 120
tctgaacggt tacacgttcg ttacccatct gacctgccat tttcttgcc tttgaacactt 180
tgcccgaggt ctggtttctga ccgatagaac ccggaacgcg gtgagacaag gagttaccgt 240
gagtagcgtc ctgggttacgg aagttccagc gcttaacggt acctgcgaaa cctttacctt 300
tagaggtgcc agttacgtca acttttttaa cgtcagcaaa c 341

```

<210> 33

<211> 176

<212> DNA

<213> Escherichia coli

<400> 33

```

aacaacaacc tggatgaacca gcgcttcggt gaaatcacga ccgaaggtag tttcggaaac 60
agtcagcgcg ctctgcgcgt ctttcaatac taattccatt gctatctcct tacgccttca 120
cagctggttt aacgatcagg tcgctaccgg ttgcacccgg gacagcacct ttaacc 176

```

<210> 34

<211> 241

<212> DNA

<213> Escherichia coli

<400> 34

```

tcgttgaaat caccgaccgaa ggtagtttcg gaaacagtc ggcgcgtctg cgcgtctttc 60
aatactaatt ccattgctat ctcttacgc cttcacagct ggtttaacga tcaggtcgct 120
accggttgca cccgggacag cacctttaac cagcagcagg ttgcgctcag cgtcaacgcg 180
tactacgtca aggctctgaa cggttacacg ttcgttaccc atctgacctg ccattttctt 240
g 241

```

<210> 35

<211> 224

<212> DNA

<213> Escherichia coli

<220>

<221> misc_feature

<222> (1)...(224)

<223> n = A,T,C or G

<400> 35

```

tgntctaata tgattacgaa aaagatatgt tgccgggagc gttgcctccc caacatataa 60
gtggctccct caagccactt cctttagaag cacaaccttg cttctaacta tataaacctt 120
ctgttatata ttacccttta tttttggggg cgtctcaacg cccattttt aataattttt 180
agtaacaat tggcatatta attagagtta ttaacaacga tate 224

```

<210> 36

<211> 413

<212> DNA

<213> Escherichia coli

<400> 36

```

aacatcctct tgtgtgaata aaacaaccgg accccatcga ggaacggagt ccggtgtcat 60
attaaaagcc cgaaaatttt actcattttt gcgggaattg caatcaacag ttgctaactc 120
tgctgtaaaa ggcgcgtcggc ggtgcagcca gtttggtgcc ggagtgcgcg cagtcaccgg 180
agcgtacacg cagtacgtga ggatgacgag cacatcccgg tgccaaaatg gcaaacaagc 240
caggccgatt agcgaccagg gaagcctggg ggcatacat ccttcattgct tctcatcatc 300
ttcgccattc cgcccttctt cattttcttc atcatgcgt gcatgtcgtc gaactgtttc 360
agaagacggt taacgtcctg cacctgcata ccgcaaccgg cagcaatacg gcg 413

```

<210> 37

<211> 509

<212> DNA

<213> Escherichia coli

<400> 37

cagcgacaac aacctggtag aacggacgct ttttagcgcc gtgacgtgct aaacgaatag	60
ttaccataac atcctcttgt gtgaataaaa caaccggacc ccatcgagga acggagtcg	120
gtgtcatatt aaaagcccga aaatcttact catcttttgcg ggaattgcaa tcaacagttg	180
ctaactctgc tgtaaaaggc cgtcggcggg gcagccagtt tggcgccgga gtgcgcgcag	240
tcaccggagc gtacacgcag tacgtgagga tgacgagcac atcccggtgc caaaatggca	300
aacaagccag gccgattagc gaccagggaa gcctgggggc atcataccct tcatgcttct	360
catcatcttc gccattccgc ccttcttcat tttcttcatc atgcgctgca tgcgctcgaa	420
ctgttttcaga agacgggttaa cgtcctgcac ctgcataccg caaccggcag caatacggcg	480
tttacgcgaa cctttgatga tttctggct	509

<210> 38

<211> 149

<212> DNA

<213> Escherichia coli

<400> 38

gatttttacc ggattaattt taaacatggt ctgatttctt ttattgagct agtcaaaatg	60
cgggtgataag agcgggattg tcccaatcca cgctcttttt tatagagaag atgacgctaa	120
attggccaga tattgtcgat gataatttg	149

<210> 39

<211> 118

<212> DNA

<213> Escherichia coli

<400> 39

gtttcatccc tggcaagcag aacggctttt tcgttattta tatcgggaga attaatatga	60
aactgcaata aattctttta tgtgatacaa gcctgggcgt tcttttttcc ttcaattg	118

<210> 40

<211> 147

<212> DNA

<213> Escherichia coli

<400> 40

gcagaacggc tttttcggtta tttatatcgg gagaattaat atgaaactgc aataaattct	60
ttaatgtgat acaagcctgg gcgttctttt ttccttcaat tgcgacaaat gtaatacttt	120
ggttaatgat tggttggtcg ttacat	147

<210> 41

<211> 224

<212> DNA

<213> Escherichia coli

<400> 41

caattgccga gcgtttcatc cctggcaagc agaacggott tttcgttatt tatatcgga	60
gaattaatat gaaactgcaa taaattcttt aatgtgatac aagcctgggc gttctttttt	120
ccttcaattg cgacaaatgt aatacttttg ttaatgattg gttggtcgtt tacataaaca	180
ctgacgtcgt aaacaccogg tatacgggg ttaccttcac tgta	224

<210> 42

<211> 506

<212> DNA

<213> Escherichia coli

<400> 42

tgaggcaatt	gccgagcgtt	tcattccctgg	caagcagaac	ggctttttcg	ttatttatat	60
cgggagaatt	aatatgaaac	tctttaatgt	gatacaagcc	tgggcgttct		120
tttttccttc	aattgcgaca	aatgtaatac	tttggttaat	gattggttgg	tcgtttacat	180
aaacactgac	gtcgtaaaaca	cccggatatag	cggggttacc	ttcactgtac	cggctgagat	240
caatattaga	tgcattctgc	cccatcagga	aggatggtc	atattcaacg	agttcagcac	300
tgaaagcagt	attgcaatac	agcagcgcg	aaaacgtggc	gatacgggtc	agatgatgat	360
aatttttagt	atattctata	gtcacgctat	gcttcctgcg	gaattatata	cttgccctgat	420
tacagcctgg	cattaccttc	aattgcgcca	ccaaagtc	taatggcgta	aaaatgcact	480
tttgcaaat	tcgctttgcc	attaag				506

<210> 43

<211> 184

<212> DNA

<213> Escherichia coli

<400> 43

caggcttgag	gaacgtctat	atccagacgt	tgatcggtta	cgtcataacg	aacagaagcc	60
tgagggataa	tttccgtcaa	attgaggcaa	ttgccgagcg	tttcatccct	ggcaagcaga	120
acggcttttt	cgttatttat	atcgggagaa	ttaatatgaa	actgcaataa	attctttaat	180
gtga						184

<210> 44

<211> 327

<212> DNA

<213> Escherichia coli

<220>

<221> misc_feature

<222> (1)...(327)

<223> n = A,T,C or G

<400> 44

ggctggaggt	gatgaccgnc	atttccctga	tgccagcagc	ctgttcggca	gataactgca	60
atgtacgatc	aggttctgtg	gtttcgggtg	tagaaaagcg	caaaacatcg	ctgctttncg	120
tcaaccgcca	gtatggattg	tgcatccga	gaaagtgtga	caacgttgtg	gactccctaa	180
cggttttcat	gatgcataac	ctccgggtta	cagcggagtc	cgcggttaaa	taaaagggaac	240
aacatgactt	acatgaaatt	aacggcggtc	aaacgcattg	ntttttttat	atattttatt	300
gtaatccagt	tttgaaaaaa	cgccagt				327

<210> 45

<211> 215

<212> DNA

<213> Escherichia coli

<400> 45

cgctgggcat	caaattcaga	catcaaggac	atccttatag	caaaaggggg	aaaatgaata	60
atgcaaaaaat	tgccgctaaa	agagaagtgt	ttaacagcaa	cggttaatta	tcatccagga	120
atacgatata	taatgacggg	atatagcgct	aagtatatat	attcatctac	ttatgcgcgc	180
ttcagatagc	gtttatacca	gcgttcgaag	gcgac			215

<210> 46

<211> 121

<212> DNA

<213> Escherichia coli

<400> 46

aaataacttt	ccgcatagct	taaaaaggag	ggtaaaatgg	caagagatga	ataacaaatt	60
ccggccagac	accagggtata	cctctgcgga	atatccgtag	tagtgggtat	tttcataatt	120
a						121

<210> 47
 <211> 160
 <212> DNA
 <213> Escherichia coli

<400> 47
 tgcaaggcag gcgctgaaag aggcgaatag tctacctgga ttatggtgaa ttgctccgcc 60
 agatgttaca gggtttattc actcatcgca tcgcgccaga tcttgtcaac gatacgttgc 120
 gccagcacgg cctgttcgcc ggcggtttgc ggaactgggg 160

<210> 48
 <211> 195
 <212> DNA
 <213> Escherichia coli

<400> 48
 tgcgggggaa tttaaactgt gaaaagattc acaaatagct gcggttagga atgtgatatc 60
 cgcagcttat cagggtgaagt aataattatt ctcaataatt aactggagag gggaatatta 120
 acgatagaaa ataagataaa caatcatgcc gatagataaa attccgaagc cgatatatgc 180
 caccatataa gcgaa 195

<210> 49
 <211> 167
 <212> DNA
 <213> Escherichia coli

<400> 49
 gtgaaaagat tcacaaatag ctgcggttag gaatgtgata tccgcagctt atcaggtgaa 60
 gtaataatta ttctcaataa ttaactggag aggggaatat taacgataga aaataagata 120
 aacaatcatg ccgatagata aaattccgaa gccgatatat gccacca 167

<210> 50
 <211> 226
 <212> DNA
 <213> Escherichia coli

<400> 50
 ataattgtact gatattaagg ctaagcgtgc gggggaattt aaactgtgaa aagattcaca 60
 aatagctgcg gttaggaatg tgatatccgc agcttatcag gtgaagtaat aattattctc 120
 aataattaac tggagagggg aatattaacg atagaaaata agataaacia tcatgccgat 180
 agataaaatt ccgaagccga tatatgccac catataagcg aaaaag 226

<210> 51
 <211> 185
 <212> DNA
 <213> Escherichia coli

<400> 51
 ccgaatgacc tgtgcggata gttaattggc atgccgacgc tggagtaggc atccatcatc 60
 tgttctgagg ttatcacttc aatctggtgc gggtaggtat ccagccggta gagtttcgcc 120
 acccggtcta tctctgccag ataaacatcc agcaggtcga acgtccagtc ggtccatcg 180
 ctcaa 185

<210> 52
 <211> 187
 <212> DNA
 <213> Escherichia coli

<400> 52
 ttctgattaa cagcggactt aatcttgagc aaagtcaatg ggcgacaatg caaattataa 60

tgctattaat	tttatactgt	tcaagcatgt	tatgtctggc	tgaagccaat	ttagccacag	120
taaccgtaa	tgatggcgaa	acttcatcaa	tattaattcg	taaagcatct	atctctgtat	180
cattaat						187

<210> 53

<211> 337

<212> DNA

<213> Escherichia coli

<400> 53

aagagggttt	agttctctcg	gtaatgcgct	aacctcaaca	ggctctcggc	tatcgttata	60
attcagcgct	tccgttacac	cactcaactt	tttgatctct	cgtaatcccg	ttctgattaa	120
cagcggactt	aatactgagc	aaagtacaat	ggcgacaatg	caaattataa	tgctattaat	180
tttatactgt	tcaagcatgt	tatgtctggc	tgaagccaat	ttagccacag	taaccgttaa	240
tgatggcgaa	acttcatcaa	tattaattcg	taaagcatct	atctctgtat	cattaataat	300
gcttctgtaa	atgccagctg	cgctgattgt	ctcacta			337

<210> 54

<211> 192

<212> DNA

<213> Escherichia coli

<400> 54

ctgagcaaag	tacaatgggc	gacaatgcaa	attataatgc	tattaatttt	atactgttca	60
agcatgttat	gtctggctga	agccaattta	gccacagtaa	ccgttaatga	tggcgaaact	120
tcataaatat	taattcgtaa	agcatctatc	tctgtatcat	taataatgct	tctgtaaatg	180
ccagctgcgc	tg					192

<210> 55

<211> 239

<212> DNA

<213> Escherichia coli

<400> 55

gattaacagc	ggacttaata	ctgagcaaag	tacaatggcg	acaatgcaaa	ttataatgct	60
attaattttt	tactgttcaa	gcatgttatg	tctggctgaa	gccaatttag	ccacagtaac	120
cggttaatga	ggcgaaaact	catcaatatt	aattcgtaaa	gcatctatct	ctgtatcatt	180
aataatgctt	ctgtaaatgc	cagctgcgct	gattgtctca	ctagcaggta	tggtatttta	239

<210> 56

<211> 240

<212> DNA

<213> Escherichia coli

<400> 56

gattaacagc	gggacttaat	actgagcaaa	gtacaatggc	gacaatgcaa	attataatgc	60
tattaattttt	atactgttca	agcatgttat	gtctggctga	agccaattta	gccacagtaa	120
ccgttaatga	tggcgaaaact	tcataaatat	taattcgtaa	agcatctatc	tctgtatcat	180
taataatgct	tctgtaaatg	ccagctgcgc	tgattgtctc	actagcagggt	atgttattta	240

<210> 57

<211> 330

<212> DNA

<213> Escherichia coli

<400> 57

cacaaccag	tgatgtggct	ggtgcgcttc	aggatgcgat	ctgcacgacc	ttttgcacgc	60
ggcataatgc	gcttcatgct	cgggccttcg	tctacgaaaa	ttttcgtaac	tttcagatcg	120
tcaatgtcag	cgccatcggt	gtgttcagcg	ttagcaatgg	cagattccag	aactttcttg	180
accagtacag	ccgctttctt	gttgggtgtag	gtcaaaatat	ccagagcctg	cgacactttc	240

ttaccgcgaa tcagggtcagc aacaaggcga acctttctgag cagaagaacg agcatggcga 300
tgtttagcga tagtttccat ctcttctctc 330

<210> 58
<211> 266
<212> DNA
<213> Escherichia coli

<400> 58
gctttcttgt tgggtgtaggt caaaatatcc agagcctgcg acactttctt accgcgaatc 60
agggtcagcaa caaggcgaac cttctgagca gaagaacgag catggcgatg tttagcgata 120
gtttccatct cttcctccta ccttatttct tcttcgcttt tttatcagca gcgtggccgc 180
gataagtacg agtcggtgcg aattcaccca gtttgtgacc aaccatttcg tcggttacia 240
ataccggaac gtgctgacga ccatta 266

<210> 59
<211> 186
<212> DNA
<213> Escherichia coli

<400> 59
gcgaatcagg tcagcaacaa ggcgaacctt ctgagcagaa gaacgagcat ggcatgttt 60
agcgatagtt tccatctctt cctcctacct tatttcttct tcgctttttt atcagcagcg 120
tggccgcgat aagtacgagt cggcgcaat tcaccagtt tgtgaccaac catttcgctg 180
gttaca 186

<210> 60
<211> 138
<212> DNA
<213> Escherichia coli

<400> 60
gaagaacgag catggcgatg tttagcgata gtttccatct cttcctccta ccttatttct 60
tcttcgcttt tttatcagca gcgtggccgc gataagtacg agtcggtgcg aattcaccca 120
gtttgtgacc aaccattt 138

<210> 61
<211> 183
<212> DNA
<213> Escherichia coli

<400> 61
tgtgttcagc gttagcaatg gcagattcca gaactttctt gaccagtaca gccgctttct 60
tgttggtgta ggtcaaaaata tccagagcct gcgacacttt cttaccgcga atcagggtcag 120
caacaaggcg aaccttctga gcagaagaac gagcatggcg atgttttagcg atagtattcca 180
tct 183

<210> 62
<211> 135
<212> DNA
<213> Escherichia coli

<400> 62
ggtcaaaaata tccagagcct gcgacacttt cttaccgcga atcagggtcag caacaaggcg 60
aaccttctga gcagaagaac gagcatggcg atgttttagcg atagtattcca tctcttctc 120
ctaccttatt tcttc 135

<210> 63
<211> 141
<212> DNA

<213> Escherichia coli

<400> 63

tgctaaacga atagttacca taacatcctc ttgtgtgaat aaaacaaccg gaccccatcg	60
aggaacggag tccggtgtca tattaagaagc ccgaaaattt tactcatttt tgcgggaatt	120
gcaatcaaca gttgctaact c	141

<210> 64

<211> 144

<212> DNA

<213> Escherichia coli

<400> 64

tgctttgctc gcctcatgac gattatgac gttttgtttt aaaggaggaa gtatcggcag	60
tagacgaatg agtacgatgt aagcgcaaat ctcaatagcc acaaaaccaa tagaatcaa	120
cagttcttcc caggtcggga agta	144

<210> 65

<211> 70

<212> DNA

<213> Escherichia coli

<400> 65

cggttagcgc cgctggtggc atcgagcatc gctcccatgc cgtttgccag ttgatagcgt	60
ccatcttgcc	70

<210> 66

<211> 175

<212> DNA

<213> Escherichia coli

<400> 66

accatacaga gaggagatca aagatgtgcc acttgaccgg aacagcggtt acagcatgtt	60
ggataaaagt atcaagttta ctcatctgct tcagtcgtgt gttattgttg tgatttatga	120
atcatagcac aggtcgtatc gacttctggc cctggcgctt taccaccaca gggcc	175

<210> 67

<211> 867

<212> DNA

<213> Escherichia coli

<220>

<221> misc_feature

<222> (1)...(867)

<223> n = A,T,C or G

<400> 67

ccagatttgc ccccgcaaan ccgacccatt gaacgccgac ctgaccgtga atcaagcgtt	60
catcaatccg gcttaaaaca atattnggca tagcgtgttc ctctttgttt tgcttattgg	120
ccttcacagg ctgtgtggta ctgcgccagg atgtcctgaa tatggttgat aatgagttcc	180
cgtggcgttg gctgcagctc gccggagcga actttcacgt actgcagcgg cagatactgg	240
ctgatcagcg gcagcgggaat tggatgaatcc gccagattac gtaccagatg agcgaagcgg	300
tcataaatct ggctgtccgg ccagtaatag cgcacgcgat ccgagtagct ataaccacgc	360
gccagacgac gcgcgttgcc ggtcacogtg gtatggctt tgccagtatt cccgggcggg	420
cgagcatcac gtcttccaag caccctgacg cagaccagaa cangttttcg ctggcaccag	480
ttctttttta atcgccgcca gagagaacag agcttacgca gggcagaaag gtcancnctg	540
ggccaacttt cagaatggca aagtgggcaa atcaccaagc ttgncgcagc gattgctgcg	600
ttttgataat cgggtagaag tgcncctcgg aaaatcagcg tttnccgtaag tttccgacc	660
catcntggnt taaaggcgct cngtttgccg gggcntgatn aatcaaatta acntttggng	720
tgatcngaat tccaacnccn gggttgnanc cancaggggn aatgatgccn tgggcnanat	780

ngnnatttaa accttggnntt tttaaaaggc ntggcctang ggctttcaac ntnggtnccc 840
 gggccngnat ncngcntgnt gaccctt 867

<210> 68
 <211> 703
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(703)
 <223> n = A,T,C or G

<400> 68
 ccgcccggggc ggggtttttt acgttgcttc agattactct gcagcagctt ctgctttctc 60
 tgaacgatca accagctcga tgtaagccat cggcgcggtg tcgcctgcac ggaagccaca 120
 cttcngaata cgagtgtaac caccggcacg gctcgcgaaa cgcgggcccc gttcgttaaa 180
 cagttttgcc acgatctcgt tatcacgagt acgggcgaat gccagacgac gattagcaac 240
 gctatcagtc ttggcaagag taatcagcgg ctcaactacg cggcgagct ctttcgcttt 300
 aggcagagtc gtcttgatga tttcatgacg aaccagtga cctgccatat tgcggaacat 360
 agcctggcga tggctgctgt tgcggttcag ttgacgacca ctcttacgat ggcgcatgac 420
 cttatccctt tcagtataaac cttaacctgt gatccggtta ctctcagcg atgcttgccg 480
 gtggccagtt ttccaggcgc atgccagag acagtccacg ggaagccagc acgtctttaa 540
 tctcagtaag agatttttta ccaagggttag gcgttttaag gagctcaacc tcggtacgct 600
 gtaccagatc accgatatag tggatagctt ctgctttaag gcagttagca gagcggacag 660
 tcaattccag atcgncaaca gggcgcaaca ggatccggat cga 703

<210> 69
 <211> 328
 <212> DNA
 <213> Escherichia coli

<400> 69
 cgttgctgcc tgcacggaag ccacacttca gaatacagat gtaaccaccg gcacggctcg 60
 cgaacgcggg gccagttcg ttaaacagtt ttgccacgat ctcttatca cgagtacggg 120
 cgaatgccag acgacgatta gcaacgctat cagtcttggc aagagtaatc agcggctcaa 180
 ctacgcggcg cagctctttc gctttaggca gagtcgtctt gatgatttca tgacgaacca 240
 gtgaacctgc catattgcgg aacatagcct ggcgatggct gctgttgccg ttcagttgac 300
 gaccactctt acgatggcgc atgacctt 328

<210> 70
 <211> 414
 <212> DNA
 <213> Escherichia coli

<400> 70
 cgggtataaaa aaaacccgcc ggggcggggt tttttaagtt gcttcagatt actctgcagc 60
 agcttctgct ttctctgaac gatcaaccag ctcatgtaa gccatcggcg cgttgctgcc 120
 tgcacggaag ccacacttca gaatacagat gtaaccaccg gcacggctcg cgaacgcgg 180
 gccagttcg ttaaacagtt ttgccacgat ctcttatca cgagtacggg cgaatgccag 240
 acgacgatta gcaacgctat cagtcttggc aagagtaatc agcggctcaa ctacgcggcg 300
 cagctctttc gctttaggca gagtcgtctt gatgatttca tgacgaacca gtgaacctgc 360
 catattgcgg aacatagcct ggcgatggct gctgttgccg ttcagttgac gacc 414

<210> 71
 <211> 327
 <212> DNA
 <213> Escherichia coli

<400> 71

cgcgaaacgc	gggccaggtt	cgtaaaca	gttttggcac	gatctcgta	tcacgagta	60
ggcggaatgc	cagacgacga	ttagcaacgc	tatcagtctt	ggcaagagta	atcaagcggc	120
tcaactacgc	ggcgagctc	tttcgcttta	ggcagagtcg	tcttgatgat	ttcatgacga	180
accagtgaac	ctgccatatt	gcggaacata	gcctggcgat	ggctgctgtt	gcggttcagt	240
tgacgaccac	tcttacgatg	gcgcatgacc	ttatccttct	caagtaaaac	cttaacctgt	300
gatccggtta	ctcgtcagcg	atgcttg				327

<210> 72

<211> 209

<212> DNA

<213> Escherichia coli

<220>

<221> misc_feature

<222> (1)...(209)

<223> n = A,T,C or G

<400> 72

caactctgtc	tntttaagca	gagtcgtctt	gatgatttca	tgacgaacca	gtgaacctgc	60
catattgcgg	aacatagcct	ggcgatggct	gctgttgccg	ttcagttgac	gaccactctt	120
acgatggcgc	atgaccttat	ccttctcagt	aaaaccttaa	cctgtgatcc	ggttactcgt	180
cagcgatgct	tgccggtggc	cagttttcc				209

<210> 73

<211> 311

<212> DNA

<213> Escherichia coli

<400> 73

aacataagga	gtgcattatg	cgcataagcta	aaattgggggt	catcgccctg	ttcctgttta	60
tggcgtagg	cgggaattgg	ggcgatcatgc	tcgcaggtta	tacctttatt	ttgcgtgctg	120
gctaagcgcc	tgaccagcc	tttcaaacag	gcgggtctgcg	atgatcgccg	cagtgccacc	180
agtaacgccc	cctggatcac	atacgcggtta	ttaaattccgc	taagcccgat	gatgatgggc	240
gtacccagcg	tgctggcccc	taccggtgag	gcgatcgctg	ccgtaccaat	gttgataatc	300
accgaagttc	g					311

<210> 74

<211> 167

<212> DNA

<213> Escherichia coli

<400> 74

cgcgaaactcg	atctggatac	cgataatggt	agcccgtttt	cagcgtgttc	aggtctacta	60
caccgcctt	ctacttttagc	caggtcagac	agacgaattt	cggtgtaat	cgctgcttta	120
cgagaagtga	agccgaattt	cggcagacga	cggtacagag	gcactcg		167

<210> 75

<211> 151

<212> DNA

<213> Escherichia coli

<400> 75

gcagaaaaac	acgtttttta	ggtttatcag	catattgcgc	tttcaattgc	gcgtactgat	60
ccagcaggga	ttgcgggct	tgctcgccct	tgctcggttg	cggactccag	ggggccagtt	120
gacgtaacgc	attggcaatt	tgttcaatgc	t			151

<210> 76

<211> 151

<212> DNA

<213> Escherichia coli

<400> 76
 gcgtcaaagt cgctgctgtc gataaaagcgc acgtcgttgg tcgccacgac gggcaaaccg 60
 cgcgcttccg ccagttccac cgccgcgtgc agatagcttt cttcatccgg cctgccggtg 120
 cggatcagct cgagaaaata gcgatccggg a 151

<210> 77
 <211> 115
 <212> DNA
 <213> Escherichia coli

<400> 77
 taaccgctat tgatcgtagg ctgaccgcag catccctggt tctccgggaa atttacgcga 60
 cagccgaggtt tttccagtag cagcacggag tctcgtgccca ttcttgattt caggg 115

<210> 78
 <211> 220
 <212> DNA
 <213> Escherichia coli

<400> 78
 taaaaatggt tgacataaac ttgccataag ccgtggggagg cacagaaaaa tcaatgatac 60
 ggaatgtggt ctactatga ccaactgaaat caatattcgg cgtcccgggt tctagcaatt 120
 cgataaattg catatgttta ctgccgatag attttaaaaa atgataaacc tcaagagggt 180
 aatggacatt aacgttatta atgacggtta acgtattaaa 220

<210> 79
 <211> 258
 <212> DNA
 <213> Escherichia coli

<400> 79
 ctaaaggatt gagttatcgc attatgccca tgaagccatg tacgcccata tacacaccga 60
 ctaagccaat caacagactg gaaaaatagg gggcgcggtt agcgagagtg ttaaaccgcg 120
 tccagcggtt tgcgacctgc tgaacgctga ttgctgcgcc aacgcctacg gtgacaagcg 180
 ttaacgccag gccaatgctg aaactgacga ccagtgttgc gccagtgtc agggctttca 240
 actgaatgca tatcaaca 258

<210> 80
 <211> 311
 <212> DNA
 <213> Escherichia coli

<400> 80
 catatatattt atcaagcttc tggtatgttt ttttatagaa cgcaaaatca gtcttgagta 60
 gtacggaagg gctattgttg taattaataa tatcatctgg ttttaggaca agtaaaaaac 120
 ccgttaagta atttgcatta atgttatacg tatttgtaa atccgatatt tgctggtatt 180
 cacacttcat cttcttattt ttatcaagcc tagatagagg tgcaacatga ttttcaattt 240
 tatatttttt atcatttatt attatatcgt atgtataatc atgtaaaata ccattcgttg 300
 ttattggcat a 311

<210> 81
 <211> 281
 <212> DNA
 <213> Escherichia coli

<400> 81
 caaaatcagt cttgagtagt acggaagggc tattgttgta attaataata tcatctggtt 60
 ttaggacaag taaaaaaccc gttaagtaat ttgcattaat gttatacgt tttgttaaatt 120
 ccgatatttg ctggtattca cacttcatct tcttattttt atcaagccta gatagaggtg 180

caacatgatt ttcaatttta tttttttat catttattat tatatcgtat gtataatcat	240
gtaaaatacc attcgttggt attggcataa atgcgaaagc a	281

<210> 82

<211> 402

<212> DNA

<213> Escherichia coli

<400> 82

aacaataaat atataacagc ggttatgagt atggctatta ttattgcgga aactaatgga	60
atcattgccg ataaaatcat tggaaatagt tttatcttat taagggtgaa aaggaggga	120
tttgataaac acataaacag tgacaataaa atcgcccaa aaagattata tagtatattt	180
aacaaaatat tattcatggc tatattgtct aaggcgtgta ttaacgccac atctgttatt	240
gttagtacaa tccatgtaat agctaataat gttaaataag ctttaattct atgctgtata	300
aaaacagatg caataaatat tgcaacagca gatatgaggt accatgcggt ttccagtga	360
aaataaaatt gttttatgta atcaagtttc attgagcatt ca	402

<210> 83

<211> 273

<212> DNA

<213> Escherichia coli

<400> 83

aatgtttatc gtatttggtta aatccgatat ttgctggtat tcacacttca tcttcttatt	60
tttatcaagc ctagatagag gtgcaacatg attttcaatt ttatatattt tatcatttat	120
tattatatcg tatgtataat catgtaaaat accattcgtt gttattggca taaatgcgaa	180
agcaaccatc aattgtgcat tgtttgattt aaattttatt tgagagtcag taacacttga	240
ggctagcata aatttatcat cttgcttgct caa	273

<210> 84

<211> 162

<212> DNA

<213> Escherichia coli

<220>

<221> misc_feature

<222> (1)...(162)

<223> n = A,T,C or G

<400> 84

gnnnnnnnnn nntttntnt tttggggccg cgtacatang ccagggatct aggagtaaga	60
atagcttcga attccctccc tggaggcacc acctaaattt tcctgaagtt gagcgaggtt	120
aatgttggca taacgataaa aaacaccgca tgaaaattcc tg	162

<210> 85

<211> 131

<212> DNA

<213> Escherichia coli

<400> 85

ccaataataa taatgtcgca gtcgtcttcc atgtcatgcc ccagatatcc agaacacaac	60
accctaacat agcgttactt aagggaatt gaccgcccac acactottat cattcgccgc	120
gatagataca a	131

<210> 86

<211> 207

<212> DNA

<213> Escherichia coli

<400> 86

gaattttcag	acggctaaca	atgagacacc	agattaaatg	atagtcgggg	agggagagaa	60
gaggaggcg	caatggctgc	gcccgaataa	taaattagtc	gcgcttcgcg	ccagtacgca	120
gcaggccgga	tgcgccttca	gaatagtcgc	gaggcatctg	caccggtgcc	tgatcgttgc	180
tggttcaga	ctctgccaga	cgattac				207

<210> 87
 <211> 247
 <212> DNA
 <213> Escherichia coli

<400> 87	
taacgcta	at
atgataagaa	120
gagacaccag	180
ccgaaaaata	240
atagtcg	247

<210> 88
 <211> 238
 <212> DNA
 <213> Escherichia coli

<400> 88	
tgaatgataa	60
aatgagacac	120
cgcccgaata	180
agaatagtcg	238

<210> 89
 <211> 582
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(582)
 <223> n = A,T,C or G

<400> 89	
ttcaaaacag	60
tgatagtcgg	120
tcgcgcttcg	180
tgcaccggtg	240
gcttcagcag	300
ccgggagagc	360
ctaactgcct	420
cgaaactgac	480
tacttggcgg	540
atattncgcc	582

<210> 90
 <211> 287
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(287)
 <223> n = A,T,C or G

<400> 90
 tgcactcaac agctggggtt gntttttcat ttttctgct ctctacctg aatgataaga 60
 aaagagattc aaaacagttt gatgttattg aattttcaga cggctaacaa tgagacacca 120
 gattaaatga tagtcgggga gggagagaag aggagggcgc aatggctgcg cccgaaaaat 180
 aaattaagtc gcgcttcgcg ccagtagcga gcaggccgga tgcgccttca gaatagtcgc 240
 gaggcattctg caccgggtgcc tgatcgttgc tggcttcaga ctctgcc 287

<210> 91
 <211> 200
 <212> DNA
 <213> Escherichia coli

<400> 91
 taccagatca ccgatatagt ggatagcttc tgctttaagg cagttagcag agcggacagt 60
 caattccaga tcgtcaacag ggcgcagcag gatcggtatg aactctggtt tctcttcttt 120
 cacttcaggc tgacgtacat cagtaagtc aacgaaagct tccagttggt cagccagaat 180
 ggttgccgca cgacgaatcg 200

<210> 92
 <211> 278
 <212> DNA
 <213> Escherichia coli

<400> 92
 ccacgatctc gttatcacga gtacgggcca atgccagacg acgattagca acgctatcag 60
 tcttggcaag agtaatcagc ggctcaacta cgcggcgag ctctttcgtt ttaggcagag 120
 tcgtcttgat gatttcatga cgaaccagtg aacctgccat attgcggaac atagcctggc 180
 gatggctgct gttgcgggtc agttgacgac cactcttagc atggcgcatg accttatact 240
 tctcagtaaa accttaacct gtgatccggt tactcgte 278

<210> 93
 <211> 424
 <212> DNA
 <213> Escherichia coli

<400> 93
 cttagccatt tagtaaccct accttacttg cggaacggga agtcaaaggc agccagcaga 60
 gcgcggcctt cttcgtcaga tttcgtagta gtggtaatgg taatatccaa accacgaacg 120
 cggctcgactt tatcgtagtc gatttctggg aagatgatct gctcacggac acctatgctg 180
 tagttaccac gaccgtcgaa agacttagcg gacaggccac ggaagtcacg gatacgaggt 240
 acagcaatag tgatcaggcg ctcaaagaac tcccacatgc gttcgccacg cagagttact 300
 ttacagccga tcggatagcc ctgacggatt ttgaagcctg caacagattt gcgtgctttg 360
 gtgatcagcg gtttttgacc ggagattgct gccaggctctg ctgctgcgtt atccagcagt 420
 tttt 424

<210> 94
 <211> 161
 <212> DNA
 <213> Escherichia coli

<400> 94
 gactgggagt taacaagcgt aactccctgg gaaatgcgag ctttaaccact cagggggttag 60
 ctttattact tagaaacggt cagacgagcg cggccttttag cagcagcagc tgccagaacc 120
 tgacgacat ttttagtagc catacgagca cggaagccgt g 161

<210> 95
 <211> 187
 <212> DNA
 <213> Escherichia coli

<400> 95
 tggctgctgg aagacgaatg tgaattgact gggagttaac aagcgtaact ccctgggaaa 60
 tgcgagctta accactcagg ggttagcttt attacttaga aacggtcaga cgagcgcggc 120
 ctttagcacg acgacgtgcc agaacctgac gaccattttt agtagccata cgagcacgga 180
 agccgtg 187

<210> 96
 <211> 236
 <212> DNA
 <213> Escherichia coli

<400> 96
 tgccagcccg ttgtggctgc tggaagacga atgtgaattg actgggagtt aacaagcgta 60
 actccctggg aaatgcgagc ttaaccactc aggggttagc tttattactt agaaacggtc 120
 agacgagcgc ggcttttagc acgacgacgt gccagaacct gacgaccatt tttagtagcc 180
 atacgagcac ggaagccgtg agaacgggtg cgcttcagta cagacgggtg aaaagt 236

<210> 97
 <211> 828
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(828)
 <223> n = A,T,C or G

<400> 97
 gcgaattcag gcggccgaga atggtaattt gcggcgtgcc agcccggtgt ggctgctgga 60
 agacgaatgt gaattgactg ggagttaaca agcgtaactc cctgggaaat gccagcttaa 120
 ccactcaggg gttagcttta ttacttatta aacggtcaga cgagcgcggg ctttatcacg 180
 accacgtgcc ngaacctgac gaccattttt agnagccata ctagcacgga agccgtgaga 240
 acggnngcgc ttcagtacan acgngtgaaa agngcctttc atggcnatth ctggggatnn 300
 cgtcnacctg cngnntaacc ataangggnn ggggccncta aacgggtcct tgagggggtt 360
 tttgaagctt gggcttttca ncctgatnca gattaaatca naacgccnga ancggctctga 420
 taaaacannc nnnncntnng cttntcnnna tttgcnacnn ntccnccacn nnngtgcatn 480
 ccnntnncan agnactncga nttnccnnn tnnngccttt nngnngcnnt atnnangctg 540
 tctcgncccn nnnccncttn nnnntttnnc cgcnnnatcc nttnactnna cccnnntnca 600
 cgnnannctn cnnccgcncn nnnnctcnat ntnttnnngn tctcnnntgn cnnnnnnntn 660
 tctnatgncg tnnccnncnn nnnctcctnn nncatgncct tctnactn nntatcnnn 720
 gtcnnttnn ncnnnnaann ncntctctc nnnnnngnnt nccatcgntc anncgnnnng 780
 ncnntnacnt cctantnnnn nnnntcnnn ntatcnnnat ctggcccg 828

<210> 98
 <211> 183
 <212> DNA
 <213> Escherichia coli

<400> 98
 gctgctcgtc ggtcgcgtcg aggttaacga acagatcgaa tacctgatcc acaaccaat 60
 caggacgcgc gccagggcgg tcaactttgt tgataacaac aatcggttc aggccgtaag 120
 caaacgcttt tttggttacg aagcgctgtt gcggcatcgg gccgtcaaata gcgtcaacca 180
 cca 183

<210> 99
 <211> 192
 <212> DNA
 <213> Escherichia coli

<400> 99

ggcatcatgc	tgtgttgccg	ggcaacgcga	aagacgtctg	gcgtcaggca	tggcaggggtg	60
agtatgggcg	tagcgctacg	ttgccatact	ggtatttgcg	agagatcttt	attcagaaac	120
cggaggtaat	ctttgatgat	gtcgtgacta	atatgagcaa	ccaaagtgtt	gttaagagag	180
gagacgtcga	ta					192

<210> 100
 <211> 242
 <212> DNA
 <213> Escherichia coli

<400> 100						
taattttgtt	ggaaagtaat	catatataaa	ttttggaacc	aaccctgcaa	tacctaaatt	60
tgtaaacatt	aatccaaaga	gacataatcc	tataagagaa	gagtttttca	cagaaataaa	120
aaaaagagga	caaaggaaaa	taaatgaagt	tattagaccg	actacaaagg	ctttttttac	180
accaatctta	tcaccaacaa	aaccaaataa	tattgtacct	gtcagtggtc	ctaaacctgc	240
ta						242

<210> 101
 <211> 177
 <212> DNA
 <213> Escherichia coli

<400> 101						
gacgcggcga	acgatttcgg	cttggtcttt	tactggaggt	aataaaacaa	cttgggattt	60
gatatctttt	cctgaaatac	ctttttgacc	agaagttggt	ttcacgcagt	tcatcattgc	120
atttcgtgct	gaggggggatg	aaaaaaatat	ttcgatatat	tctggtaaag	catctttt	177

<210> 102
 <211> 250
 <212> DNA
 <213> Escherichia coli

<400> 102						
gacctgtttt	tctatgggtg	cggcgtaggc	gaagagttgc	tcgacgcggc	gaacgatttc	60
ggcttggtct	tttactggag	gtaataaaac	aacttgggat	ttgatatctt	ttcctgaaat	120
acctttttga	ccagaagttg	ttttcacgca	gttcatcatt	gcatttcgtg	ctgaggggga	180
tgaaaaaaat	atttcgatat	attctggtaa	agcatctttg	gttaatcgag	ctcgaataag	240
tttatcagga						250

<210> 103
 <211> 194
 <212> DNA
 <213> Escherichia coli

<400> 103						
ttaggtcgaa	cacctttcgg	cgcgaacaag	ccctgggtatt	cattggcgat	gctgtgtcga	60
atcacctgct	caggtgaaaa	accctgctgg	cggaaatctt	ccagctcccg	tatcgccccg	120
ttagcgccct	gctccgttcg	aatcggtttt	cgaatgcct	ggcgaaattc	aaccactca	180
cgccaaagcg	agac					194

<210> 104
 <211> 173
 <212> DNA
 <213> Escherichia coli

<400> 104						
tccataaatc	cctcttaatt	tcacgtatcg	aataacgttg	ttttaatcta	gctatgagga	60
acaaataaaa	taaaaatatt	atttttaata	ctgaagcaac	atctttggct	gctttctttt	120
ttaatattgc	tgcccgattc	attttctgat	atcgccatt	tttattgcgg	gta	173

<210> 105
 <211> 173
 <212> DNA
 <213> Escherichia coli

<400> 105
 tccataaaatc cctcttaatt tcacgtatcg aataacgttg ttttaatcta gctatgagga 60
 acaaataaaa taaaaatatt atttttaata ctgaagcaac atcttttggt gctttctttt 120
 ttaatatggc tggccgattc attttctgat atcggccatt tttattgcgg gta 173

<210> 106
 <211> 142
 <212> DNA
 <213> Escherichia coli

<400> 106
 aacagctcca gcgccaacag cgctccaacg cccgccgagg gcagggtgga gagaatcgtc 60
 agcggatgta cgtaactctc gtaaaggata cccagcacga tatacaccgt ggcatggcg 120
 gcgataatca ggatcacctg cg 142

<210> 107
 <211> 263
 <212> DNA
 <213> Escherichia coli

<400> 107
 aaaatcttat tcagcgctt catttggtt gggcctttaa tcccttagag ccatccggtt 60
 gagcaagggt ggcgtaacct gatcatcaca ataatatcga ccacaatagt ggtgacgccc 120
 gagcacgata tactgcatca gttgcggctg ttgcggcatg atgaattgcg gaaatagcgc 180
 cgccagaaac acaatacttt tgggattggt gagattcaca aaaactgcgc gctggaacaa 240
 atgtcgacgc gattgagtag ggg 263

<210> 108
 <211> 235
 <212> DNA
 <213> Escherichia coli

<400> 108
 tcggaagcct gaatgcgat acgtagcga gcttcgacgc gttcgtccag cttattgacc 60
 cacaatatgct gatcgcccag cgccagcgcg gtcatcgcgt aatgcggatg atgctcaagc 120
 accgtcactt tcagaatgct actttgttgc tctttcgga gccacggatt catcacgcta 180
 ctgccccaca ctctctccag cgcgcaaaag gctttcacct gaccgttttc cagta 235

<210> 109
 <211> 147
 <212> DNA
 <213> Escherichia coli

<400> 109
 gccagatga cactttttgt gtaatggccg gagttcacat ttttaattta gatcaaagg 60
 gggaagaata agcagaaaaa gcccgccata acagcgggca ggagggattt agaactgata 120
 aaccagacct aaagcgacaa tatcatc 147

<210> 110
 <211> 241
 <212> DNA
 <213> Escherichia coli

<400> 110
 tcataaaacc tcctgtttta gtatccgcat aaagtgtaac gccagatgac actttttgtg 60

taatgacgga gttcacat	ttt	taatttaga tcaaaggagg	aagaataagc agaaaaagcc	120
cgccataaca gcgggcagga	ggatttagaa ctgataaacc	agacctaaag cgacaatatc		180
atcggtagag atgccattgg	cagcgtagaa gctgtcatct	tcatccaaca ggttgatttt		240
a				241

<210> 111
 <211> 125
 <212> DNA
 <213> Escherichia coli

<400> 111			
tccgcataaa gtgtaacgcc	agatgacact ttttgtgtaa	tgacggagtt cacat	111
atttagatca aaggaggaag	aataagcaga aaaagcccgc	cataacagcg ggcaggagga	120
ttag			125

<210> 112
 <211> 218
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(218)
 <223> n = A,T,C or G

<400> 112				
taatgaccga gttcacat	ttt	taatttana tcaaangagg	aaagaataag cngaaaaagc	60
ccgccataac agcgggcagg	aggatttaga actgataaac	cagacctaaa gcgacaatat		120
catcggtaga gatgccattg	gcagcggtana agctgtcatc	ttcatccaac aggttgattt		180
tatagtcaac gtaggtggac	atgtttttat tgaatatg			218

<210> 113
 <211> 148
 <212> DNA
 <213> Escherichia coli

<400> 113			
cgcataaagt gtaacgccag	atgacacttt ttgtgtaatg	acggagttca cattttta	113
ttagatcaaa ggaggaagaa	taagcagaaa aagcccgcga	taacagcggg caggaggatt	120
tagaactgat aaaccagacc	taaagcga		148

<210> 114
 <211> 193
 <212> DNA
 <213> Escherichia coli

<400> 114			
tgcggtattg cgcaggccaa	agaaagcaag cgaagggtgc	aggtcgctca tttcgacttc	60
gggccagcgt ggcacaaaga	ccaatggtga actgccatga	caggtattgg cccagcagc	120
ggaactcaca aggcaccata	acgtcccctc cctgataacg	ctgatactgt ggtcgcggtt	180
atgccagttg gca			193

<210> 115
 <211> 117
 <212> DNA
 <213> Escherichia coli

<400> 115			
tgccatgaca ggtattggcc	ccagcagcgg aactcacaag	gcaccataac gtcccctccc	60
tgataacgct gatactgtgg	tcgcggttat gccagttggc	atcttcacgt aaataga	117

<210> 116
 <211> 133
 <212> DNA
 <213> Escherichia coli

<400> 116
 taacctgccc gcgcaaactgt gttattcgat aaggctttct gaaggggtga tcaagttgcg 60
 gggtcaggca gctttcataa taggcctgaa tctccatcat gcgagtgcga tgacgctggg 120
 aacgacgcca ggc 133

<210> 117
 <211> 288
 <212> DNA
 <213> Escherichia coli

<400> 117
 taatctagct atgaggaaca aataaaataa aaatattatt tttaatactg aagcaacatc 60
 tttggctgct ttctttttta atattgctgg ccgattcatt ttctgatata gccattttt 120
 attgcgggta tcaggccagt ttatgggttag ccattaattc cagcgctgcg actaacgcag 180
 agtgatccaa ctggctgcca ccgtttgccc cagcaggtatt aaataactcc tggcaggtcg 240
 cagtgtttgg caggttcagc gcaagtgtt tgcactttg cagtgcc 288

<210> 118
 <211> 246
 <212> DNA
 <213> Escherichia coli

<400> 118
 taatttcacg tatcgaataa cgttgtttta atctagctat gaggaacaaa taaaataaaa 60
 atattatttt taatactgaa gcaacatctt tggctgcttt cttttttaat attgctggcc 120
 gattcatttt ctgatatcgg ccatttttat tgcgggtatc aggccagttt atgggttagcc 180
 attaattcca gcgcctgcac taacgcagag tgatccaact ggctgccacc gtttgccgca 240
 caggtta 246

<210> 119
 <211> 525
 <212> DNA
 <213> Escherichia coli

<400> 119
 taatttcacg tatcgaataa cgttgtttta atctagctat gaggaacaaa taaaataaaa 60
 atattatttt taatactgaa gcaacatctt tggctgcttt cttttttaat attgctggcc 120
 gattcatttt ctgatatcgg ccatttttat tgcgggtatc aggccagttt atgggttagcc 180
 attaattcca gcgcctgcac taacgcagag tgatccaact ggctgccacc gtttgccgca 240
 caggtattaa ataactcctg gcaggtcgca gtgtttggca gggtcagcgc aagtgtttc 300
 gcactttgca gtgccaggtt gagatcttcc tgggtgcagag cgattttgaa gcccgatta 360
 aaggtgcggt taatcatacg ctgcctatga acttcagaa tacgtgagga agcaaagccg 420
 cccatcagcg cctggcgcac acgtaccggg tccgcaccgg cttttgaagc aaatagcagg 480
 gtttcagaaa ccgcttcaat attgagcgcc acgataatct gattt 525

<210> 120
 <211> 161
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(161)
 <223> n = A,T,C or G

```

<400> 120
tcttaatttc acgtatcgaa taacgntgnt ttaatctagc tatgaggnac aaataaaata      60
aaaatattat ttttaatact gaagcaacat ctttggctgc tttctttttt aatattgctg      120
gccgattcat tttctgatat cggccatttt tattgcgggt a                          161

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```

<210> 121
<211> 535
<212> DNA
<213> Escherichia coli

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<220>
<221> misc_feature
<222> (1)...(535)
<223> n = A,T,C or G

```

```

<400> 121
cagtatcaat cagcgactgg cgctgtgctt ctgctgcac tactgcgacg ctatgctgtg      60
cctcggtatc cgtcacccat ttctcaccat cccatttata gtatggcggt aatggggcga      120
tagtcgcggg acgcatacaa acataaccgc tggatgttat gtgtctatcg agaatcaaag      180
tggaagtcc tttgtaagt ataagacagg aatcacttat aacgataatc agttagtata      240
tgtatctatc actgttgatg ataatatcag cacttggttc tggagggggg ttgttggtgg      300
caatgatgca ttttaagttat cgnctgcaga tagaggagat attacaataa acaacgaatc      360
agggcatttg atagtcaata ccgcaattct atcaggagat atagtcactc taagaggagg      420
agaaattagg ttggtattat agcttggtgc cgccatgatt ggcgcgcaat ttaaacttag      480
tgctttacat cgctattgnc ttgattttct tgaattattc tataaattaa aaaaa          535

```

```

<210> 122
<211> 267
<212> DNA
<213> Escherichia coli

```

```

<400> 122
ccattttttc aatgaaaatt aaaaagggga tttttgagaa gggtagaatg tcgtttgttt      60
ttttctttat tatgtctggt gacgcggggg gatagaacgt ctgtgcatat agtagtgaat      120
ttattcaggt ctacattatt ctctattttg gtcagtttta tgagttcatt tacagccata      180
ctcattaaat catctgttat cgaaaattta tatatgctca tagcagataa tattgcttgc      240
tgaattatct cttcagaaat atccgct                                267

```

```

<210> 123
<211> 203
<212> DNA
<213> Escherichia coli

```

```

<400> 123
ttttttcttt attatgtctg gtggacgccg ggggataga accgtctgtg catatagtag      60
tgaatttatt caggtctaca ttattctcta ttttggcagt tttatgagtt catttacagc      120
catactcatt aaatcatctg ttatcgaaaa tttatatatg ctcatagcag ataattattgc      180
ttgctgaatt atctcttcag aaa                                203

```

```

<210> 124
<211> 247
<212> DNA
<213> Escherichia coli

```

```

<400> 124
ccttaatgtg tatgacctgg attcatagta tcaattgcc a ttttttcaat gaaaattaaa      60
aaggggattt ttgagaaggg tagaatgtcg tttgtttttt tctttattat gtctggtgac      120
gcggggggat agaacgtctg tgcatatagt agtgaattta ttcagggtcta cattattctc      180
tattttggtc agttttatga gttcatttac agccatactc attaaatcat ctgttatcga      240

```

aaatttta

247

<210> 125

<211> 145

<212> DNA

<213> Escherichia coli

<400> 125

aaattaaaaa	ggggattttt	gagaagggtg	gaatgtcgtt	tgtttttttc	tttattatgt	60
ctggtgacgc	gggggatag	aacgtctgtg	catatagtag	tgaatttatt	caggtctaca	120
ttattctcta	ttttggtcag	tttta				145

<210> 126

<211> 469

<212> DNA

<213> Escherichia coli

<400> 126

aatgagaatg	attggccttc	tttatgattt	taaggattat	gcttctaaaa	tggcggagaa	60
catggcgagg	cttgctgcct	tacttcatta	cttcagcggt	gatggaggcg	atatatctgt	120
taccgggtaa	tgactccaac	ttattgatag	tgttttatgt	tcagataatg	cccgatgact	180
ttgtcatgct	gctccaccga	ttttgagaac	gacagcgact	tccgtcccag	ccgtgccagg	240
tgctgcctca	gattcagggt	atgccgctca	attcgtcgcg	tatatcgctt	gctgattacg	300
tgacgctttc	ccttcaggcg	ggattcatac	agcggccagc	catccgtcat	ccatatcacc	360
acgtcaaagg	gtgacagcag	gctcataaga	cgccccagcg	tcgccatagt	gcgttcaccg	420
aatacgtgcg	caacaaccgt	cttcgggagc	ctgtcatacg	cgtaaaaca		469

<210> 127

<211> 596

<212> DNA

<213> Escherichia coli

<220>

<221> misc_feature

<222> (1)...(596)

<223> n = A,T,C or G

<400> 127

cgatcagtta	tcctgtgtgc	tgcaacattt	ccacgagaag	ctatcattgt	tatatcta	60
gctaagtcocg	gattattcaa	tattagagag	tcaaataatc	tttgtgatgc	tgtatcggtc	120
caccattttg	tcaatgcttt	tgacagatta	tcactctgct	gctgctgtgc	agggcttttg	180
ggccatggaa	ttggcaaggg	gaatgtgcta	ggaaaaactt	ctaaccacag	aggatctgta	240
ttcgtaactg	gattcaacgg	atactgataa	aaattccatc	cccccttcag	cccaatcgga	300
tcctgagtga	tataccgccc	ctgcagcggg	tcataatagc	ggtggcgggt	gtaatacagg	360
ccggactcct	catcatactg	ctgccccggc	aggcggataa	gctgctgcag	ctgatgcggg	420
ttctcttcat	tcagcagggt	gccccattca	tcgtattctg	cgcaccatc	tggtgcccct	480
ccttgctgat	aagggccagc	ggcaggccgc	gatggtcgca	gtggtacang	tggttttttc	540
gcgccggcgt	gtacaccggg	tccatctggt	tttgcatctg	ctccacggnc	angccg	596

<210> 128

<211> 963

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(963)

<400> 128

gtg atg atc	aaa acg	cgt ttt	tct cgc	tgg cta	acg ttt	ttt acg	ttc	48
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Met	Met	Ile	Lys	Thr	Arg	Phe	Ser	Arg	Trp	Leu	Thr	Phe	Phe	Thr	Phe		
1				5					10						15		
gcc	gct	gcc	gtg	gcg	ctg	gcg	cta	ccg	gca	aaa	gcc	aac	acc	tgg	ccg		96
Ala	Ala	Ala	Val	Ala	Leu	Ala	Leu	Pro	Ala	Lys	Ala	Asn	Thr	Trp	Pro		
			20					25					30				
ctg	ccg	cca	gcg	ggc	agt	cgt	ctg	gtt	ggc	gaa	aac	aaa	ttt	cat	gtg		144
Leu	Pro	Pro	Ala	Gly	Ser	Arg	Leu	Val	Gly	Glu	Asn	Lys	Phe	His	Val		
		35					40				45						
gtg	gaa	aat	gac	ggg	ggg	tct	ctg	gaa	gcc	atc	gcc	aaa	aaa	tac	aac		192
Val	Glu	Asn	Asp	Gly	Gly	Ser	Leu	Glu	Ala	Ile	Ala	Lys	Lys	Tyr	Asn		
	50					55				60							
gtc	ggc	ttt	ctc	gct	ctg	tta	cag	gct	aac	ccc	ggc	gtt	gat	cct	tac		240
Val	Gly	Phe	Leu	Ala	Leu	Leu	Gln	Ala	Asn	Pro	Gly	Val	Asp	Pro	Tyr		
	65				70					75					80		
gta	ccg	cgc	gcg	ggc	agc	gtg	tta	acg	atc	ccg	ttg	caa	acc	cta	ctt		288
Val	Pro	Arg	Ala	Gly	Ser	Val	Leu	Thr	Ile	Pro	Leu	Gln	Thr	Leu	Leu		
			85					90						95			
cca	gat	gcg	ccg	cgc	gaa	ggc	att	gtg	atc	aac	att	gcg	gag	ctg	cgt		336
Pro	Asp	Ala	Pro	Arg	Glu	Gly	Ile	Val	Ile	Asn	Ile	Ala	Glu	Leu	Arg		
		100					105					110					
ctc	tat	tac	tac	ccg	ccg	ggg	aaa	aat	tcg	gta	acc	gtg	tat	cca	ata		384
Leu	Tyr	Tyr	Tyr	Pro	Pro	Gly	Lys	Asn	Ser	Val	Thr	Val	Tyr	Pro	Ile		
		115				120						125					
ggg	att	ggg	cag	tta	ggg	ggg	gac	acg	ctg	aca	ccg	aca	atg	gtg	acc		432
Gly	Ile	Gly	Gln	Leu	Gly	Gly	Asp	Thr	Leu	Thr	Pro	Thr	Met	Val	Thr		
	130				135					140							
acc	gtt	tca	gac	aaa	cgt	gca	aac	cca	acc	tgg	acg	cca	acg	gca	aac		480
Thr	Val	Ser	Asp	Lys	Arg	Ala	Asn	Pro	Thr	Trp	Thr	Pro	Thr	Ala	Asn		
	145			150						155					160		
atc	cgc	gcc	cgt	tat	aaa	gca	cag	gga	att	gag	ttg	cct	gcg	gta	gtg		528
Ile	Arg	Ala	Arg	Tyr	Lys	Ala	Gln	Gly	Ile	Glu	Leu	Pro	Ala	Val	Val		
			165					170						175			
ccg	gct	gga	ctg	gat	aac	cca	atg	ggc	cat	cat	gcg	att	cgt	ctg	gcg		576
Pro	Ala	Gly	Leu	Asp	Asn	Pro	Met	Gly	His	His	Ala	Ile	Arg	Leu	Ala		
		180					185					190					
gcc	tat	ggc	ggc	gtt	tat	ttg	ctt	cat	ggg	acg	aac	gcc	gat	ttc	ggc		624
Ala	Tyr	Gly	Gly	Val	Tyr	Leu	Leu	His	Gly	Thr	Asn	Al					

Ile Asn Thr Pro	Ile Lys Val Ser Ala Glu Pro Asn Gly Ala Arg Leu	
245	250	255
gtt gaa gta cat cag ccg ctg tca gag aag att gat gac gat ccg cag	816	
Val Glu Val His Gln Pro Leu Ser Glu Lys Ile Asp Asp Asp Pro Gln		
260	265	270
ctg ctg cca att acg ctg aat agc gca atg caa tca ttt aaa gat gca	864	
Leu Leu Pro Ile Thr Leu Asn Ser Ala Met Gln Ser Phe Lys Asp Ala		
275	280	285
gca caa act gac gct gaa gtg atg caa cat gtg atg gat gtc cgt tcc	912	
Ala Gln Thr Asp Ala Glu Val Met Gln His Val Met Asp Val Arg Ser		
290	295	300
ggg atg ccg gtg gat gtc cgc cgt cat caa gtg agc cca caa acg ctg	960	
Gly Met Pro Val Asp Val Arg Arg His Gln Val Ser Pro Gln Thr Leu		
305	310	315
taa		963
*		
<210> 129		
<211> 2187		
<212> DNA		
<213> Escherichia coli		
<220>		
<221> CDS		
<222> (1)...(2187)		
<400> 129		
atg att act cgt att cct cgt agt tct ttc tct gca aat att aat aat	48	
Met Ile Thr Arg Ile Pro Arg Ser Ser Phe Ser Ala Asn Ile Asn Asn		
1	5	10
15		
aca gcc cag aca aat gaa cac caa acc ctg agt gaa ttg ttt tat aaa	96	
Thr Ala Gln Thr Asn Glu His Gln Thr Leu Ser Glu Leu Phe Tyr Lys		
20	25	30
gaa ctc gag gat aaa ttt tct ggc aag gag ctg gcg acg cct cta tta	144	
Glu Leu Glu Asp Lys Phe Ser Gly Lys Glu Leu Ala Thr Pro Leu Leu		
35	40	45
aaa agc ttc tca gag aac tgt aga caa aat ggt cgt cat atc ttt agc	192	
Lys Ser Phe Ser Glu Asn Cys Arg Gln Asn Gly Arg His Ile Phe Ser		
50	55	60
aac aag gat ttt gtc att aaa ttt tcc acg tcc gtc tta caa gct gat	240	
Asn Lys Asp Phe Val Ile Lys Phe Ser Thr Ser Val Leu Gln Ala Asp		
65	70	75
80		
aag aaa gaa att acg ata att aat aaa aac gaa aac acg aca ctt act	288	
Lys Lys Glu Ile Thr Ile Ile Asn Lys Asn Glu Asn Thr Thr Leu Thr		
85	90	95
caa acc att gcc cca ata ttt gaa aaa tac cta atg gaa att tta cct	336	
Gln Thr Ile Ala Pro Ile Phe Glu Lys Tyr Leu Met Glu Ile Leu Pro		

100	105	110	
caa cgc tca gac act ctt gat aaa caa gaa tta aac cta aaa tca gat			384
Gln Arg Ser Asp Thr Leu Asp Lys Gln Glu Leu Asn Leu Lys Ser Asp			
115	120	125	
aga aaa gaa aaa gaa ttc cca aga att aaa ctt aat ggt caa tgt tat			432
Arg Lys Glu Lys Glu Phe Pro Arg Ile Lys Leu Asn Gly Gln Cys Tyr			
130	135	140	
ttt ccg ggg cga ccc caa aac cgt ata gta tgc cga cac att gct gca			480
Phe Pro Gly Arg Pro Gln Asn Arg Ile Val Cys Arg His Ile Ala Ala			
145	150	155	160
caa tat att aat gat att tat cag aat gtt gat tac aaa ccc cat caa			528
Gln Tyr Ile Asn Asp Ile Tyr Gln Asn Val Asp Tyr Lys Pro His Gln			
165	170	175	
gat gat tac tct tca gct gaa aaa ttt ctc acg cac ttc aac aaa aaa			576
Asp Asp Tyr Ser Ser Ala Glu Lys Phe Leu Thr His Phe Asn Lys Lys			
180	185	190	
tgc aaa aac cag act ttg gcg ttg gtt tcc agc cgt cct gag ggg cgt			624
Cys Lys Asn Gln Thr Leu Ala Leu Val Ser Ser Arg Pro Glu Gly Arg			
195	200	205	
tgc gtt gct gcc tgc ggt gat ttc ggg cta gtt atg aaa gca tat ttt			672
Cys Val Ala Ala Cys Gly Asp Phe Gly Leu Val Met Lys Ala Tyr Phe			
210	215	220	
gac aag atg gaa tca aat ggc atc agt gtt atg gca gcc ata tta ctg			720
Asp Lys Met Glu Ser Asn Gly Ile Ser Val Met Ala Ala Ile Leu Leu			
225	230	235	240
gtg gat aac cat gct ttg acg gtc cgg cta aga ata aag aac aca act			768
Val Asp Asn His Ala Leu Thr Val Arg Leu Arg Ile Lys Asn Thr Thr			
245	250	255	
gaa gga tgt acc cat tac gtg gtt tcg gtt tat gat cct aat gta act			816
Glu Gly Cys Thr His Tyr Val Val Ser Val Tyr Asp Pro Asn Val Thr			
260	265	270	
aac gat aaa ata aga att atg agc gaa agc aaa gag aat att aaa cac			864
Asn Asp Lys Ile Arg Ile Met Ser Glu Ser Lys Glu Asn Ile Lys His			
275	280	285	
tat tct ctg atg gat ttt atg aat gta gat tat agc ctc ctg aaa tgg			912
Tyr Ser Leu Met Asp Phe Met Asn Val Asp Tyr Ser Leu Leu Lys Trp			
290	295	300	
tca aat gat cat gtt att aat caa tct gtt gca ata att cca gca ctt			960
Ser Asn Asp His Val Ile Asn Gln Ser Val Ala Ile Ile Pro Ala Leu			
305	310	315	320
ccg aaa gaa cag cta ttg atg tta aaa gga tct gtg gat gaa ata acc			1008
Pro Lys Glu Gln Leu Leu Met Leu Lys Gly Ser Val Asp Glu Ile Thr			
325	330	335	
cct cca tta tca cct gca acg atg aat ttg cta atg gca att ggt cag			1056
Pro Pro Leu Ser Pro Ala Thr Met Asn Leu Leu Met Ala Ile Gly Gln			

340	345	350	
aat cac caa ctt acg caa ctg atg att caa ctc cag aaa atg cca gaa Asn His Gln Leu Thr Gln Leu Met Ile Gln Leu Gln Lys Met Pro Glu 355 360 365			1104
cta cat aga aca gaa atg ttg act gcc tat aat agt att aac ctg cca Leu His Arg Thr Glu Met Leu Thr Ala Tyr Asn Ser Ile Asn Leu Pro 370 375 380			1152
ggt tta tat ttg gct ata aat tat ggt aat gcg gat atc gtt gag act Gly Leu Tyr Leu Ala Ile Asn Tyr Gly Asn Ala Asp Ile Val Glu Thr 385 390 395 400			1200
att ttc aat tca ttg tca gaa aca gga tat gaa gga tta ctc tcg aaa Ile Phe Asn Ser Leu Ser Glu Thr Gly Tyr Glu Gly Leu Leu Ser Lys 405 410 415			1248
aaa aat ctc atg cat att ctg gag gca aaa gat aaa aat ggt ttt tct Lys Asn Leu Met His Ile Leu Glu Ala Lys Asp Lys Asn Gly Phe Ser 420 425 430			1296
gga tta ttt tta gcg ata tca cgt aag gat aaa aat gtt gta acc tcg Gly Leu Phe Leu Ala Ile Ser Arg Lys Asp Lys Asn Val Val Thr Ser 435 440 445			1344
att ctg aac gcc tta cct aaa ctg gcc gca aca cat cat tta gat aac Ile Leu Asn Ala Leu Pro Lys Leu Ala Ala Thr His His Leu Asp Asn 450 455 460			1392
gaa caa gtg tat aaa ttc ctg agt gcc aaa aat aga acg tcc agc cat Glu Gln Val Tyr Lys Phe Leu Ser Ala Lys Asn Arg Thr Ser Ser His 465 470 475 480			1440
gtt tta tac cat gtt atg gcg aat ggt gat gcc gac atg ctg aaa att Val Leu Tyr His Val Met Ala Asn Gly Asp Ala Asp Met Leu Lys Ile 485 490 495			1488
gtt ttg aac gcg tta cct ttg tta att cgc aca tgt cat ttg act aaa Val Leu Asn Ala Leu Pro Leu Leu Ile Arg Thr Cys His Leu Thr Lys 500 505 510			1536
gaa cag gta ctc gat ctc ctg aag gca aag gat ttt tat ggt tgc cca Glu Gln Val Leu Asp Leu Leu Lys Ala Lys Asp Phe Tyr Gly Cys Pro 515 520 525			1584
gga cta tat ctg gcg atg caa aat gga cat agc gat atc gtg aaa gtt Gly Leu Tyr Leu Ala Met Gln Asn Gly His Ser Asp Ile Val Lys Val 530 535 540			1632
att ctt gaa gca ttg ccc agc cta gcc cag gaa att aac att tca gct Ile Leu Glu Ala Leu Pro Ser Leu Ala Gln Glu Ile Asn Ile Ser Ala 545 550 555 560			1680
tcc gat att gta gat ctt ctg acc gct aaa agt ctt gcg cgc gac acg Ser Asp Ile Val Asp Leu Leu Thr Ala Lys Ser Leu Ala Arg Asp Thr 565 570 575			1728
ggt ttg ttt atg gcc atg cag cgc gga cac atg aac gtt att aat act Gly Leu Phe Met Ala Met Gln Arg Gly His Met Asn Val Ile Asn Thr			1776

580	585	590	
att ttt aac gca tta ccc act ctg ttt aat acg ttt aaa ttc gat aaa			1824
Ile Phe Asn Ala Leu Pro Thr Leu Phe Asn Thr Phe Lys Phe Asp Lys			
595	600	605	
aaa aat atg aag ccc ctc ctc ctg gca aat aat tct aat gaa tat ccc			1872
Lys Asn Met Lys Pro Leu Leu Leu Ala Asn Asn Ser Asn Glu Tyr Pro			
610	615	620	
ggt ttg ttt tca gcg ata cag cat aaa caa caa aat gtt gta gag acg			1920
Gly Leu Phe Ser Ala Ile Gln His Lys Gln Gln Asn Val Val Glu Thr			
625	630	635	640
ggt tat ctt gct tta tct gac cat gca cgc ctg ttt gga ttt acc gct			1968
Val Tyr Leu Ala Leu Ser Asp His Ala Arg Leu Phe Gly Phe Thr Ala			
645	650	655	
gaa gat att atg gat ttt tgg caa cac aaa gcc cca caa aaa tac tct			2016
Glu Asp Ile Met Asp Phe Trp Gln His Lys Ala Pro Gln Lys Tyr Ser			
660	665	670	
gcc ttt gag ttg gct ttt gaa ttt ggt cac cgg gtt att gct gaa tta			2064
Ala Phe Glu Leu Ala Phe Glu Phe Gly His Arg Val Ile Ala Glu Leu			
675	680	685	
atc ctt aat aca tta aat aag atg gct gaa agc ttt ggc ttt acg gat			2112
Ile Leu Asn Thr Leu Asn Lys Met Ala Glu Ser Phe Gly Phe Thr Asp			
690	695	700	
aac cct cga tac att gcg gag aaa aat tat atg gaa gct tta ctc aaa			2160
Asn Pro Arg Tyr Ile Ala Glu Lys Asn Tyr Met Glu Ala Leu Leu Lys			
705	710	715	720
aaa gca tct ccc cat acc gta cgc taa			2187
Lys Ala Ser Pro His Thr Val Arg *			
725			
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<211> 255			
<212> DNA			
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<221> CDS			
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<400> 130			
atg acc gat aaa atc cgt act ctg caa ggt cgc gtt gtt agc gac aaa			48
Met Thr Asp Lys Ile Arg Thr Leu Gln Gly Arg Val Val Ser Asp Lys			
1	5	10	15
atg gag aaa tcc att gtt gtt gct atc gaa cgt ttt gtg aaa cac ccg			96
Met Glu Lys Ser Ile Val Val Ala Ile Glu Arg Phe Val Lys His Pro			
20	25	30	
atc tac ggt aaa ttc atc aag cgt acg acc aaa ctg cac gta cat gac			144
Ile Tyr Gly Lys Phe Ile Lys Arg Thr Thr Lys Leu His Val His Asp			
35	40	45	

gag aac aac gaa tgc ggt atc ggt gac gtg gtt gaa atc cgc gaa tgc 192
 Glu Asn Asn Glu Cys Gly Ile Gly Asp Val Val Glu Ile Arg Glu Cys
 50 55 60

cgt ccg ctg tcc aag act aaa tcc tgg acg ctg gtt cgc gtt gta gag 240
 Arg Pro Leu Ser Lys Thr Lys Ser Trp Thr Leu Val Arg Val Val Glu
 65 70 75 80

aaa gcg gtt ctg taa 255
 Lys Ala Val Leu *

<210> 131
 <211> 192
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(192)

<400> 131
 atg aaa gca aaa gag ctg cgt gag aag agc gtt gaa gag ctg aac acc 48
 Met Lys Ala Lys Glu Leu Arg Glu Lys Ser Val Glu Glu Leu Asn Thr
 1 5 10 15

gag ctg ctg aac ctg ctg cgt gag cag ttc aac ctg cgt atg cag gct 96
 Glu Leu Leu Asn Leu Leu Arg Glu Gln Phe Asn Leu Arg Met Gln Ala
 20 25 30

gca agt ggc cag ctg caa cag tct cac ctg ttg aag caa gtg cgt cgc 144
 Ala Ser Gly Gln Leu Gln Gln Ser His Leu Leu Lys Gln Val Arg Arg
 35 40 45

gat gtc gca cgc gtt aag act tta ctg aac gag aag gcg ggt gcg taa 192
 Asp Val Ala Arg Val Lys Thr Leu Leu Asn Glu Lys Ala Gly Ala *
 50 55 60

<210> 132
 <211> 411
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(411)

<400> 132
 atg tta caa cca aag cgt aca aaa ttc cgt aaa atg cac aaa ggc cgt 48
 Met Leu Gln Pro Lys Arg Thr Lys Phe Arg Lys Met His Lys Gly Arg
 1 5 10 15

aac cgc ggt ctg gcg cag ggt acg gat gtt agc ttc ggc agc ttc ggt 96
 Asn Arg Gly Leu Ala Gln Gly Thr Asp Val Ser Phe Gly Ser Phe Gly
 20 25 30

ctg aaa gct gtt ggc cgt ggt cgt ctg act gcc cgt cag atc gaa gca 144

Leu Lys Ala Val Gly Arg Gly Arg Leu Thr Ala Arg Gln Ile Glu Ala
 35 40 45
 gca cgt cgt gct atg acc cgt gca gtt aag cgt caa ggt aag atc tgg 192
 Ala Arg Arg Ala Met Thr Arg Ala Val Lys Arg Gln Gly Lys Ile Trp
 50 55 60
 atc cgt gtg ttc ccg gac aaa ccg atc act gaa aag ccg ctg gca gtg 240
 Ile Arg Val Phe Pro Asp Lys Pro Ile Thr Glu Lys Pro Leu Ala Val
 65 70 75 80
 cgt atg ggt aaa ggt aaa ggt aac gtg gag tat tgg gtt gcc ttg att 288
 Arg Met Gly Lys Gly Lys Gly Asn Val Glu Tyr Trp Val Ala Leu Ile
 85 90 95
 cag ccg ggt aaa gtc ctg tat gaa atg gac ggt gtt ccg gaa gag ctg 336
 Gln Pro Gly Lys Val Leu Tyr Glu Met Asp Gly Val Pro Glu Glu Leu
 100 105 110
 gcc cgt gaa gca ttc aag ctg gca gca gcg aaa ctg ccg att aaa acc 384
 Ala Arg Glu Ala Phe Lys Leu Ala Ala Ala Lys Leu Pro Ile Lys Thr
 115 120 125
 acc ttt gta act aag acg gtg atg taa 411
 Thr Phe Val Thr Lys Thr Val Met *
 130 135

 <210> 133
 <211> 702
 <212> DNA
 <213> Escherichia coli

 <220>
 <221> CDS
 <222> (1)...(702)

 <400> 133
 atg ggt cag aaa gta cat cct aat ggt att cgc ctg ggt att gta aaa 48
 Met Gly Gln Lys Val His Pro Asn Gly Ile Arg Leu Gly Ile Val Lys
 1 5 10 15
 cca tgg aac tct acc tgg ttt gcg aac acc aaa gaa ttc gct gac aac 96
 Pro Trp Asn Ser Thr Trp Phe Ala Asn Thr Lys Glu Phe Ala Asp Asn
 20 25 30
 ctg gac agc gat ttt aaa gta cgt cag tac ctg act aag gaa ctg gct 144
 Leu Asp Ser Asp Phe Lys Val Arg Gln Tyr Leu Thr Lys Glu Leu Ala
 35 40 45
 aaa gcg tcc gta tct cgt atc gtt atc gag cgt ccg gct aag agc atc 192
 Lys Ala Ser Val Ser Arg Ile Val Ile Glu Arg Pro Ala Lys Ser Ile
 50 55 60
 cgt gta acc att cac act gct cgc ccg ggt atc gtt atc ggt aaa aaa 240
 Arg Val Thr Ile His Thr Ala Arg Pro Gly Ile Val Ile Gly Lys Lys
 65 70 75 80
 ggt gaa gac gta gaa aaa ctg cgt aag gtc gta gcg gac atc gct ggc 288
 Gly Glu Asp Val Glu Lys Leu Arg Lys Val Val Ala Asp Ile Ala Gly

85	90	95	
gtt cct gca cag atc aac atc gcc gaa gtt cgt aag cct gaa ctg gac Val Pro Ala Gln Ile Asn Ile Ala Glu Val Arg Lys Pro Glu Leu Asp 100 105 110			336
gca aaa ctg gtt gct gac agc atc act tct cag ctg gaa cgt cgc gtt Ala Lys Leu Val Ala Asp Ser Ile Thr Ser Gln Leu Glu Arg Arg Val 115 120 125			384
atg ttc cgt cgt gct atg aag cgt gct gta cag aac gca atg cgt ctg Met Phe Arg Arg Ala Met Lys Arg Ala Val Gln Asn Ala Met Arg Leu 130 135 140			432
ggc gct aaa ggt att aaa gtt gaa gtt agc ggc cgt ctg ggc ggc gcg Gly Ala Lys Gly Ile Lys Val Glu Val Ser Gly Arg Leu Gly Gly Ala 145 150 155 160			480
gaa atc gca cgt acc gaa tgg tac cgc gaa ggt cgc gta ccg ctg cac Glu Ile Ala Arg Thr Glu Trp Tyr Arg Glu Gly Arg Val Pro Leu His 165 170 175			528
act ctg cgt gct gac atc gac tac aac acc tct gaa gcg cac acc act Thr Leu Arg Ala Asp Ile Asp Tyr Asn Thr Ser Glu Ala His Thr Thr 180 185 190			576
tac ggt gta atc ggc gtt aaa gtg tgg atc ttc aaa ggc gag atc ctg Tyr Gly Val Ile Gly Val Lys Val Trp Ile Phe Lys Gly Glu Ile Leu 195 200 205			624
ggt ggt atg gct gct gtt gaa caa ccg gaa aaa ccg gct gct cag cct Gly Gly Met Ala Ala Val Glu Gln Pro Glu Lys Pro Ala Ala Gln Pro 210 215 220			672
aaa aag cag cag cgt aaa ggc cgt aaa taa Lys Lys Gln Gln Arg Lys Gly Arg Lys *			702
225 230			
<210> 134			
<211> 333			
<212> DNA			
<213> Escherichia coli			
<220>			
<221> CDS			
<222> (1)...(333)			
<400> 134			
atg gaa act atc gct aaa cat cgc cat gct cgt tct tct gct cag aag Met Glu Thr Ile Ala Lys His Arg His Ala Arg Ser Ser Ala Gln Lys 1 5 10 15			48
gtt cgc ctt gtt gct gac ctg att cgc ggt aag aaa gtg tcg cag gct Val Arg Leu Val Ala Asp Leu Ile Arg Gly Lys Lys Val Ser Gln Ala 20 25 30			96
ctg gat att ttg acc tac acc aac aag aaa gcg gct gta ctg gtc aag Leu Asp Ile Leu Thr Tyr Thr Asn Lys Lys Ala Ala Val Leu Val Lys 35 40 45			144

aaa gtt ctg gaa tct gcc att gct aac gct gaa cac aac gat ggc gct 192
 Lys Val Leu Glu Ser Ala Ile Ala Asn Ala Glu His Asn Asp Gly Ala
 50 55 60

gac att gac gat ctg aaa gtt acg aaa att ttc gta gac gaa ggc ccg 240
 Asp Ile Asp Asp Leu Lys Val Thr Lys Ile Phe Val Asp Glu Gly Pro
 65 70 75 80

agc atg aag cgc att atg ccg cgt gca aaa ggt cgt gca gat cgc atc 288
 Ser Met Lys Arg Ile Met Pro Arg Ala Lys Gly Arg Ala Asp Arg Ile
 85 90 95

ctg aag cgc acc agc cac atc act gtg gtt gtg tcc gat cgc tga 333
 Leu Lys Arg Thr Ser His Ile Thr Val Val Val Ser Asp Arg *
 100 105 110

<210> 135
 <211> 279
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(279)

<400> 135
 atg cca cgt tct ctc aag aaa ggt cct ttt att gac ctg cac ttg ctg 48
 Met Pro Arg Ser Leu Lys Lys Gly Pro Phe Ile Asp Leu His Leu Leu
 1 5 10 15

aag aag gta gag aaa gcg gtg gaa agc gga gac aag aag ccc ctg cgc 96
 Lys Lys Val Glu Lys Ala Val Glu Ser Gly Asp Lys Lys Pro Leu Arg
 20 25 30

act tgg tcc cgt cgt tca acg atc ttt cct aac atg atc ggt ttg acc 144
 Thr Trp Ser Arg Arg Ser Thr Ile Phe Pro Asn Met Ile Gly Leu Thr
 35 40 45

atc gct gtc cat aat ggt cgt cag cac gtt ccg gta ttt gta acc gac 192
 Ile Ala Val His Asn Gly Arg Gln His Val Pro Val Phe Val Thr Asp
 50 55 60

gaa atg gtt ggt cac aaa ctg ggt gaa ttc gca ccg act cgt act tat 240
 Glu Met Val Gly His Lys Leu Gly Glu Phe Ala Pro Thr Arg Thr Tyr
 65 70 75 80

cgc ggc cac gct gct gat aaa aaa gcg aag aag aaa taa 279
 Arg Gly His Ala Ala Asp Lys Lys Ala Lys Lys Lys *
 85 90

<210> 136
 <211> 822
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS

<222> (1)...(822)

<400> 136

atg gca gtt gtt aaa tgt aaa ccg aca tct ccg ggt cgt cgc cac gta	48
Met Ala Val Val Lys Cys Lys Pro Thr Ser Pro Gly Arg Arg His Val	
1 5 10 15	
ggt aaa gtg gtt aac cct gag ctg cac aag ggc aaa cct ttt gct ccg	96
Val Lys Val Val Asn Pro Glu Leu His Lys Gly Lys Pro Phe Ala Pro	
20 25 30	
ttg ctg gaa aaa aac agc aaa tcc ggt ggt cgt aac aac aat ggc cgt	144
Leu Leu Glu Lys Asn Ser Lys Ser Gly Gly Arg Asn Asn Asn Gly Arg	
35 40 45	
atc acc act cgt cat atc ggt ggt ggc cac aag cag gct tac cgt att	192
Ile Thr Thr Arg His Ile Gly Gly Gly His Lys Gln Ala Tyr Arg Ile	
50 55 60	
ggt gac ttc aaa cgc aac aaa gac ggt atc ccg gca gtt gtt gaa cgt	240
Val Asp Phe Lys Arg Asn Lys Asp Gly Ile Pro Ala Val Val Glu Arg	
65 70 75 80	
ctt gag tac gat ccg aac cgt tcc gcg aac atc gcg ctg gtt ctg tac	288
Leu Glu Tyr Asp Pro Asn Arg Ser Ala Asn Ile Ala Leu Val Leu Tyr	
85 90 95	
aaa gac ggt gaa cgc cgt tac atc ctg gcc cct aaa ggc ctg aaa gct	336
Lys Asp Gly Glu Arg Arg Tyr Ile Leu Ala Pro Lys Gly Leu Lys Ala	
100 105 110	
ggc gac cag att cag tct ggc gtt gat gct gca atc aaa cca ggt aac	384
Gly Asp Gln Ile Gln Ser Gly Val Asp Ala Ala Ile Lys Pro Gly Asn	
115 120 125	
acc ctg ccg atg cgc aac atc ccg gtt ggt tct act gtt cat aac gta	432
Thr Leu Pro Met Arg Asn Ile Pro Val Gly Ser Thr Val His Asn Val	
130 135 140	
gaa atg aaa cca ggt aaa ggc ggt cag ctg gca cgt tcc gct ggt act	480
Glu Met Lys Pro Gly Lys Gly Gly Gln Leu Ala Arg Ser Ala Gly Thr	
145 150 155 160	
tac gtt cag atc gtt gct cgt gat ggt gct tat gtc acc ctg cgt ctg	528
Tyr Val Gln Ile Val Ala Arg Asp Gly Ala Tyr Val Thr Leu Arg Leu	
165 170 175	
cgt tct ggt gaa atg cgt aaa gta gaa gca gac tgc cgt gca act ctg	576
Arg Ser Gly Glu Met Arg Lys Val Glu Ala Asp Cys Arg Ala Thr Leu	
180 185 190	
ggc gaa gtt ggc aat gct gag cat atg ctg cgc gtt ctg ggt aaa gca	624
Gly Glu Val Gly Asn Ala Glu His Met Leu Arg Val Leu Gly Lys Ala	
195 200 205	
ggt gct gca cgc tgg cgt ggt gtt cgt ccg acc gtt cgc ggt acc gcg	672
Gly Ala Ala Arg Trp Arg Gly Val Arg Pro Thr Val Arg Gly Thr Ala	
210 215 220	
atg aac ccg gta gac cac cca cat ggt ggt ggt gaa ggt cgt aac ttt	720

Met Asn Pro Val Asp His Pro His Gly Gly Gly Glu Gly Arg Asn Phe	
225 230 235 240	
ggt aag cac ccg gta act ccg tgg ggc gtt cag acc aaa ggt aag aag	768
Gly Lys His Pro Val Thr Pro Trp Gly Val Gln Thr Lys Gly Lys Lys	
245 250 255	
acc cgc agc aac aag cgt act gat aaa ttc atc gta cgt cgc cgt agc	816
Thr Arg Ser Asn Lys Arg Thr Asp Lys Phe Ile Val Arg Arg Arg Ser	
260 265 270	
aaa taa	822
Lys *	
<210> 137	
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<212> DNA	
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atg att cgt gaa gaa cgt ctg ctg aag gtg ctg cgt gca ccg cac gtt	48
Met Ile Arg Glu Glu Arg Leu Leu Lys Val Leu Arg Ala Pro His Val	
1 5 10 15	
tct gaa aaa gcg tct act gcg atg gaa aaa tcc aac acc atc gta ctc	96
Ser Glu Lys Ala Ser Thr Ala Met Glu Lys Ser Asn Thr Ile Val Leu	
20 25 30	
aaa gtt gct aaa gac gcg acc aaa gca gaa atc aaa gct gct gtg cag	144
Lys Val Ala Lys Asp Ala Thr Lys Ala Glu Ile Lys Ala Ala Val Gln	
35 40 45	
aaa ctg ttt gaa gtc gaa gtc gaa gtc gtt aac acc ctg gta gtt aaa	192
Lys Leu Phe Glu Val Glu Val Glu Val Val Asn Thr Leu Val Val Lys	
50 55 60	
ggg aaa gtt aaa cgt cac gga cag cgt atc ggt cgt cgt agc gac tgg	240
Gly Lys Val Lys Arg His Gly Gln Arg Ile Gly Arg Arg Ser Asp Trp	
65 70 75 80	
aaa aaa gct tac gtc acc ctg aaa gaa ggc cag aat ctg gac ttc gtt	288
Lys Lys Ala Tyr Val Thr Leu Lys Glu Gly Gln Asn Leu Asp Phe Val	
85 90 95	
ggc ggc gct gag taa	303
Gly Gly Ala Glu *	
100	
<210> 138	
<211> 606	
<212> DNA	
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<220>

<221> CDS

<222> (1)...(606)

<400> 138

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Met Glu Leu Val Leu Lys Asp Ala Gln Ser Ala Leu Thr Val Ser Glu	
1 5 10 15	
act acc ttc ggt cgt gat ttc aac gaa gcg ctg gtt cac cag gtt gtt	96
Thr Thr Phe Gly Arg Asp Phe Asn Glu Ala Leu Val His Gln Val Val	
20 25 30	
gtt gct tat gca gct ggt gct cgt cag ggt act cgt gct cag aag act	144
Val Ala Tyr Ala Ala Gly Ala Arg Gln Gly Thr Arg Ala Gln Lys Thr	
35 40 45	
cgt gct gaa gta act ggt tcc ggt aaa aaa ccg tgg cgc cag aaa ggc	192
Arg Ala Glu Val Thr Gly Ser Gly Lys Lys Pro Trp Arg Gln Lys Gly	
50 55 60	
acc ggc cgt gcg cgt tct ggt tct atc aag agc ccg atc tgg cgt tct	240
Thr Gly Arg Ala Arg Ser Gly Ser Ile Lys Ser Pro Ile Trp Arg Ser	
65 70 75 80	
ggt ggc gtg acc ttt gct gct cgt ccg cag gac cac agt caa aaa gtt	288
Gly Gly Val Thr Phe Ala Ala Arg Pro Gln Asp His Ser Gln Lys Val	
85 90 95	
aac aag aag atg tac cgc ggc gcg ctg aaa agc atc ctg tcc gaa ctg	336
Asn Lys Lys Met Tyr Arg Gly Ala Leu Lys Ser Ile Leu Ser Glu Leu	
100 105 110	
gta cgt cag gat cgt ctg atc gtt gtc gag aag ttc tct gta gaa gcg	384
Val Arg Gln Asp Arg Leu Ile Val Val Glu Lys Phe Ser Val Glu Ala	
115 120 125	
ccg aaa act aag ctg ctg gca cag aaa ctg aaa gac atg gct ctg gaa	432
Pro Lys Thr Lys Leu Leu Ala Gln Lys Leu Lys Asp Met Ala Leu Glu	
130 135 140	
gat gtg ctg atc atc acc ggt gag ctg gac gaa aac ctg ttc ctg gct	480
Asp Val Leu Ile Ile Thr Gly Glu Leu Asp Glu Asn Leu Phe Leu Ala	
145 150 155 160	
gcg cgc aac ctg cac aag gtt gac gta cgc gat gca act ggt atc gac	528
Ala Arg Asn Leu His Lys Val Asp Val Arg Asp Ala Thr Gly Ile Asp	
165 170 175	
ccg gtt agc ctg atc gcc ttc gac aaa gtc gta atg act gct gat gct	576
Pro Val Ser Leu Ile Ala Phe Asp Lys Val Val Met Thr Ala Asp Ala	
180 185 190	
gtt aag caa gtt gag gag atg ctg gca tga	606
Val Lys Gln Val Glu Glu Met Leu Ala *	
195 200	

<210> 139

<211> 630

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(639)

<400> 139

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Met	Ile	Gly	Leu	Val	Gly	Lys	Lys	Val	Gly	Met	Thr	Arg	Ile	Phe	Thr	
1			5						10					15		

gaa	gac	ggc	ggt	tct	atc	cca	gta	acc	gta	atc	gaa	ggt	gaa	gca	aac	96
Glu	Asp	Gly	Val	Ser	Ile	Pro	Val	Thr	Val	Ile	Glu	Val	Glu	Ala	Asn	
			20					25					30			

cgc	ggt	act	cag	ggt	aaa	gac	ctg	gct	aac	gat	ggc	tac	cgt	gct	att	144
Arg	Val	Thr	Gln	Val	Lys	Asp	Leu	Ala	Asn	Asp	Gly	Tyr	Arg	Ala	Ile	
		35					40					45				

cag	gtg	acc	acc	ggt	gct	aaa	aaa	gct	aac	cgt	gtg	acc	aag	cct	gaa	192
Gln	Val	Thr	Thr	Gly	Ala	Lys	Lys	Ala	Asn	Arg	Val	Thr	Lys	Pro	Glu	
	50					55					60					

gct	ggc	cac	ttc	gct	aaa	gct	ggc	gta	gaa	gct	ggc	cgt	ggt	ctg	tgg	240
Ala	Gly	His	Phe	Ala	Lys	Ala	Gly	Val	Glu	Ala	Gly	Arg	Gly	Leu	Trp	
65					70				75					80		

gaa	ttc	cgc	ctg	gct	gaa	ggc	gaa	gag	ttc	act	gta	ggt	cag	agc	att	288
Glu	Phe	Arg	Leu	Ala	Glu	Gly	Glu	Glu	Phe	Thr	Val	Gly	Gln	Ser	Ile	
			85					90						95		

agc	ggt	gaa	ctg	ttt	gct	gac	ggt	aaa	aaa	ggt	gac	gta	act	ggc	acc	336
Ser	Val	Glu	Leu	Phe	Ala	Asp	Val	Lys	Lys	Val	Asp	Val	Thr	Gly	Thr	
		100					105						110			

tct	aaa	ggt	aaa	ggt	ttc	gca	ggt	acc	ggt	aag	cgc	tgg	aac	ttc	cgt	384
Ser	Lys	Gly	Lys	Gly	Phe	Ala	Gly	Thr	Val	Lys	Arg	Trp	Asn	Phe	Arg	
	115						120					125				

acc	cag	gac	gct	act	cac	ggt	aac	tcc	ttg	tct	cac	cgc	ggt	ccg	ggt	432
Thr	Gln	Asp	Ala	Thr	His	Gly	Asn	Ser	Leu	Ser	His	Arg	Val	Pro	Gly	
	130					135					140					

tct	atc	ggt	cag	aac	cag	act	ccg	ggc	aaa	gtg	ttc	aaa	ggc	aag	aaa	480
Ser	Ile	Gly	Gln	Asn	Gln	Thr	Pro	Gly	Lys	Val	Phe	Lys	Gly	Lys	Lys	
145				150					155					160		

atg	gca	ggt	cag	atg	ggt	aac	gaa	cgt	gta	acc	ggt	cag	agc	ctt	gac	528
Met	Ala	Gly	Gln	Met	Gly	Asn	Glu	Arg	Val	Thr	Val	Gln	Ser	Leu	Asp	
			165					170						175		

gta	gta	cgc	ggt	gac	gct	gag	cgc	aac	ctg	ctg	ctg	ggt	aaa	ggt	gct	576
Val	Val	Arg	Val	Asp	Ala	Glu	Arg	Asn	Leu	Leu	Leu	Val	Lys	Gly	Ala	
			180					185					190			

gtc	ccg	ggt	gca	acc	ggt	agc	gac	ctg	atc	ggt	aaa	cca	gct	gtg	aag	624
Val	Pro	Gly	Ala	Thr	Gly	Ser	Asp	Leu	Ile	Val	Lys	Pro	Ala	Val	Lys	
	195						200					205				

gcg taa
Ala * * *

630

<210> 140
<211> 312
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(312)

<400> 140
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Met Gln Asn Gln Arg Ile Arg Ile Arg Leu Lys Ala Phe Asp His Arg
1 5 10 15
ctg atc gat caa gca acc gcg gaa atc gtc gag act gcc aag cgc act 96
Leu Ile Asp Gln Ala Thr Ala Glu Ile Val Glu Thr Ala Lys Arg Thr
20 25 30
ggt gcg cag gtc cgt ggt ccg atc ccg ctg ccg aca cgc aaa gag cgc 144
Gly Ala Gln Val Arg Gly Pro Ile Pro Leu Pro Thr Arg Lys Glu Arg
35 40 45
ttc act gtt ctg atc tcc ccg cac gtc aac aaa gac gcg cgc gat cag 192
Phe Thr Val Leu Ile Ser Pro His Val Asn Lys Asp Ala Arg Asp Gln
50 55 60
tac gaa atc cgt act cac ttg cgt ctg gtt gac atc gtt gag cca acc 240
Tyr Glu Ile Arg Thr His Leu Arg Leu Val Asp Ile Val Glu Pro Thr
65 70 75 80
gag aaa acc gtt gat gct ctg atg cgt ctg gat ctg gct gcc ggt gta 288
Glu Lys Thr Val Asp Ala Leu Met Arg Leu Asp Leu Ala Ala Gly Val
85 90 95
gac gtg cag atc agc ctg ggt taa 312
Asp Val Gln Ile Ser Leu Gly *
100

<210> 141
<211> 4710
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(4710)

<400> 141
gtg aac aca ata cac ttg cgc tgt ctc ttc agg atg aat ccc ctg gtc 48
Met Asn Thr Ile His Leu Arg Cys Leu Phe Arg Met Asn Pro Leu Val
1 5 10 15
tgg tgc ctg tgg gct gat gtt gca gca aag cta agg tcg ctt aaa cgc 96
Trp Cys Leu Trp Ala Asp Val Ala Ala Lys Leu Arg Ser Leu Lys Arg

20	25	30	
tac tca gta ttc act ttt cag agg atg aaa ttt atg aac agg acc agt			144
Tyr Ser Val Phe Thr Phe Gln Arg Met Lys Phe Met Asn Arg Thr Ser			
35	40	45	
ccc tat tat tgt cgc cgc tca gta ctt tcc tta ttg ata tct gcc ttg			192
Pro Tyr Tyr Cys Arg Arg Ser Val Leu Ser Leu Leu Ile Ser Ala Leu			
50	55	60	
ata tat gcc ccg ccc ggg atg gct gcc ttc act act aat gtt att ggt			240
Ile Tyr Ala Pro Pro Gly Met Ala Ala Phe Thr Thr Asn Val Ile Gly			
65	70	75	80
gtg gta aac gat gag act gta gat ggc aac caa aaa gtg gat gaa cga			288
Val Val Asn Asp Glu Thr Val Asp Gly Asn Gln Lys Val Asp Glu Arg			
85	90	95	
ggg aca aca aat aac act cat att atc aac cat ggc cag cag aat gtt			336
Gly Thr Thr Asn Asn Thr His Ile Ile Asn His Gly Gln Gln Asn Val			
100	105	110	
cat ggc ggg gta tct aat gga agt ctt att gaa tct ggt gga tat caa			384
His Gly Gly Val Ser Asn Gly Ser Leu Ile Glu Ser Gly Gly Tyr Gln			
115	120	125	
gat ata gga agt cat aac aat ttt gtg ggg cag gct aat aat aca acc			432
Asp Ile Gly Ser His Asn Asn Phe Val Gly Gln Ala Asn Asn Thr Thr			
130	135	140	
att aac ggt ggc aga cag tca att cat gac ggg ggt att tcc aca ggt			480
Ile Asn Gly Gly Arg Gln Ser Ile His Asp Gly Gly Ile Ser Thr Gly			
145	150	155	160
acg aca atc gag agt ggc aat cag gac gtt tat aaa ggg ggt atc agc			528
Thr Thr Ile Glu Ser Gly Asn Gln Asp Val Tyr Lys Gly Gly Ile Ser			
165	170	175	
aat gga acg aca att aag ggc ggt gct tca cgc gta gag gga ggg agt			576
Asn Gly Thr Thr Ile Lys Gly Gly Ala Ser Arg Val Glu Gly Gly Ser			
180	185	190	
gcg aat gga ata ctc att gat ggt ggt agc cag ata gta aaa gtt caa			624
Ala Asn Gly Ile Leu Ile Asp Gly Gly Ser Gln Ile Val Lys Val Gln			
195	200	205	
ggg cat gct gat ggt aca acg ata aat aag tct ggc tct cag gac gta			672
Gly His Ala Asp Gly Thr Thr Ile Asn Lys Ser Gly Ser Gln Asp Val			
210	215	220	
gta caa gga agt ctg gca acg aac aca acc ata aat ggt ggt cga cag			720
Val Gln Gly Ser Leu Ala Thr Asn Thr Thr Ile Asn Gly Gly Arg Gln			
225	230	235	240
tat gtt gaa cag agc aca gta gaa aca aca acc att aaa aat ggc ggt			768
Tyr Val Glu Gln Ser Thr Val Glu Thr Thr Thr Ile Lys Asn Gly Gly			
245	250	255	
gag caa aga gta tat gag agc cgt gcg ctg gac acg acg att gaa ggc			816
Glu Gln Arg Val Tyr Glu Ser Arg Ala Leu Asp Thr Thr Ile Glu Gly			

260	265	270	
gga act cag tct ctg aat agt aag tca acg gca aaa aat acg cat atc Gly Thr Gln Ser Leu Asn Ser Lys Ser Thr Ala Lys Asn Thr His Ile 275 280 285			864
tat tct ggt ggc acg caa att gtt gat aac acc agc acc tcg gat gtt Tyr Ser Gly Gly Thr Gln Ile Val Asp Asn Thr Ser Thr Ser Asp Val 290 295 300			912
att gaa gtt tat tct ggt ggc gtg ctt gat gtt agg ggt ggt acg gca Ile Glu Val Tyr Ser Gly Gly Val Leu Asp Val Arg Gly Gly Thr Ala 305 310 315 320			960
aca aat gtt acc cag cac gat ggt gca att tta aaa act aac act aac Thr Asn Val Thr Gln His Asp Gly Ala Ile Leu Lys Thr Asn Thr Asn 325 330 335			1008
ggt acg acg gtg agc ggt acg aat agt gaa ggt gca ttc tcc atc cac Gly Thr Thr Val Ser Gly Thr Asn Ser Ser Glu Gly Ala Phe Ser Ile His 340 345 350			1056
aat cac gtg gca gac aat gtg ttg ctg gaa aac ggt ggt cat tta gac Asn His Val Ala Asp Asn Val Leu Leu Glu Asn Gly Gly His Leu Asp 355 360 365			1104
ata aac gca tat ggt tcg gca aac aag acg att att aaa gat aaa gga Ile Asn Ala Tyr Gly Ser Ala Asn Lys Thr Ile Ile Lys Asp Lys Gly 370 375 380			1152
aca atg tca gtt tta acc aat gct aaa gct gat gcg acc cga ata gat Thr Met Ser Val Leu Thr Asn Ala Lys Ala Asp Ala Thr Arg Ile Asp 385 390 395 400			1200
aat ggc ggg gtt atg gat gtt gca gga aac gcg aca aat acc ata att Asn Gly Gly Val Met Asp Val Ala Gly Asn Ala Thr Asn Thr Ile Ile 405 410 415			1248
aat ggt ggc aca cag aat att aat aat tat ggc ata gcc aca ggc acc Asn Gly Gly Thr Gln Asn Ile Asn Asn Tyr Gly Ile Ala Thr Gly Thr 420 425 430			1296
aat atc aac agc gga acg caa aat atc aaa agc ggc ggg aaa gct gac Asn Ile Asn Ser Gly Thr Gln Asn Ile Lys Ser Gly Gly Lys Ala Asp 435 440 445			1344
aca aca att ata tcc tcc ggg agc cgg cag gtt gtt gag aaa gat ggt Thr Thr Ile Ile Ser Ser Gly Ser Arg Gln Val Val Glu Lys Asp Gly 450 455 460			1392
acg gca att ggc agc aat att agc gcc gga ggc tcg ctg att gtc tat Thr Ala Ile Gly Ser Asn Ile Ser Ala Gly Gly Ser Leu Ile Val Tyr 465 470 475 480			1440
acc ggc ggt att gca cat ggg gtt aac cag gag acg ggc agt gct tta Thr Gly Gly Ile Ala His Gly Val Asn Gln Glu Thr Gly Ser Ala Leu 485 490 495			1488
gtt gcc aac acg ggt gca ggg act gat atc gaa gga tac aac aag ctc Val Ala Asn Thr Gly Ala Gly Thr Asp Ile Glu Gly Tyr Asn Lys Leu			1536

500	505	510	
tct cac ttc act att acc gga ggg gag gct aat tat gtt gtg ctg gaa Ser His Phe Thr Ile Thr Gly Gly Glu Ala Asn Tyr Val Val Leu Glu 515 520 525			1584
aat acc ggc gaa ctg acg gta gtg gct aaa acc tcg gcg aaa aat act Asn Thr Gly Glu Leu Thr Val Val Ala Lys Thr Ser Ala Lys Asn Thr 530 535 540			1632
acc att gat act ggc ggt aag ctg att gtc cag aag gag gct aaa aca Thr Ile Asp Thr Gly Gly Lys Leu Ile Val Gln Lys Glu Ala Lys Thr 545 550 555 560			1680
gat agc acc aga ctt aat aat ggc ggc gtt ctg gag gtt cag gac ggt Asp Ser Thr Arg Leu Asn Asn Gly Gly Val Leu Glu Val Gln Asp Gly 565 570 575			1728
ggt gag gct aag cat gtt gag caa caa tcc ggc ggc gca tta att gct Gly Glu Ala Lys His Val Glu Gln Gln Ser Gly Gly Ala Leu Ile Ala 580 585 590			1776
tcc acg acc tcc gga aca ctt atc gaa gga acc aac agt tat ggt gat Ser Thr Thr Ser Gly Thr Leu Ile Glu Gly Thr Asn Ser Tyr Gly Asp 595 600 605			1824
gct ttc tac atc agg aat tca gaa gct aaa aat gta gtg ctg gaa aac Ala Phe Tyr Ile Arg Asn Ser Glu Ala Lys Asn Val Val Leu Glu Asn 610 615 620			1872
gct ggc tca tta aca gtc gtc act ggt tcc cgc gca gtt gac acg att Ala Gly Ser Leu Thr Val Val Thr Gly Ser Arg Ala Val Asp Thr Ile 625 630 635 640			1920
att aat gcc aac ggc aaa atg gat gtt tat gga aaa gat gtt ggc act Ile Asn Ala Asn Gly Lys Met Asp Val Tyr Gly Lys Asp Val Gly Thr 645 650 655			1968
gta ctc aat agt gct ggc acc caa aca ata tat gcc agt gcc act tct Val Leu Asn Ser Ala Gly Thr Gln Thr Ile Tyr Ala Ser Ala Thr Ser 660 665 670			2016
gat aaa gca aat atc aaa ggt ggc aag caa acg gta tat ggt tta gcc Asp Lys Ala Asn Ile Lys Gly Gly Lys Gln Thr Val Tyr Gly Leu Ala 675 680 685			2064
act gaa gca aat atc gaa agt ggt gaa caa att gtt gat ggt ggg tca Thr Glu Ala Asn Ile Glu Ser Gly Glu Gln Ile Val Asp Gly Gly Ser 690 695 700			2112
aca gag aaa aca cac atc aat ggt ggc acg caa acc gtt cag aat tat Thr Glu Lys Thr His Ile Asn Gly Gly Thr Gln Thr Val Gln Asn Tyr 705 710 715 720			2160
ggt aag gca atc aat acc gat atc gtc tct ggc cta caa caa att atg Gly Lys Ala Ile Asn Thr Asp Ile Val Ser Gly Leu Gln Gln Ile Met 725 730 735			2208
gca aac ggg aca gcg gaa ggt tcc att att aat ggg ggt tca cag gta Ala Asn Gly Thr Ala Glu Gly Ser Ile Ile Asn Gly Gly Ser Gln Val			2256

740	745	750	
gtt aat gag ggc ggc ctg gct gaa aac tcg gtg ctt aat gac ggc ggc Val Asn Glu Gly Gly Leu Ala Glu Asn Ser Val Leu Asn Asp Gly Gly 755 760 765			2304
aca ctc gat gtg cgg gag aaa ggc agc gca acg ggg ata cag cag agt Thr Leu Asp Val Arg Glu Lys Gly Ser Ala Thr Gly Ile Gln Gln Ser 770 775 780			2352
agc cag ggc gct ttg gtt gca acc acc agg gcg acg cgg gtc aca gga Ser Gln Gly Ala Leu Val Ala Thr Thr Arg Ala Thr Arg Val Thr Gly 785 790 795 800			2400
aca cgc gcg gat ggc gtc gcg ttc agc atc gag cag ggt gcg gcg aac Thr Arg Ala Asp Gly Val Ala Phe Ser Ile Glu Gln Gly Ala Ala Asn 805 810 815			2448
aat atc ctg ctg gca aat ggc ggc gtg tta acc gtg gag tca gac acc Asn Ile Leu Leu Ala Asn Gly Gly Val Leu Thr Val Glu Ser Asp Thr 820 825 830			2496
tct tct gac aaa aca cag gtc aat atg ggc gga cgg gag atc gtc aaa Ser Ser Asp Lys Thr Gln Val Asn Met Gly Gly Arg Glu Ile Val Lys 835 840 845			2544
aca aaa gcc act gcg aca ggc acg acg ctc acc ggc ggt gaa caa att Thr Lys Ala Thr Ala Thr Gly Thr Thr Leu Thr Gly Gly Glu Gln Ile 850 855 860			2592
gtc gag ggt gtg gcg aat gag aca aca att aac gac ggc gga ata caa Val Glu Gly Val Ala Asn Glu Thr Thr Ile Asn Asp Gly Gly Ile Gln 865 870 875 880			2640
aca gtt tca gct aac gga gag gca ata aaa aca aag atc aat gaa ggc Thr Val Ser Ala Asn Gly Glu Ala Ile Lys Thr Lys Ile Asn Glu Gly 885 890 895			2688
ggc acg ctg aca gtc aac gat aat ggc aaa gcg aca gat atc gtc cag Gly Thr Leu Thr Val Asn Asp Asn Gly Lys Ala Thr Asp Ile Val Gln 900 905 910			2736
aac agc ggt gcc gct ctc cag acg agc acg gct aac ggt att gaa atc Asn Ser Gly Ala Ala Leu Gln Thr Ser Thr Ala Asn Gly Ile Glu Ile 915 920 925			2784
agc ggt act cac cag tac ggt act ttt tcc att tcc ggc aat tta gcg Ser Gly Thr His Gln Tyr Gly Thr Phe Ser Ile Ser Gly Asn Leu Ala 930 935 940			2832
acc aat atg ttg ctg gaa aat ggc ggt aat tta ttg gta tta gca ggt Thr Asn Met Leu Leu Glu Asn Gly Gly Asn Leu Leu Val Leu Ala Gly 945 950 955 960			2880
acc gaa gct cgc gac tcc acg gtt ggc aag ggt ggg gca atg caa aac Thr Glu Ala Arg Asp Ser Thr Val Gly Lys Gly Gly Ala Met Gln Asn 965 970 975			2928
ctg ggt cag gac tcc gcc aca aag gtt aac tct ggc ggg caa tat acc Leu Gly Gln Asp Ser Ala Thr Lys Val Asn Ser Gly Gly Gln Tyr Thr			2976

980	985	990	
ctt ggg cgg tca aaa gat gag ttt cag gct ctg gcc cgg gca gaa gat Leu Gly Arg Ser Lys Asp Glu Phe Gln Ala Leu Ala Arg Ala Glu Asp 995 1000 1005			3024
ctc cag gtc gct ggc ggt acg gca atc gtc tac gca ggt acg ctg gcg Leu Gln Val Ala Gly Gly Thr Ala Ile Val Tyr Ala Gly Thr Leu Ala 1010 1015 1020			3072
gat gca tcg gtc agt ggc gcg aca gga agc ctg tcg tta atg acg cca Asp Ala Ser Val Ser Gly Ala Thr Gly Ser Leu Ser Leu Met Thr Pro 1025 1030 1035 1040			3120
cgg gat aat gtt acg cca gtt aaa ctc gaa ggg gcg gtc cgg att acc Arg Asp Asn Val Thr Pro Val Lys Leu Glu Gly Ala Val Arg Ile Thr 1045 1050 1055			3168
gat agc gcg aca ttg act ctg gga aat ggc gtc gat acc acg ctt gcc Asp Ser Ala Thr Leu Thr Leu Gly Asn Gly Val Asp Thr Thr Leu Ala 1060 1065 1070			3216
gac ctg acg gct gcc agc cgg ggc agt gtc tgg ctt aac agc aat aat Asp Leu Thr Ala Ala Ser Arg Gly Ser Val Trp Leu Asn Ser Asn Asn 1075 1080 1085			3264
tcc tgt gca ggt acc agc aac tgc gaa tat aga gta aac agt ttg cta Ser Cys Ala Gly Thr Ser Asn Cys Glu Tyr Arg Val Asn Ser Leu Leu 1090 1095 1100			3312
ctc aac gac ggt gat gtt tat ttg tca gca caa aca gca gcg cct gcc Leu Asn Asp Gly Asp Val Tyr Leu Ser Ala Gln Thr Ala Ala Pro Ala 1105 1110 1115 1120			3360
aca act aac ggt atc tac aat acg ctg aca acc aat gaa ctt tcc ggt Thr Thr Asn Gly Ile Tyr Asn Thr Leu Thr Thr Asn Glu Leu Ser Gly 1125 1130 1135			3408
agc ggt aat ttc tac ctg cat acc aac gtt gca ggc tcc cgg ggc gat Ser Gly Asn Phe Tyr Leu His Thr Asn Val Ala Gly Ser Arg Gly Asp 1140 1145 1150			3456
caa ctg gtc gtc aac aac aac gcc act ggt aat ttt aaa atc ttt gtt Gln Leu Val Val Asn Asn Asn Ala Thr Gly Asn Phe Lys Ile Phe Val 1155 1160 1165			3504
cag gat acc ggc gtc agc cca cag tct gac gac gcg atg acg ctg gtg Gln Asp Thr Gly Val Ser Pro Gln Ser Asp Asp Ala Met Thr Leu Val 1170 1175 1180			3552
aaa aca ggg gga ggg gat gct tcg ttt acg ctg ggc aat acc ggc ggt Lys Thr Gly Gly Gly Asp Ala Ser Phe Thr Leu Gly Asn Thr Gly Gly 1185 1190 1195 1200			3600
ttc gtt gat ctt ggg acc tat gag tat gtc ctg aaa agt gac ggc aac Phe Val Asp Leu Gly Thr Tyr Glu Tyr Val Leu Lys Ser Asp Gly Asn 1205 1210 1215			3648
agc aac tgg aac ctg acc aat gat gtc aaa ccc aac ccg gac ccc atc Ser Asn Trp Asn Leu Thr Asn Asp Val Lys Pro Asn Pro Asp Pro Ile			3696

1220	1225	1230	
cca aat cca aag cca gac cca aaa ccc gat cca aag cca gac cca aat			3744
Pro Asn Pro Lys Pro Asp Pro Lys Pro Asp Pro Lys Pro Asp Pro Asn			
1235	1240	1245	
cca aaa cca gac cct act ccc gat cca acg ccg aca ccc gtt ccg gag			3792
Pro Lys Pro Asp Pro Thr Pro Asp Pro Thr Pro Thr Pro Val Pro Glu			
1250	1255	1260	
aaa cgc att acg cct tct acg gca gcc gta ctc aat atg gca gca aca			3840
Lys Arg Ile Thr Pro Ser Thr Ala Ala Val Leu Asn Met Ala Ala Thr			
1265	1270	1275	1280
tta ccg ttg gta ttt gat gct gag cta aac agt att cgc gag cgg ttg			3888
Leu Pro Leu Val Phe Asp Ala Glu Leu Asn Ser Ile Arg Glu Arg Leu			
1285	1290	1295	
aac ata atg aaa gcg agt cca cac aac aat aat gtc tgg ggg gcg acg			3936
Asn Ile Met Lys Ala Ser Pro His Asn Asn Asn Val Trp Gly Ala Thr			
1300	1305	1310	
tat aac acc cgt aat aat gtc acc acc gat gcg ggt gcc ggg ttt gag			3984
Tyr Asn Thr Arg Asn Asn Val Thr Thr Asp Ala Gly Ala Gly Phe Glu			
1315	1320	1325	
cag acg ctg acc gga atg aca gtg ggg atc gac agc cgt aat gat att			4032
Gln Thr Leu Thr Gly Met Thr Val Gly Ile Asp Ser Arg Asn Asp Ile			
1330	1335	1340	
cct gaa gga att acc acg cta ggc gct ttt atg ggc tat tcc cat tca			4080
Pro Glu Gly Ile Thr Thr Leu Gly Ala Phe Met Gly Tyr Ser His Ser			
1345	1350	1355	1360
cat atc ggt ttt gat cgc gga gga cat ggc agt gtg ggc agt tat tct			4128
His Ile Gly Phe Asp Arg Gly Gly His Gly Ser Val Gly Ser Tyr Ser			
1365	1370	1375	
ctg ggc ggc tat gcc agt tgg gaa cat gaa agt ggt ttc tat ctg gac			4176
Leu Gly Gly Tyr Ala Ser Trp Glu His Glu Ser Gly Phe Tyr Leu Asp			
1380	1385	1390	
ggt gtc gtg aag ctg aac cgt ttt aaa agt aac gta gca ggt aaa atg			4224
Gly Val Val Lys Leu Asn Arg Phe Lys Ser Asn Val Ala Gly Lys Met			
1395	1400	1405	
agc agc ggt gga gcc gcc aat ggc agt tac cac agc aac ggg ctg ggc			4272
Ser Ser Gly Gly Ala Ala Asn Gly Ser Tyr His Ser Asn Gly Leu Gly			
1410	1415	1420	
ggt cac att gaa acc ggg atg cga ttt acc gat ggt aac tgg aac ctg			4320
Gly His Ile Glu Thr Gly Met Arg Phe Thr Asp Gly Asn Trp Asn Leu			
1425	1430	1435	1440
acg ccg tat gca tcg tta acg ggg ttc acc gct gat aac ccc gaa tat			4368
Thr Pro Tyr Ala Ser Leu Thr Gly Phe Thr Ala Asp Asn Pro Glu Tyr			
1445	1450	1455	
cat tta tcc aat ggc atg aaa tcg aaa tca gtc gat acc cgc agt ata			4416
His Leu Ser Asn Gly Met Lys Ser Lys Ser Val Asp Thr Arg Ser Ile			

1460	1465	1470	
tat cgt gaa ctg ggc gca acg ctg agt tac aac atg cgt ctg ggg aac			4464
Tyr Arg Glu Leu Gly Ala Thr Leu Ser Tyr Asn Met Arg Leu Gly Asn			
1475	1480	1485	
ggt atg gaa gtt gag ccg tgg ctg aag gcg gct gtg cgc aaa gaa ttt			4512
Gly Met Glu Val Glu Pro Trp Leu Lys Ala Ala Val Arg Lys Glu Phe			
1490	1495	1500	
gtc gat gat aac cgg gtg aaa gtg aat agt gac ggt aat ttc gtc aat			4560
Val Asp Asp Asn Arg Val Lys Val Asn Ser Asp Gly Asn Phe Val Asn			
1505	1510	1515	1520
tat ttg tcg ggc aga cgt gga ata tac cag gca ggt att aaa gcc tca			4608
Tyr Leu Ser Gly Arg Arg Gly Ile Tyr Gln Ala Gly Ile Lys Ala Ser			
1525	1530	1535	
ttc agc agt acg tta agc ggg cat ctt ggg gtg ggg tat agc cat agt			4656
Phe Ser Ser Thr Leu Ser Gly His Leu Gly Val Gly Tyr Ser His Ser			
1540	1545	1550	
gcc ggt gtg gaa tcc ccg tgg aac gcg gta gct ggt gtg aac tgg tcg			4704
Ala Gly Val Glu Ser Pro Trp Asn Ala Val Ala Gly Val Asn Trp Ser			
1555	1560	1565	
ttc tga			4710
Phe *			

<210> 142
 <211> 117
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(117)

<400> 142	
atg aaa gtt cgt gct tcc gtc aag aaa tta tgc cgt aac tgc aaa atc	48
Met Lys Val Arg Ala Ser Val Lys Lys Leu Cys Arg Asn Cys Lys Ile	
1 5 10 15	
ggt aag cgt gat ggt gtc atc cgt gtg att tgc agt gcc gag ccg aag	96
Val Lys Arg Asp Gly Val Ile Arg Val Ile Cys Ser Ala Glu Pro Lys	
20 25 30	
cat aaa cag cgc caa ggc tga	117
His Lys Gln Arg Gln Gly *	
35	

<210> 143
 <211> 1332
 <212> DNA
 <213> Escherichia coli
 <220>

<221> CDS

<222> (1)...(1332)

<400> 143

atg gct aaa caa ccg gga tta gat ttt caa agt gcc aaa ggt ggc tta	48
Met Ala Lys Gln Pro Gly Leu Asp Phe Gln Ser Ala Lys Gly Gly Leu	
1 5 10 15	
ggc gag ctg aaa cgc aga ctg ctg ttt gtt atc ggt gcg ctg att gtg	96
Gly Glu Leu Lys Arg Arg Leu Leu Phe Val Ile Gly Ala Leu Ile Val	
20 25 30	
ttc cgt att ggc tct ttt att ccg atc cct ggt att gat gcc gct gta	144
Phe Arg Ile Gly Ser Phe Ile Pro Ile Pro Gly Ile Asp Ala Ala Val	
35 40 45	
ctt gcc aaa ctg ctt gag caa cag cga ggc acc atc att gag atg ttt	192
Leu Ala Lys Leu Leu Glu Gln Gln Arg Gly Thr Ile Ile Glu Met Phe	
50 55 60	
aac atg ttc tct ggt ggt gct ctc agc cgt gct tct atc ttt gct ctg	240
Asn Met Phe Ser Gly Gly Ala Leu Ser Arg Ala Ser Ile Phe Ala Leu	
65 70 75 80	
ggg atc atg ccg tat att tcg gcg tcg atc att atc cag ctg ctg acg	288
Gly Ile Met Pro Tyr Ile Ser Ala Ser Ile Ile Ile Gln Leu Leu Thr	
85 90 95	
gtg gtt cac cca acg ttg gca gaa att aag aaa gaa ggg gag tct ggt	336
Val Val His Pro Thr Leu Ala Glu Ile Lys Lys Glu Gly Glu Ser Gly	
100 105 110	
cgt cgt aag atc agc cag tac acc cgc tac ggt act ctg gtg ctg gca	384
Arg Arg Lys Ile Ser Gln Tyr Thr Arg Tyr Gly Thr Leu Val Leu Ala	
115 120 125	
ata ttc cag tcg atc ggt att gct acc ggt ctg ccg aat atg cct ggt	432
Ile Phe Gln Ser Ile Gly Ile Ala Thr Gly Leu Pro Asn Met Pro Gly	
130 135 140	
atg caa ggc ctg gtg att aac ccg ggc ttt gca ttc tac ttc acc gct	480
Met Gln Gly Leu Val Ile Asn Pro Gly Phe Ala Phe Tyr Phe Thr Ala	
145 150 155 160	
gtt gta agt ctg gtc aca gga acc atg ttc ctg atg tgg ttg ggc gaa	528
Val Val Ser Leu Val Thr Gly Thr Met Phe Leu Met Trp Leu Gly Glu	
165 170 175	
cag att act gaa cga ggt atc ggc aac ggt att tca atc att atc ttc	576
Gln Ile Thr Glu Arg Gly Ile Gly Asn Gly Ile Ser Ile Ile Ile Phe	
180 185 190	
gcc ggt att gtc gcg gga ctc ccg cca gcc att gcc cat act atc gag	624
Ala Gly Ile Val Ala Gly Leu Pro Pro Ala Ile Ala His Thr Ile Glu	
195 200 205	
caa gcg cgt caa ggc gac ctg cac ttc ctc gtg ttg ctg ttg gtt gca	672
Gln Ala Arg Gln Gly Asp Leu His Phe Leu Val Leu Leu Leu Val Ala	
210 215 220	

gta tta gta ttt gca gtg acg ttc ttt gtt gta ttt gtt gag cgt ggt Val Leu Val Phe Ala Val Thr Phe Phe Val Val Phe Val Glu Arg Gly 225 230 235 240	720
caa cgc cgc att gtg gta aac tac gcg aaa cgt cag caa ggt cgt cgt Gln Arg Arg Ile Val Val Asn Tyr Ala Lys Arg Gln Gln Gly Arg Arg 245 250 255	768
gtc tat gct gca cag agc aca cat tta ccg ctg aaa gtg aat atg gcg Val Tyr Ala Ala Gln Ser Thr His Leu Pro Leu Lys Val Asn Met Ala 260 265 270	816
ggg gta atc ccg gca atc ttc gct tcc agt att att ctg ttc ccg gcg Gly Val Ile Pro Ala Ile Phe Ala Ser Ser Ile Ile Leu Phe Pro Ala 275 280 285	864
acc atc gcg tca tgg ttc ggg ggc ggt act ggt tgg aac tgg ctg aca Thr Ile Ala Ser Trp Phe Gly Gly Gly Thr Gly Trp Asn Trp Leu Thr 290 295 300	912
aca att tcg ctg tat ttg cag cct ggg caa ccg ctt tat gtg tta ctc Thr Ile Ser Leu Tyr Leu Gln Pro Gly Gln Pro Leu Tyr Val Leu Leu 305 310 315 320	960
tat gcg tct gca atc atc ttc ttc tgt ttc ttc tac acg gcg ttg gtt Tyr Ala Ser Ala Ile Ile Phe Phe Cys Phe Phe Tyr Thr Ala Leu Val 325 330 335	1008
ttc aac ccg cgt gaa aca gca gat aac ctg aag aag tcc ggt gca ttt Phe Asn Pro Arg Glu Thr Ala Asp Asn Leu Lys Lys Ser Gly Ala Phe 340 345 350	1056
gta cca gga att cgt ccg gga gag caa acg gcg aag tat atc gat aaa Val Pro Gly Ile Arg Pro Gly Glu Gln Thr Ala Lys Tyr Ile Asp Lys 355 360 365	1104
gta atg acc cgc ctg acc ctg gtt ggt gcg ctg tat att acc ttt atc Val Met Thr Arg Leu Thr Leu Val Gly Ala Leu Tyr Ile Thr Phe Ile 370 375 380	1152
tgc ctg atc ccg gag ttc atg cgt gat gca atg aaa gta ccg ttc tac Cys Leu Ile Pro Glu Phe Met Arg Asp Ala Met Lys Val Pro Phe Tyr 385 390 395 400	1200
ttc ggt ggg acc tca ctg ctt atc gtt gtt gtc gtg att atg gac ttt Phe Gly Gly Thr Ser Leu Leu Ile Val Val Val Val Ile Met Asp Phe 405 410 415	1248
atg gct caa gtg caa act ctg atg atg tcc agt cag tat gag tct gca Met Ala Gln Val Gln Thr Leu Met Met Ser Ser Gln Tyr Glu Ser Ala 420 425 430	1296
ttg aag aag gcg aac ctg aaa ggc tac ggc cga taa Leu Lys Lys Ala Asn Leu Lys Gly Tyr Gly Arg *	1332
435 440	

<210> 144

<211> 435

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(435)

<400> 144

atg	cgt	tta	aat	act	ctg	tct	ccg	gcc	gaa	ggc	tcc	aaa	aag	gcg	ggc	48
Met	Arg	Leu	Asn	Thr	Leu	Ser	Pro	Ala	Glu	Gly	Ser	Lys	Lys	Ala	Gly	
1				5					10					15		

aaa	cgc	ctg	ggc	cgt	ggc	atc	ggc	tct	ggc	ctc	ggc	aaa	acc	ggc	ggc	96
Lys	Arg	Leu	Gly	Arg	Gly	Ile	Gly	Ser	Gly	Leu	Gly	Lys	Thr	Gly	Gly	
		20						25					30			

cgt	ggc	cac	aaa	ggc	cag	aag	tct	cgt	tct	ggc	ggc	gta	cgt	cgc		144
Arg	Gly	His	Lys	Gly	Gln	Lys	Ser	Arg	Ser	Gly	Gly	Gly	Val	Arg	Arg	
		35					40					45				

ggc	ttc	gag	ggc	ggc	cag	atg	cct	ctg	tac	cgt	cgt	ctg	ccg	aaa	ttc	192
Gly	Phe	Glu	Gly	Gly	Gln	Met	Pro	Leu	Tyr	Arg	Arg	Leu	Pro	Lys	Phe	
	50					55					60					

ggc	ttc	act	tct	cgt	aaa	gca	gcg	att	aca	gcc	gaa	att	cgt	ctg	tct	240
Gly	Phe	Thr	Ser	Arg	Lys	Ala	Ala	Ile	Thr	Ala	Glu	Ile	Arg	Leu	Ser	
	65				70					75					80	

gac	ctg	gct	aaa	gta	gaa	ggc	ggc	gta	gta	gac	ctg	aac	acg	ctg	aaa	288
Asp	Leu	Ala	Lys	Val	Glu	Gly	Gly	Val	Val	Asp	Leu	Asn	Thr	Leu	Lys	
			85					90						95		

gcg	gct	aac	att	atc	ggc	atc	cag	atc	gag	ttc	gcg	aaa	gtg	atc	ctg	336
Ala	Ala	Asn	Ile	Ile	Gly	Ile	Gln	Ile	Glu	Phe	Ala	Lys	Val	Ile	Leu	
		100					105						110			

gct	ggc	gaa	gta	acg	act	ccg	gta	act	ggt	cgt	ggc	ctg	cgt	ggt	act	384
Ala	Gly	Glu	Val	Thr	Thr	Pro	Val	Thr	Val	Arg	Gly	Leu	Arg	Val	Thr	
		115					120					125				

aaa	ggc	gct	cgt	gct	gct	atc	gaa	gct	gct	ggc	ggc	aaa	atc	gag	gaa	432
Lys	Gly	Ala	Arg	Ala	Ala	Ile	Glu	Ala	Ala	Gly	Gly	Lys	Ile	Glu	Glu	
	130					135					140					

taa																435
*																

<210> 145

<211> 180

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(180)

<400> 145

atg	gca	aag	act	att	aaa	att	act	caa	acc	cgc	agt	gca	atc	ggc	cgt	48
Met	Ala	Lys	Thr	Ile	Lys	Ile	Thr	Gln	Thr	Arg	Ser	Ala	Ile	Gly	Arg	

1	5	10	15	
ctg ccg aaa cac aag gca acg ctg ctt ggc ctg ggt ctg cgt cgt att				96
Leu Pro Lys His Lys Ala Thr Leu Leu Gly Leu Gly Leu Arg Arg Ile				
20		25	30	
ggt cac acc gta gag cgc gag gat act cct gct att cgc ggt atg atc				144
Gly His Thr Val Glu Arg Glu Asp Thr Pro Ala Ile Arg Gly Met Ile				
35		40	45	
aac gcg gtt tcc ttc atg gtt aaa gtt gag gag taa				180
Asn Ala Val Ser Phe Met Val Lys Val Glu Glu *				
50		55		
<210> 146				
<211> 504				
<212> DNA				
<213> Escherichia coli				
<220>				
<221> CDS				
<222> (1)...(504)				
<400> 146				
atg gct cac atc gaa aaa caa gct ggc gaa ctg cag gaa aag ctg atc				48
Met Ala His Ile Glu Lys Gln Ala Gly Glu Leu Gln Glu Lys Leu Ile				
1	5	10	15	
gcg gta aac cgc gta tct aaa acc gtt aaa ggt ggt cgt att ttc tcc				96
Ala Val Asn Arg Val Ser Lys Thr Val Lys Gly Gly Arg Ile Phe Ser				
20		25	30	
ttc aca gct ctg act gta gtt ggc gat ggt aac ggt cgc gtt ggt ttt				144
Phe Thr Ala Leu Thr Val Val Gly Asp Gly Asn Gly Arg Val Gly Phe				
35		40	45	
ggt tac ggt aaa gcg cgt gaa gtt cca gca gcg atc cag aaa gcg atg				192
Gly Tyr Gly Lys Ala Arg Glu Val Pro Ala Ala Ile Gln Lys Ala Met				
50		55	60	
gaa aaa gcc cgt cgc aat atg att aac gtc gcg ctg aat aac gcc act				240
Glu Lys Ala Arg Arg Asn Met Ile Asn Val Ala Leu Asn Asn Gly Thr				
65		70	75	80
ctg caa cac cct gtt aaa ggt gtt cac acg ggt tct cgc gta ttc atg				288
Leu Gln His Pro Val Lys Gly Val His Thr Gly Ser Arg Val Phe Met				
85		90	95	
cag ccg gct tcc gaa ggt acc ggt atc atc gcc ggt ggt gca atg cgc				336
Gln Pro Ala Ser Glu Gly Thr Gly Ile Ile Ala Gly Gly Ala Met Arg				
100		105	110	
gcc gtt ctg gaa gtc gct ggg gtt cat aac gtt ctg gct aaa gcc tat				384
Ala Val Leu Glu Val Ala Gly Val His Asn Val Leu Ala Lys Ala Tyr				
115		120	125	
ggt tcc acc aac ccg atc aac gtg gtt cgt gca act att gat ggc ctg				432
Gly Ser Thr Asn Pro Ile Asn Val Val Arg Ala Thr Ile Asp Gly Leu				
130		135	140	

gaa aat atg aat tct cca gaa atg gtc gct gcc aag cgt ggt aaa tcc 480
 Glu Asn Met Asn Ser Pro Glu Met Val Ala Ala Lys Arg Gly Lys Ser
 145 150 155 160

ggt gaa gaa att ctg ggg aaa taa 504
 Val Glu Glu Ile Leu Gly Lys *
 165

<210> 147

<211> 354

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(354)

<400> 147

atg gat aag aaa tct gct cgt atc cgt cgt gcg acc cgc gca cgc cgc 48
 Met Asp Lys Lys Ser Ala Arg Ile Arg Arg Ala Thr Arg Ala Arg Arg
 1 5 10 15

aag ctc cag gag ctg ggc gca act cgc ctg gtg gta cat cgt acc ccg 96
 Lys Leu Gln Glu Leu Gly Ala Thr Arg Leu Val Val His Arg Thr Pro
 20 25 30

cgt cac att tac gca cag gta att gca ccg aac ggt tct gaa gtt ctg 144
 Arg His Ile Tyr Ala Gln Val Ile Ala Pro Asn Gly Ser Glu Val Leu
 35 40 45

gta gct gct tct act gta gaa aaa gct atc gct gaa caa ctg aag tac 192
 Val Ala Ala Ser Thr Val Glu Lys Ala Ile Ala Glu Gln Leu Lys Tyr
 50 55 60

acc ggt aac aaa gac gcg gct gca gct gtg ggt aaa gct gtc gct gaa 240
 Thr Gly Asn Lys Asp Ala Ala Ala Val Gly Lys Ala Val Ala Glu
 65 70 75 80

cgc gct ctg gaa aaa ggc atc aaa gat gta tcc ttt gac cgt tcc ggg 288
 Arg Ala Leu Glu Lys Gly Ile Lys Asp Val Ser Phe Asp Arg Ser Gly
 85 90 95

ttc caa tat cat ggt cgt gtc cag gca ctg gca gat gct gcc cgt gaa 336
 Phe Gln Tyr His Gly Arg Val Gln Ala Leu Ala Asp Ala Ala Arg Glu
 100 105 110

gct ggc ctt cag ttc taa 354
 Ala Gly Leu Gln Phe *
 115

<210> 148

<211> 534

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(534)

<400> 148

atg tct cgt gtt gct aaa gca ccg gtc gtt gtt cct gcc ggc gtt gac 48
 Met Ser Arg Val Ala Lys Ala Pro Val Val Val Pro Ala Gly Val Asp
 1 5 10 15

gta aaa atc aac ggt cag gtt att acg atc aaa ggt aaa aac ggc gag 96
 Val Lys Ile Asn Gly Gln Val Ile Thr Ile Lys Gly Lys Asn Gly Glu
 20 25 30

ctg act cgt act ctc aac gat gct gtt gaa gtt aaa cat gca gat aat 144
 Leu Thr Arg Thr Leu Asn Asp Ala Val Glu Val Lys His Ala Asp Asn
 35 40 45

acc ctg acc ttc ggt ccg cgt gat ggt tac gca gac ggt tgg gca cag 192
 Thr Leu Thr Phe Gly Pro Arg Asp Gly Tyr Ala Asp Gly Trp Ala Gln
 50 55 60

gct ggt acc gcg cgt gcc ctg ctg aac tca atg gtt atc ggt gtt acc 240
 Ala Gly Thr Ala Arg Ala Leu Leu Asn Ser Met Val Ile Gly Val Thr
 65 70 75 80

gaa ggc ttc act aag aag ctg cag ctg gtt ggt gta ggt tac cgt gca 288
 Glu Gly Phe Thr Lys Lys Leu Gln Leu Val Gly Val Gly Tyr Arg Ala
 85 90 95

gcg gtt aaa ggc aat gtg att aac ctg tct ctg ggt ttc tct cat cct 336
 Ala Val Lys Gly Asn Val Ile Asn Leu Ser Leu Gly Phe Ser His Pro
 100 105 110

gtt gac cat cag ctg cct gcg ggt atc act gct gaa tgt ccg act cag 384
 Val Asp His Gln Leu Pro Ala Gly Ile Thr Ala Glu Cys Pro Thr Gln
 115 120 125

act gaa atc gtg ctg aaa ggc gct gat aag cag gtg atc ggc cag gtt 432
 Thr Glu Ile Val Leu Lys Gly Ala Asp Lys Gln Val Ile Gly Gln Val
 130 135 140

gca gcg gat ctg cgc gcc tac cgt cgt cct gag cct tat aaa ggc aag 480
 Ala Ala Asp Leu Arg Ala Tyr Arg Arg Pro Glu Pro Tyr Lys Gly Lys
 145 150 155 160

ggt gtt cgt tac gcc gac gaa gtc gtg cgt acc aaa gag gct aag aag 528
 Gly Val Arg Tyr Ala Asp Glu Val Val Arg Thr Lys Glu Ala Lys Lys
 165 170 175

aag taa 534
 Lys *

<210> 149

<211> 393

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(393)

<400> 149

atg agc atg caa gat ccg atc gcg gat atg ctg acc cgt atc cgt aac 48
 Met Ser Met Gln Asp Pro Ile Ala Asp Met Leu Thr Arg Ile Arg Asn
 1 5 10 15

ggt cag gcc gcg aac aaa gct gcg gtc acc atg cct tcc tcc aag ctg 96
 Gly Gln Ala Ala Asn Lys Ala Ala Val Thr Met Pro Ser Ser Lys Leu
 20 25 30

aaa gtg gca atc gcc aac gtg ctg aag gaa gaa ggt ttt att gaa gat 144
 Lys Val Ala Ile Ala Asn Val Leu Lys Glu Glu Gly Phe Ile Glu Asp
 35 40 45

ttt aaa gtt gaa ggc gac acc aag cct gaa ctg gaa ctt act ctg aag 192
 Phe Lys Val Glu Gly Asp Thr Lys Pro Glu Leu Glu Leu Thr Leu Lys
 50 55 60

tat ttc cag ggc aaa gct gtt gta gaa agc att cag cgt gtc agc cgc 240
 Tyr Phe Gln Gly Lys Ala Val Val Glu Ser Ile Gln Arg Val Ser Arg
 65 70 75 80

cca ggt ctg cgc atc tat aaa cgt aaa gat gag ctg ccg aaa gtt atg 288
 Pro Gly Leu Arg Ile Tyr Lys Arg Lys Asp Glu Leu Pro Lys Val Met
 85 90 95

gcg ggt ctg ggt atc gca gtt gtt tct acc tct aaa ggt gtt atg act 336
 Ala Gly Leu Gly Ile Ala Val Val Ser Thr Ser Lys Gly Val Met Thr
 100 105 110

gat cgt gca gcg cgc cag gct ggt ctt ggt ggc gaa att atc tgc tac 384
 Asp Arg Ala Ala Arg Gln Ala Gly Leu Gly Gly Glu Ile Ile Cys Tyr
 115 120 125

gta gcc taa 393
 Val Ala *
 130

<210> 150

<211> 306

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)... (306)

<400> 150

atg gct aag caa tca atg aaa gca cgc gaa gta aaa cgc gta gct tta 48
 Met Ala Lys Gln Ser Met Lys Ala Arg Glu Val Lys Arg Val Ala Leu
 1 5 10 15

gct gat aaa tac ttc gcg aaa cgc gct gaa ctg aaa gcg atc atc tct 96
 Ala Asp Lys Tyr Phe Ala Lys Arg Ala Glu Leu Lys Ala Ile Ile Ser
 20 25 30

gat gtg aac gct tcc gac gaa gat cgt tgg aac gct gtt ctc aag ctg 144
 Asp Val Asn Ala Ser Asp Glu Asp Arg Trp Asn Ala Val Leu Lys Leu
 35 40 45

cag act ctg ccg cgt gat tcc agc ccg tct cgt cag cgt aac cgc tgc 192
 Gln Thr Leu Pro Arg Asp Ser Ser Pro Ser Arg Gln Arg Asn Arg Cys
 50 55 60

cgt caa aca ggt cgt ccg cat ggt ttc ctg cgg aag ttc ggg ttg agc 240
 Arg Gln Thr Gly Arg Pro His Gly Phe Leu Arg Lys Phe Gly Leu Ser
 65 70 75 80

cgt att aag gtc cgt gaa gcc gct atg cgc ggt gaa atc ccg ggt ctg 288
 Arg Ile Lys Val Arg Glu Ala Ala Met Arg Gly Glu Ile Pro Gly Leu
 85 90 95

aaa aag gct agc tgg taa 306
 Lys Lys Ala Ser Trp *
 100

<210> 151
 <211> 540
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(540)

<400> 151

atg gcg aaa ctg cat gat tac tac aaa gac gaa gta gtt aaa aaa ctc 48
 Met Ala Lys Leu His Asp Tyr Tyr Lys Asp Glu Val Val Lys Lys Leu
 1 5 10 15

atg act gag ttt aac tac aat tct gtc atg caa gtc cct cgg gtc gag 96
 Met Thr Glu Phe Asn Tyr Asn Ser Val Met Gln Val Pro Arg Val Glu
 20 25 30

aag atc acc ctg aac atg ggt gtt ggt gaa gcg atc gct gac aaa aaa 144
 Lys Ile Thr Leu Asn Met Gly Val Gly Glu Ala Ile Ala Asp Lys Lys
 35 40 45

ctg ctg gat aac gca gca gca gac ctg gca gca atc tcc ggt caa aaa 192
 Leu Leu Asp Asn Ala Ala Ala Asp Leu Ala Ala Ile Ser Gly Gln Lys
 50 55 60

ccg ctg atc acc aaa gca cgc aaa tct gtt gca ggc ttc aaa atc cgt 240
 Pro Leu Ile Thr Lys Ala Arg Lys Ser Val Ala Gly Phe Lys Ile Arg
 65 70 75 80

cag ggc tat ccg atc ggc tgt aaa gta act ctg cgt ggc gaa cgc atg 288
 Gln Gly Tyr Pro Ile Gly Cys Lys Val Thr Leu Arg Gly Glu Arg Met
 85 90 95

tgg gag ttc ttt gag cgc ctg atc act att gct gta cct cgt atc cgt 336
 Trp Glu Phe Phe Glu Arg Leu Ile Thr Ile Ala Val Pro Arg Ile Arg
 100 105 110

gac ttc cgt ggc ctg tcc gct aag tct ttc gac ggt cgt ggt aac tac 384
 Asp Phe Arg Gly Leu Ser Ala Lys Ser Phe Asp Gly Arg Gly Asn Tyr
 115 120 125

```

agc atg ggt gtc cgt gag cag atc atc ttc cca gaa atc gac tac gat      432
Ser Met Gly Val Arg Glu Gln Ile Ile Phe Pro Glu Ile Asp Tyr Asp
   130                      135                      140

aaa gtc gac cgc gtt cgt ggt ttg gat att acc att acc act act gcg      480
Lys Val Asp Arg Val Arg Gly Leu Asp Ile Thr Ile Thr Thr Thr Ala
   145                      150                      155                      160

aaa tct gac gaa gaa ggc cgc gct ctg ctg gct gcc ttt gac ttc ccg      528
Lys Ser Asp Glu Glu Gly Arg Ala Leu Leu Ala Ala Phe Asp Phe Pro
           165                      170                      175

ttc cgc aag taa      540
Phe Arg Lys  *
```

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<210> 152
<211> 315
<212> DNA
<213> Escherichia coli
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<220>
<221> CDS
<222> (1)...(315)
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<400> 152
atg gca gcg aaa atc cgt cgt gat gac gaa gtt atc gtg tta acc ggt      48
Met Ala Ala Lys Ile Arg Arg Asp Asp Glu Val Ile Val Leu Thr Gly
   1                      5                      10                      15

aaa gat aaa ggt aaa cgc ggt aaa gtt aag aat gtc ctg tct tcc ggc      96
Lys Asp Lys Gly Lys Arg Gly Lys Val Lys Asn Val Leu Ser Ser Gly
           20                      25                      30

aag gtc att gtt gaa ggt atc aac ctg gtt aag aaa cat cag aag ccg      144
Lys Val Ile Val Glu Gly Ile Asn Leu Val Lys Lys His Gln Lys Pro
           35                      40                      45

gtt ccg gcc ctg aac caa ccg ggt ggc atc gtt gaa aaa gaa gcc gct      192
Val Pro Ala Leu Asn Gln Pro Gly Gly Ile Val Glu Lys Glu Ala Ala
   50                      55                      60

att cag gtt tcc aac gta gca atc ttc aat gcg gca acc ggc aag gct      240
Ile Gln Val Ser Asn Val Ala Ile Phe Asn Ala Ala Thr Gly Lys Ala
   65                      70                      75                      80

gac cgt gta ggc ttt aga ttc gaa gac ggt aaa aaa gtc cgt ttc ttc      288
Asp Arg Val Gly Phe Arg Phe Glu Asp Gly Lys Lys Val Arg Phe Phe
           85                      90                      95

aag tct aac agc gaa act atc aag taa      315
Lys Ser Asn Ser Glu Thr Ile Lys  *
           100
```

```

<210> 153
<211> 372
<212> DNA
<213> Escherichia coli
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<220>

<221> CDS

<222> (1)...(372)

<400> 153

atg atc caa gaa cag act atg ctg aac gtc gcc gac aac tcc ggt gca	48
Met Ile Gln Glu Gln Thr Met Leu Asn Val Ala Asp Asn Ser Gly Ala	
1 5 10 15	
cg t cgc gta atg tgt atc aag gtt ctg ggt ggc tcg cac cgt cgc tac	96
Arg Arg Val Met Cys Ile Lys Val Leu Gly Gly Ser His Arg Arg Tyr	
20 25 30	
gca ggc gta ggc gac atc atc aag atc acc atc aaa gaa gca att ccg	144
Ala Gly Val Gly Asp Ile Ile Lys Ile Thr Ile Lys Glu Ala Ile Pro	
35 40 45	
cg t ggt aag gtc aaa aaa ggt gat gtg ctg aag gcg gta gtg gtg cgc	192
Arg Gly Lys Val Lys Lys Gly Asp Val Leu Lys Ala Val Val Val Arg	
50 55 60	
acc aag aag ggt gtt cgt cgc ccg gac ggt tct gtc att cgc ttc gat	240
Thr Lys Lys Gly Val Arg Arg Pro Asp Gly Ser Val Ile Arg Phe Asp	
65 70 75 80	
ggt aat gct tgt gtt ctt ctg aac aac aac agc gag cag cct atc ggt	288
Gly Asn Ala Cys Val Leu Leu Asn Asn Asn Ser Glu Gln Pro Ile Gly	
85 90 95	
acg cgt att ttt ggg ccg gta act cgt gag ctt cgt agt gag aag ttc	336
Thr Arg Ile Phe Gly Pro Val Thr Arg Glu Leu Arg Ser Glu Lys Phe	
100 105 110	
atg aaa att atc tct ctg gca cca gaa gta ctc taa	372
Met Lys Ile Ile Ser Leu Ala Pro Glu Val Leu *	
115 120	

<210> 154

<211> 1191

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1191)

<400> 154

atg aaa ata aaa aca ggt gca cgc atc ctc gca tta tcc gca tta acg	48
Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr	
1 5 10 15	
acg atg atg ttt tcc gcc tcg gct ctc gcc aaa atc gaa gaa ggt aaa	96
Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys	
20 25 30	
ctg gta atc tgg att aac ggc gat aaa ggc tat aac ggt ctc gct gaa	144
Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu	
35 40 45	

gtc ggt aag aaa ttc gag aaa gat acc gga att aaa gtc acc gtt gag Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu 50 55 60	192
cat ccg gat aaa ctg gaa gag aaa ttc cca cag gtt gcg gca act ggc His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly 65 70 75 80	240
gat ggc cct gac att atc ttc tgg gca cac gac cgc ttt ggt ggc tac Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr 85 90 95	288
gct caa tct ggc ctg ttg gct gaa atc acc ccg gac aaa gcg ttc cag Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln 100 105 110	336
gac aag ctg tat ccg ttt acc tgg gat gcc gta cgt tac aac ggc aag Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys 115 120 125	384
ctg att gct tac ccg atc gct gtt gaa gcg tta tcg ctg att tat aac Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn 130 135 140	432
aaa gat ctg ctg ccg aac ccg cca aaa acc tgg gaa gag atc ccg gcg Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala 145 150 155 160	480
ctg gat aaa gaa ctg aaa gcg aaa ggt aag agc gcg ctg atg ttc aac Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn 165 170 175	528
ctg caa gaa ccg tac ttc acc tgg ccg ctg att gct gct gac ggg ggt Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly 180 185 190	576
tat gcg ttc aag tat gaa aac ggc aag tac gac att aaa gac gtg ggc Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly 195 200 205	624
gtg gat aac gct ggc gcg aaa gcg ggt ctg acc ttc ctg gtt gac ctg Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu 210 215 220	672
att aaa aac aaa cac atg aat gca gac acc gat tac tcc atc gca gaa Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu 225 230 235 240	720
gct gcc ttt aat aaa ggc gaa aca gcg atg acc atc aac ggc ccg tgg Ala Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp 245 250 255	768
gca tgg tcc aac atc gac acc agc aaa gtg aat tat ggt gta acg gta Ala Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val 260 265 270	816
ctg ccg acc ttc aag ggt caa cca tcc aaa ccg ttc gtt ggc gtg ctg Leu Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu 275 280 285	864

agc gca ggt att aac gcc gcc agt ccg aac aaa gag ctg gcg aaa gag 912
 Ser Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu
 290 295 300

ttc ctc gaa aac tat ctg ctg act gat gaa ggt ctg gaa gcg gtt aat 960
 Phe Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn
 305 310 315 320

aaa gac aaa ccg ctg ggt gcc gta gcg ctg aag tct tac gag gaa gag 1008
 Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu
 325 330 335

ttg gcg aaa gat cca cgt att gcc gcc acc atg gaa aac gcc cag aaa 1056
 Leu Ala Lys Asp Pro Arg Ile Ala Ala Thr Met Glu Asn Ala Gln Lys
 340 345 350

ggt gaa atc atg ccg aac atc ccg cag atg tcc gct ttc tgg tat gcc 1104
 Gly Glu Ile Met Pro Asn Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala
 355 360 365

gtg cgt act gcg gtg atc aac gcc gcc agc ggt cgt cag act gtc gat 1152
 Val Arg Thr Ala Val Ile Asn Ala Ala Ser Gly Arg Gln Thr Val Asp
 370 375 380

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<211> 1545

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1545)

<400> 155

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tgg tca gtg cta ggt ctg ctc ggc ctg ctg gtg ggt tac ctt gtt gtt 96
 Trp Ser Val Leu Gly Leu Leu Gly Leu Leu Val Gly Tyr Leu Val Val
 20 25 30

tta atg tac gca caa ggg gaa tac ctg ttc gcc att acc acg ctg ata 144
 Leu Met Tyr Ala Gln Gly Glu Tyr Leu Phe Ala Ile Thr Thr Leu Ile
 35 40 45

ttg agt tca gcg ggg ctg tat att ttc gcc aat cgt aaa gcc tac gcc 192
 Leu Ser Ser Ala Gly Leu Tyr Ile Phe Ala Asn Arg Lys Ala Tyr Ala
 50 55 60

tgg cgc tat gtt tac ccg gga atg gct gga atg gga tta ttc gtc ctc 240
 Trp Arg Tyr Val Tyr Pro Gly Met Ala Gly Met Gly Leu Phe Val Leu
 65 70 75 80

ttc cct ctg gtc tgc acc atc gcc att gcc ttc acc aac tac agc agc Phe Pro Leu Val Cys Thr Ile Ala Ile Ala Phe Thr Asn Tyr Ser Ser 85 90 95	288
act aac cag ctg act ttt gaa cgt gcg cag gaa gtg ttg tta gat cgc Thr Asn Gln Leu Thr Phe Glu Arg Ala Gln Glu Val Leu Leu Asp Arg 100 105 110	336
tcc tgg caa gca ggc aaa acc tat aac ttt ggt ctt tac ccg gcg ggc Ser Trp Gln Ala Gly Lys Thr Tyr Asn Phe Gly Leu Tyr Pro Ala Gly 115 120 125	384
gat gag tgg caa ctg gcg ctc agc gac ggc gaa acc ggc aaa aat tac Asp Glu Trp Gln Leu Ala Leu Ser Asp Gly Glu Thr Gly Lys Asn Tyr 130 135 140	432
ctc tcc gac gct ttt aaa ttt ggc ggc gag caa aaa ctg caa ctg aaa Leu Ser Asp Ala Phe Lys Phe Gly Gly Glu Gln Lys Leu Gln Leu Lys 145 150 155 160	480
gaa acg acc gcc cag ccc gaa ggc gaa cgc gcg aat ctg cgc gtg att Glu Thr Thr Ala Gln Pro Glu Gly Glu Arg Ala Asn Leu Arg Val Ile 165 170 175	528
acc cag aat cgt cag gcg ctg agt gac att acc gcc att ctg ccg gat Thr Gln Asn Arg Gln Ala Leu Ser Asp Ile Thr Ala Ile Leu Pro Asp 180 185 190	576
ggc aac aaa gtg atg atg agc tcc ctg cgc cag ttt tct ggc acg cag Gly Asn Lys Val Met Met Ser Ser Leu Arg Gln Phe Ser Gly Thr Gln 195 200 205	624
ccg ctc tac aca ctc gac ggt gac ggc acg ttg acg aat aat cag agc Pro Leu Tyr Thr Leu Asp Gly Asp Gly Thr Leu Thr Asn Asn Gln Ser 210 215 220	672
ggc gtg aaa tat cgt ccg aat aac caa att ggc ttt tac cag tcc att Gly Val Lys Tyr Arg Pro Asn Asn Gln Ile Gly Phe Tyr Gln Ser Ile 225 230 235 240	720
acc gcc gac ggc aac tgg ggt gat gaa aag cta agc ccc ggt tac acc Thr Ala Asp Gly Asn Trp Gly Asp Glu Lys Leu Ser Pro Gly Tyr Thr 245 250 255	768
gtg acc acc ggc tgg aaa aac ttt acc cgc gtc ttt acc gac gaa ggc Val Thr Thr Gly Trp Lys Asn Phe Thr Arg Val Phe Thr Asp Glu Gly 260 265 270	816
att cag aaa ccg ttc ctc gcc att ttc gtc tgg acc gtg gtg ttc tcg Ile Gln Lys Pro Phe Leu Ala Ile Phe Val Trp Thr Val Val Phe Ser 275 280 285	864
ctg atc act gtc ttt tta acg gtg gcg gtc ggc atg gtt ctg gcg tgt Leu Ile Thr Val Phe Leu Thr Val Ala Val Gly Met Val Leu Ala Cys 290 295 300	912
ctg gtg cag tgg gaa gcg ttg cgc ggc aaa gcg gtc tat cgc gtc ctg Leu Val Gln Trp Glu Ala Leu Arg Gly Lys Ala Val Tyr Arg Val Leu 305 310 315 320	960

ctg att ctg ccc tac gcg gtg cca tcg ttc att tca atc ttg att ttc Leu Ile Leu Pro Tyr Ala Val Pro Ser Phe Ile Ser Ile Leu Ile Phe 325 330 335	1008
aaa ggg ttg ttt aac cag agc ttc ggt gaa atc aac atg atg ttg agc Lys Gly Leu Phe Asn Gln Ser Phe Gly Glu Ile Asn Met Met Leu Ser 340 345 350	1056
gcg ctg ttt ggc gtg aag ccc gcc tgg ttc agc gat ccg acc acc gcc Ala Leu Phe Gly Val Lys Pro Ala Trp Phe Ser Asp Pro Thr Thr Ala 355 360 365	1104
cgc acg atg cta att atc gtc aat acc tgg ctg ggt tat ccg tac atg Arg Thr Met Leu Ile Ile Val Asn Thr Trp Leu Gly Tyr Pro Tyr Met 370 375 380	1152
atg atc ctc tgc atg ggc ttg ctg aaa gcg att ccg gac gat ttg tat Met Ile Leu Cys Met Gly Leu Leu Lys Ala Ile Pro Asp Asp Leu Tyr 385 390 395 400	1200
gaa gcc tca gca atg gat ggc gca ggt ccg ttc cag aac ttc ttt aag Glu Ala Ser Ala Met Asp Gly Ala Gly Pro Phe Gln Asn Phe Phe Lys 405 410 415	1248
att acg ctg ccg ctg ctg att aaa ccg ctg acg ccg ctg atg atc gcc Ile Thr Leu Pro Leu Leu Ile Lys Pro Leu Thr Pro Leu Met Ile Ala 420 425 430	1296
agc ttc gcc ttt aac ttt aac aac ttc gtg ctg att caa ctg tta acc Ser Phe Ala Phe Asn Phe Asn Asn Phe Val Leu Ile Gln Leu Leu Thr 435 440 445	1344
aac ggc ggc ccg gat cgt ctt ggc acg acc acg cca gcc ggt tat acc Asn Gly Gly Pro Asp Arg Leu Gly Thr Thr Thr Pro Ala Gly Tyr Thr 450 455 460	1392
gac ctg ctt gtt aac tac acc tac cgc atc gct ttt gaa ggc ggc ggg Asp Leu Leu Val Asn Tyr Thr Tyr Arg Ile Ala Phe Glu Gly Gly Gly 465 470 475 480	1440
ggt cag gac ttc ggt ctg gcg gca gca att gcc acg ctg atc ttc ctg Gly Gln Asp Phe Gly Leu Ala Ala Ala Ile Ala Thr Leu Ile Phe Leu 485 490 495	1488
ctg gtg ggt gcg ctg gcg ata gtg aac ctg aaa gcc acg cga atg aag Leu Val Gly Ala Leu Ala Ile Val Asn Leu Lys Ala Thr Arg Met Lys 500 505 510	1536
ttt gat taa Phe Asp *	1545

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<211> 891

<212> DNA

<213> Escherichia coli

<220>

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<222> (1)...(891)

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1 5 10 15	
cac ctg cta ctg cta ctt ttt atc gca gcg att atg ttc ccg ctg ctg	96
His Leu Leu Leu Leu Leu Phe Ile Ala Ala Ile Met Phe Pro Leu Leu	
20 25 30	
atg gtc gtc gct atc tcg ctg cgt cag gga aac ttt gcg acc ggc agc	144
Met Val Val Ala Ile Ser Leu Arg Gln Gly Asn Phe Ala Thr Gly Ser	
35 40 45	
ctg atc ccg gag caa atc tcc tgg gat cac tgg aaa ctg gcg tta ggt	192
Leu Ile Pro Glu Gln Ile Ser Trp Asp His Trp Lys Leu Ala Leu Gly	
50 55 60	
ttt agc gtt gaa cag gct gat ggt cgc att acg cca ccg cca ttc ccg	240
Phe Ser Val Glu Gln Ala Asp Gly Arg Ile Thr Pro Pro Pro Phe Pro	
65 70 75 80	
gta ctg ctg tgg ctg tgg aac tcg gta aag gtc gcc ggg att tcc gcg	288
Val Leu Leu Trp Leu Trp Asn Ser Val Lys Val Ala Gly Ile Ser Ala	
85 90 95	
att ggc att gtg gcg ctc tcc acc acc tgc gcc tac gct ttc gcc cgt	336
Ile Gly Ile Val Ala Leu Ser Thr Thr Cys Ala Tyr Ala Phe Ala Arg	
100 105 110	
atg cgc ttt cca ggc aaa gcg acg ctg ctg aaa gga atg ctg att ttc	384
Met Arg Phe Pro Gly Lys Ala Thr Leu Leu Lys Gly Met Leu Ile Phe	
115 120 125	
cag atg ttc ccg gca gta ctt tca ctg gtc gcg ttg tat gcg ttg ttt	432
Gln Met Phe Pro Ala Val Leu Ser Leu Val Ala Leu Tyr Ala Leu Phe	
130 135 140	
gat cgt ctg ggt gag tac att cca ttc att ggc ctg aat act cac ggc	480
Asp Arg Leu Gly Glu Tyr Ile Pro Phe Ile Gly Leu Asn Thr His Gly	
145 150 155 160	
ggc gta att ttc gcg tat ctg ggt ggg att gcg ctg cat gtc tgg acc	528
Gly Val Ile Phe Ala Tyr Leu Gly Gly Ile Ala Leu His Val Trp Thr	
165 170 175	
atc aaa ggc tat ttc gaa acc atc gac agt tcg ctg gaa gaa gct gct	576
Ile Lys Gly Tyr Phe Glu Thr Ile Asp Ser Ser Leu Glu Glu Ala Ala	
180 185 190	
gcg ctg gat ggt gcg aca ccg tgg cag gcc ttc cgc ctt gtc ctg ttg	624
Ala Leu Asp Gly Ala Thr Pro Trp Gln Ala Phe Arg Leu Val Leu Leu	
195 200 205	
ccg ctg tca gta ccg att ctg gcg gtg gta ttc atc ctg tcg ttt atc	672
Pro Leu Ser Val Pro Ile Leu Ala Val Val Phe Ile Leu Ser Phe Ile	
210 215 220	
gct gcc att act gaa gtt ccg gtc gcg tcg ctg tta ctg cgt gac gta	720

-65-

115	120	125	
aaa gtt ctc ctg caa caa ctg att tcg acc atc tct aac tgg aag aat			432
Lys Val Leu Leu Gln Gln Leu Ile Ser Thr Ile Ser Asn Trp Lys Asn			
130	135	140	
gat ctc aaa aca ccg tcc cag gcg gca gca agt gcg att ggc gag cgg			480
Asp Leu Lys Thr Pro Ser Gln Ala Ala Ala Ser Ala Ile Gly Glu Arg			
145	150	155	160
gac cgt att ttt gcc cat tgt tat ggg ctg tat gat gca cac ctg aaa			528
Asp Arg Ile Phe Ala His Cys Tyr Gly Leu Tyr Asp Ala His Leu Lys			
165	170	175	
gcc tgt aac gtt ctc gac ttc gat gat ctg att tta ttg ccg acg ttg			576
Ala Cys Asn Val Leu Asp Phe Asp Asp Leu Ile Leu Leu Pro Thr Leu			
180	185	190	
ctg ctg caa gcc aat gaa gaa gtc cgc aag cgc tgg cag aac aaa att			624
Leu Leu Gln Ala Asn Glu Glu Val Arg Lys Arg Trp Gln Asn Lys Ile			
195	200	205	
cgc tat ctg ctg gtg gat gag tat cag gac acc aac acc agc cag tat			672
Arg Tyr Leu Leu Val Asp Glu Tyr Gln Asp Thr Asn Thr Ser Gln Tyr			
210	215	220	
gag ctg gtg aaa ctg ctg gtg ggc agc cgc gcg cgc ttt acc gtg gtg			720
Glu Leu Val Lys Leu Leu Val Gly Ser Arg Ala Arg Phe Thr Val Val			
225	230	235	240
ggg gac gat gac cag tcg atc tac tcc tgg cgc ggt gca cgt ccg caa			768
Gly Asp Asp Asp Gln Ser Ile Tyr Ser Trp Arg Gly Ala Arg Pro Gln			
245	250	255	
aac ctg gtg ctg ctg agt cag gat ttt ccg gcg ctg aag gtg att aag			816
Asn Leu Val Leu Leu Ser Gln Asp Phe Pro Ala Leu Lys Val Ile Lys			
260	265	270	
ctt gag cag aac tat cgc tct tcc ggg cgt att ctg aaa gcg gcg aac			864
Leu Glu Gln Asn Tyr Arg Ser Ser Gly Arg Ile Leu Lys Ala Ala Asn			
275	280	285	
atc ctg atc gcc aat aac ccg cac gtc ttt gaa aag cgt ctg ttc tcc			912
Ile Leu Ile Ala Asn Asn Pro His Val Phe Glu Lys Arg Leu Phe Ser			
290	295	300	
gaa ctg ggt tat ggc gcg gag cta aaa gta tta agc gcg aat aac gaa			960
Glu Leu Gly Tyr Gly Ala Glu Leu Lys Val Leu Ser Ala Asn Asn Glu			
305	310	315	320
gaa cat gag gct gag cgc gtt act ggc gag ctg atc gcc cat cac ttc			1008
Glu His Glu Ala Glu Arg Val Thr Gly Glu Leu Ile Ala His His Phe			
325	330	335	
gtc aat aaa acg cag tac aaa gat tac gcc att ctt tat cgc ggt aac			1056
Val Asn Lys Thr Gln Tyr Lys Asp Tyr Ala Ile Leu Tyr Arg Gly Asn			
340	345	350	
cat cag tcg ccg gtg ttt gaa aaa ttc ctg atg caa aac cgc atc ccg			1104
His Gln Ser Arg Val Phe Glu Lys Phe Leu Met Gln Asn Arg Ile Pro			

355	360	365	
tac aaa ata tct ggt ggt acg tct ttt ttc tct cgt cct gaa atc aag Tyr Lys Ile Ser Gly Gly Thr Ser Phe Phe Ser Arg Pro Glu Ile Lys 370 375 380			1152
gac ttg ctg gct tat ctg cgc gtg ctg act aac ccg gac gat gac agc Asp Leu Leu Ala Tyr Leu Arg Val Leu Thr Asn Pro Asp Asp Asp Ser 385 390 395 400			1200
gca ttt ctg cgt atc gtt aac acg ccg aag cga gag att ggc ccg gct Ala Phe Leu Arg Ile Val Asn Thr Pro Lys Arg Glu Ile Gly Pro Ala 405 410 415			1248
acg ctg aaa aag ctg ggt gag tgg gcg atg acg cgc aat aaa agc atg Thr Leu Lys Lys Leu Gly Glu Trp Ala Met Thr Arg Asn Lys Ser Met 420 425 430			1296
ttt acc gcc agc ttt gat atg ggc ctg agt cag acg ctt agc gga cgt Phe Thr Ala Ser Phe Asp Met Gly Leu Ser Gln Thr Leu Ser Gly Arg 435 440 445			1344
ggt tat gaa gca ttg acc cgc ttc act cac tgg ttg gca gaa atc cag Gly Tyr Glu Ala Leu Thr Arg Phe Thr His Trp Leu Ala Glu Ile Gln 450 455 460			1392
cgt ctg gcg gag cgg gag ccg att gcc gcg gtg cgt gat ctg atc cat Arg Leu Ala Glu Arg Glu Pro Ile Ala Ala Val Arg Asp Leu Ile His 465 470 475 480			1440
ggc atg gat tat gaa tcc tgg ctg tac gaa aca tcg ccc agc ccg aaa Gly Met Asp Tyr Glu Ser Trp Leu Tyr Glu Thr Ser Pro Ser Pro Lys 485 490 495			1488
gcc gcc gaa atg cgc atg aag aac gtc aac caa ctg ttt agc tgg atg Ala Ala Glu Met Arg Met Lys Asn Val Asn Gln Leu Phe Ser Trp Met 500 505 510			1536
acg gag atg ctg gaa ggc agt gaa ctg gat gag ccg atg acg ctc acc Thr Glu Met Leu Glu Gly Ser Glu Leu Asp Glu Pro Met Thr Leu Thr 515 520 525			1584
cag gtg gtg acg cgc ttt act ttg cgc gac atg atg gag cgt ggt gag Gln Val Val Thr Arg Phe Thr Leu Arg Asp Met Met Glu Arg Gly Glu 530 535 540			1632
agt gaa gaa gag ctg gat cag gtg caa ctg atg act ctc cac gcg tcg Ser Glu Glu Glu Leu Asp Gln Val Gln Leu Met Thr Leu His Ala Ser 545 550 555 560			1680
aaa ggg ctg gag ttt cct tat gtc tac atg gtc ggt atg gaa gaa ggg Lys Gly Leu Glu Phe Pro Tyr Val Tyr Met Val Gly Met Glu Glu Gly 565 570 575			1728
ttt ttg ccg cac cag agc agc atc gat gaa gat aat atc gat gag gag Phe Leu Pro His Gln Ser Ser Ile Asp Glu Asp Asn Ile Asp Glu Glu 580 585 590			1776
cgg cgg ctg gcc tat gtc ggc att acc cgc gcc cag aag gaa ttg acc Arg Arg Leu Ala Tyr Val Gly Ile Thr Arg Ala Gln Lys Glu Leu Thr			1824

595	600	605	
ttt acg ctg tgt aaa gaa cgc cgt cag tac ggc gaa ctg gtg cgc ccg Phe Thr Leu Cys Lys Glu Arg Arg Gln Tyr Gly Glu Leu Val Arg Pro 610 615 620			1872
gag ccg agc cgc ttt ttg ctg gag ctg ccg cag gat gat ctg att tgg Glu Pro Ser Arg Phe Leu Leu Glu Leu Pro Gln Asp Asp Leu Ile Trp 625 630 635 640			1920
gaa cag gag cgc aaa gtg gtc agc gcc gaa gaa cgg atg cag aaa ggg Glu Gln Glu Arg Lys Val Val Ser Ala Glu Glu Arg Met Gln Lys Gly 645 650 655			1968
caa agc cat ctg gcg aat ctg aaa gcg atg atg gcg gca aaa cga ggg Gln Ser His Leu Ala Asn Leu Lys Ala Met Met Ala Ala Lys Arg Gly 660 665 670			2016
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ctc agt cag aca ttt gca gaa aaa ttt act gtg acc gag gaa tta ctg Leu Ser Gln Thr Phe Ala Glu Lys Phe Thr Val Thr Glu Glu Leu Leu 20 25 30			96
cag tct tta aaa aaa aca gcg tta tcc gga gat gaa gaa agc att gag Gln Ser Leu Lys Lys Thr Ala Leu Ser Gly Asp Glu Glu Ser Ile Glu 35 40 45			144
tta ctg cat aat att gcg tta ggt tat gat aaa ttt ggg aaa gaa gct Leu Leu His Asn Ile Ala Leu Gly Tyr Asp Lys Phe Gly Lys Glu Ala 50 55 60			192
gaa gat att ctt tac cat att gtt aga acc cca aca aat gag acc cta Glu Asp Ile Leu Tyr His Ile Val Arg Thr Pro Thr Asn Glu Thr Leu 65 70 75 80			240
tcg att atc cga ctt atc aaa aat gct tgt tta aaa tta tat aat ctg Ser Ile Ile Arg Leu Ile Lys Asn Ala Cys Leu Lys Leu Tyr Asn Leu 85 90 95			288
gca cat atc gca acc aac tcc ccc ctc aaa tca cat gat tca gat gat Ala His Ile Ala Thr Asn Ser Pro Leu Lys Ser His Asp Ser Asp Asp 100 105 110			336

ctc ctg ttc aaa aaa cta ttc tcc cct tcg aaa tta atg aca att atc Leu Leu Phe Lys Lys Leu Phe Ser Pro Ser Lys Leu Met Thr Ile Ile 115 120 125	384
ggt gat gaa att cct ctt ata tct gaa aaa cag tcg ctt tca aag gtg Gly Asp Glu Ile Pro Leu Ile Ser Glu Lys Gln Ser Leu Ser Lys Val 130 135 140	432
ctt tta aat gat gag aat aat gaa ctg agt gat ggt aca aac ttc tgg Leu Leu Asn Asp Glu Asn Asn Glu Leu Ser Asp Gly Thr Asn Phe Trp 145 150 155 160	480
gat aaa aat cgt caa tta acc aca gat gaa ata gct tgc tat ctt cag Asp Lys Asn Arg Gln Leu Thr Thr Asp Glu Ile Ala Cys Tyr Leu Gln 165 170 175	528
aag atc gcc gct aat gca aaa aat act caa gtc aat tat cct act ggt Lys Ile Ala Ala Asn Ala Lys Asn Thr Gln Val Asn Tyr Pro Thr Gly 180 185 190	576
ctc tac gtc ccc tac tcc acc aga act cac ctg gaa gac gct ctc aat Leu Tyr Val Pro Tyr Ser Thr Arg Thr His Leu Glu Asp Ala Leu Asn 195 200 205	624
gaa aat att aag agc gat cca tca tgg ccg aat gaa gtc cag tta ttc Glu Asn Ile Lys Ser Asp Pro Ser Trp Pro Asn Glu Val Gln Leu Phe 210 215 220	672
ccc ata aat act ggc gga cac tgg ata tta gtt tcg cta cag aaa ata Pro Ile Asn Thr Gly Gly His Trp Ile Leu Val Ser Leu Gln Lys Ile 225 230 235 240	720
gta aat aaa aaa aat aat aaa cta caa ata aaa tgc gtc ata ttc aac Val Asn Lys Lys Asn Asn Lys Leu Gln Ile Lys Cys Val Ile Phe Asn 245 250 255	768
tca ttg cgt gca cta ggc tat gat aaa gaa aat tca ctt aag cgt gtc Ser Leu Arg Ala Leu Gly Tyr Asp Lys Glu Asn Ser Leu Lys Arg Val 260 265 270	816
att aat agt ttt aat tct gaa ctc atg gga gaa atg tcg aat aat aat Ile Asn Ser Phe Asn Ser Glu Leu Met Gly Glu Met Ser Asn Asn Asn 275 280 285	864
ata aaa gtt cat tta aat gaa cca gag ata ata ttt tta cat gcc gat Ile Lys Val His Leu Asn Glu Pro Glu Ile Ile Phe Leu His Ala Asp 290 295 300	912
ctt cag caa tac tta agc caa agt tgc ggt gca ttt gtg tgc atg gca Leu Gln Gln Tyr Leu Ser Gln Ser Cys Gly Ala Phe Val Cys Met Ala 305 310 315 320	960
gcc cag gaa gtg att gaa caa agg gaa agc aat tct gac agc gcc ccc Ala Gln Glu Val Ile Glu Gln Arg Glu Ser Asn Ser Asp Ser Ala Pro 325 330 335	1008
tat acg tta tta aaa aac cat gct gac aga ttt aaa aaa tat tca gca Tyr Thr Leu Leu Lys Asn His Ala Asp Arg Phe Lys Lys Tyr Ser Ala 340 345 350	1056

gaa gag cag tac gaa att gat ttt caa cat cga ctg gca aac aga aat 1104
 Glu Glu Gln Tyr Glu Ile Asp Phe Gln His Arg Leu Ala Asn Arg Asn
 355 360 365
 tgt tat tta gat aaa tat ggc gat gca aat atc aat cat tat tat aga 1152
 Cys Tyr Leu Asp Lys Tyr Gly Asp Ala Asn Ile Asn His Tyr Tyr Arg
 370 375 380
 aac tta gaa atg aaa cac tca caa ccc aaa aat aga gca tcc ggc aaa 1200
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 Arg Val Ser *

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 ggc aac ctg atc tcg gtg att ggg gga ttc ctg ctg gcc tca aag ggc 96
 Gly Asn Leu Ile Ser Val Ile Gly Gly Phe Leu Leu Ala Ser Lys Gly
 20 25 30
 agc att gat tat ccc ctg ttt atc tac acg ctg gtt ggg gtg tca ctg 144
 Ser Ile Asp Tyr Pro Leu Phe Ile Tyr Thr Leu Val Gly Val Ser Leu
 35 40 45
 gtt gtg gcg tcg ggt tgt gtg ttt aac aac tac atc gac agg gat atc 192
 Val Val Ala Ser Gly Cys Val Phe Asn Asn Tyr Ile Asp Arg Asp Ile
 50 55 60
 gac aga aag atg gaa agg acg aag aat cgg gtg ctg gtg aaa ggc ctg 240
 Asp Arg Lys Met Glu Arg Thr Lys Asn Arg Val Leu Val Lys Gly Leu
 65 70 75 80
 atc tct cct gct gtc tcg ctg gtg tac gcc acg ttg ctg ggt att gct 288
 Ile Ser Pro Ala Val Ser Leu Val Tyr Ala Thr Leu Leu Gly Ile Ala
 85 90 95
 ggc ttt atg ctg ctg tgg ttt ggc gcg aat ccg ctg gcc tgc tgg ctg 336
 Gly Phe Met Leu Leu Trp Phe Gly Ala Asn Pro Leu Ala Cys Trp Leu
 100 105 110
 ggg gtg atg ggc ttt gtg gtt tat gtc ggc gtt tat agc ctg tac atg 384
 Gly Val Met Gly Phe Val Val Tyr Val Gly Val Tyr Ser Leu Tyr Met
 115 120 125

aaa cgc cac tct gtc tac ggc acg ttg att ggt tcg ctc tcc ggc gct 432
 Lys Arg His Ser Val Tyr Gly Thr Leu Ile Gly Ser Leu Ser Gly Ala
 130 135 140

gcg ccg ccg gtg atc ggc tac tgt gcg gta acc ggt gag ttc gat agc 480
 Ala Pro Pro Val Ile Gly Tyr Cys Ala Val Thr Gly Glu Phe Asp Ser
 145 150 155 160

ggc gca gcg atc ctg ctg gct atc ttc agc ctg tgg cag atg cct cac 528
 Gly Ala Ala Ile Leu Leu Ala Ile Phe Ser Leu Trp Gln Met Pro His
 165 170 175

tcc tat gcc atc gcc att ttc cgc ttt aag gat tac cag gcg gca aac 576
 Ser Tyr Ala Ile Ala Ile Phe Arg Phe Lys Asp Tyr Gln Ala Ala Asn
 180 185 190

att ccg gta ttg cca gtg gta aaa ggc att tcg gtg gcg aag aat cac 624
 Ile Pro Val Leu Pro Val Val Lys Gly Ile Ser Val Ala Lys Asn His
 195 200 205

atc acg ctg tat atc atc gcc ttt gcc gtt gcc acg ctg atg ctc tct 672
 Ile Thr Leu Tyr Ile Ile Ala Phe Ala Val Ala Thr Leu Met Leu Ser
 210 215 220

ctt ggc ggt tac gct ggg tat aaa tat ctg gtg gtc gcc gcg gcg gtt 720
 Leu Gly Gly Tyr Ala Gly Tyr Lys Tyr Leu Val Val Ala Ala Ala Val
 225 230 235 240

agc gtc tgg tgg tta ggt atg gct ctg cgc ggt tat aaa gtt gct gat 768
 Ser Val Trp Trp Leu Gly Met Ala Leu Arg Gly Tyr Lys Val Ala Asp
 245 250 255

gac aga atc tgg gcg cgc aag ctg ttc ggc ttc tct atc atc gcc atc 816
 Asp Arg Ile Trp Ala Arg Lys Leu Phe Gly Phe Ser Ile Ile Ala Ile
 260 265 270

act gcc ctc tcg gtg atg atg tcc gtt gat ttt atg gta ccg gac tcg 864
 Thr Ala Leu Ser Val Met Met Ser Val Asp Phe Met Val Pro Asp Ser
 275 280 285

cat acg ctg ctg gct gct gtg tgg taa 891
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<213> Escherichia coli

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gca ggc act gta ttg ctc agt ggc tgt aat tct gcg ctg tta gat ccc 96

Ala	Gly	Thr	Val	Leu	Leu	Ser	Gly	Cys	Asn	Ser	Ala	Leu	Leu	Asp	Pro	
			20					25					30			
aaa	gga	cag	att	ggt	ctg	gag	caa	cgt	tca	ctg	ata	ctg	acg	gca	ttt	144
Lys	Gly	Gln	Ile	Gly	Leu	Glu	Gln	Arg	Ser	Leu	Ile	Leu	Thr	Ala	Phe	
		35					40					45				
ggc	ctg	atg	ttg	att	gtc	gtt	att	ccc	gca	atc	ttg	atg	gct	gtt	ggt	192
Gly	Leu	Met	Leu	Ile	Val	Ile	Ile	Pro	Ala	Ile	Leu	Met	Ala	Val	Gly	
	50					55					60					
ttc	gcc	tgg	aag	tac	cgt	gcg	agc	aat	aaa	gat	gct	aag	tac	agc	ccg	240
Phe	Ala	Trp	Lys	Tyr	Arg	Ala	Ser	Asn	Lys	Asp	Ala	Lys	Tyr	Ser	Pro	
65					70					75					80	
aac	tgg	tca	cac	tcc	aat	aaa	gtg	gaa	gct	gtg	gtc	tgg	acg	gta	cct	288
Asn	Trp	Ser	His	Ser	Asn	Lys	Val	Glu	Ala	Val	Val	Trp	Thr	Val	Pro	
			85						90					95		
atc	tta	atc	atc	atc	ttc	ctt	gca	gta	ctg	acc	tgg	aaa	acc	act	cac	336
Ile	Leu	Ile	Ile	Ile	Phe	Leu	Ala	Val	Leu	Thr	Trp	Lys	Thr	Thr	His	
			100					105					110			
gct	ctt	gag	cct	agc	aag	ccg	ctg	gca	cac	gac	gag	aag	ccc	att	acc	384
Ala	Leu	Glu	Pro	Ser	Lys	Pro	Leu	Ala	His	Asp	Glu	Lys	Pro	Ile	Thr	
		115					120					125				
atc	gaa	gtg	gtt	tcc	atg	gac	tgg	aaa	tgg	ttc	ttc	atc	tac	ccg	gaa	432
Ile	Glu	Val	Val	Ser	Met	Asp	Trp	Lys	Trp	Phe	Phe	Ile	Tyr	Pro	Glu	
	130					135					140					
cag	ggc	att	gct	acc	gtg	aat	gaa	atc	gct	ttc	ccg	gcg	aac	act	ccg	480
Gln	Gly	Ile	Ala	Thr	Val	Asn	Glu	Ile	Ala	Phe	Pro	Ala	Asn	Thr	Pro	
145					150					155					160	
gtg	tac	ttc	aaa	gtg	acc	tcc	aac	tcc	gtg	atg	aac	tcc	ttc	ttc	att	528
Val	Tyr	Phe	Lys	Val	Thr	Ser	Asn	Ser	Val	Met	Asn	Ser	Phe	Phe	Ile	
				165					170					175		
ccg	cgt	ctg	ggt	agc	cag	att	tat	gcc	atg	gcc	ggt	atg	cag	act	cgc	576
Pro	Arg	Leu	Gly	Ser	Gln	Ile	Tyr	Ala	Met	Ala	Gly	Met	Gln	Thr	Arg	
			180					185					190			
ctg	cat	ctg	atc	gcc	aac	gaa	ccc	ggc	act	tat	gac	ggt	atc	tcc	gcc	624
Leu	His	Leu	Ile	Ala	Asn	Glu	Pro	Gly	Thr	Tyr	Asp	Gly	Ile	Ser	Ala	
		195					200					205				
agc	tac	agc	ggc	ccg	ggc	ttc	tca	ggc	atg	aag	ttc	aaa	gct	att	gca	672
Ser	Tyr	Ser	Gly	Pro	Gly	Phe	Ser	Gly	Met	Lys	Phe	Lys	Ala	Ile	Ala	
	210					215					220					
aca	ccg	gat	cgc	gcc	gca	ttc	gac	cag	tgg	gtc	gca	aaa	gcg	aag	cag	720
Thr	Pro	Asp	Arg	Ala	Ala	Phe	Asp	Gln	Trp	Val	Ala	Lys	Ala	Lys	Gln	
225					230					235					240	
tcg	ccg	aac	acc	atg	tct	gac	atg	gct	gcg	ttc	gaa	aaa	ctg	gcc	gcg	768
Ser	Pro	Asn	Thr	Met	Ser	Asp	Met	Ala	Ala	Phe	Glu	Lys	Leu	Ala	Ala	
				245					250					255		
cct	agc	gaa	tac	aac	cag	gtg	gaa	tat	ttc	tcc	aac	gtg	aaa	cca	gac	816

Pro Ser Glu Tyr Asn Gln Val Glu Tyr Phe Ser Asn Val Lys Pro Asp	
260 265 270	
ttg ttt gcc gat gta att aac aag ttt atg gct cac ggt aag agc atg	864
Leu Phe Ala Asp Val Ile Asn Lys Phe Met Ala His Gly Lys Ser Met	
275 280 285	
gac atg acc cag cca gaa ggt gag cac agc gca cac gaa ggt atg gaa	912
Asp Met Thr Gln Pro Glu Gly Glu His Ser Ala His Glu Gly Met Glu	
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Gly Met Asp Met Ser His Ala Glu Ser Ala His *	
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1 5 10 15	
gtc atg gtt acg atc gct ggc att att ttg gga ggt ctg gcg ctc gtt	96
Val Met Val Thr Ile Ala Gly Ile Ile Leu Gly Gly Leu Ala Leu Val	
20 25 30	
ggc ctg atc act tac ttc ggt aag tgg acc tac ctg tgg aaa gag tgg	144
Gly Leu Ile Thr Tyr Phe Gly Lys Trp Thr Tyr Leu Trp Lys Glu Trp	
35 40 45	
ctg acc tcc gtc gac cat aaa cgc ctc ggt atc atg tat atc atc gtg	192
Leu Thr Ser Val Asp His Lys Arg Leu Gly Ile Met Tyr Ile Ile Val	
50 55 60	
gcg att gtg atg ttg ctg cgt ggt ttt gct gac gcc att atg atg cgt	240
Ala Ile Val Met Leu Leu Arg Gly Phe Ala Asp Ala Ile Met Met Arg	
65 70 75 80	
agc cag cag gct ctt gcc tcg gcg ggc gaa gcg ggc ttc ctg cca cct	288
Ser Gln Gln Ala Leu Ala Ser Ala Gly Glu Ala Gly Phe Leu Pro Pro	
85 90 95	
cac cac tac gat cag atc ttt acc gcg cac ggc gtg att atg atc ttc	336
His His Tyr Asp Gln Ile Phe Thr Ala His Gly Val Ile Met Ile Phe	
100 105 110	
ttc gtg gcg atg cct ttc gtt atc ggt ctg atg aac ctg gtg gtt ccg	384
Phe Val Ala Met Pro Phe Val Ile Gly Leu Met Asn Leu Val Val Pro	
115 120 125	
ctg cag atc ggc gcg cgt gac gtt gcg ttc ccg ttc ctc aac aac tta	432
Leu Gln Ile Gly Ala Arg Asp Val Ala Phe Pro Phe Leu Asn Asn Leu	

130	135	140	
agc ttc tgg ttt acc gtt gtt ggt gtg att ctg gtt aac gtt tct ctc Ser Phe Trp Phe Thr Val Val Gly Val Ile Leu Val Asn Val Ser Leu 145 150 155 160			480
ggc gtg ggc gaa ttt gcg cag acc ggc tgg ctg gcc tat cca ccg cta Gly Val Gly Glu Phe Ala Gln Thr Gly Trp Leu Ala Tyr Pro Pro Leu 165 170 175			528
tcg gga ata gag tac agt ccg gga gtc ggt gtc gat tac tgg ata tgg Ser Gly Ile Glu Tyr Ser Pro Gly Val Gly Val Asp Tyr Trp Ile Trp 180 185 190			576
agt ctc cag cta tcc ggt ata ggt acg acg ctt acc ggt atc aac ttc Ser Leu Gln Leu Ser Gly Ile Met Thr Thr Leu Thr Gly Ile Asn Phe 195 200 205			624
ttc gtt acc att ctg aag atg cgc gca ccg ggc atg acc atg ttc aag Phe Val Thr Ile Leu Lys Met Arg Ala Pro Gly Met Thr Met Phe Lys 210 215 220			672
atg cca gta ttt acc tgg gca tca ctg tgc gcg aac gta ctg att att Met Pro Val Phe Thr Trp Ala Ser Leu Cys Ala Asn Val Leu Ile Ile 225 230 235 240			720
gct tcc ttc cca att ctg acg gtt acc gtc gcg ttg ttg acc ctg gat Ala Ser Phe Pro Ile Leu Thr Val Thr Val Ala Leu Leu Thr Leu Asp 245 250 255			768
cgc tat ctg ggc acc cat ttc ttt acc aac gat atg ggt ggc aac atg Arg Tyr Leu Gly Thr His Phe Phe Thr Asn Asp Met Gly Gly Asn Met 260 265 270			816
atg atg tac atc aac ctg att tgg gcc tgg ggc cac ccg gaa gtt tac Met Met Tyr Ile Asn Leu Ile Trp Ala Trp Gly His Pro Glu Val Tyr 275 280 285			864
atc ctg atc ctg cct gtt ttc ggt gtg ttc tcc gaa att gcg gca acc Ile Leu Ile Leu Pro Val Phe Gly Val Phe Ser Glu Ile Ala Ala Thr 290 295 300			912
ttc tcg cgt aaa cgt ctg ttt ggt tat acc tcg ctg gta tgg gca acc Phe Ser Arg Lys Arg Leu Phe Gly Tyr Thr Ser Leu Val Trp Ala Thr 305 310 315 320			960
gtc tgt atc acc gtg ctg tcg ttc atc gtt tgg ctg cac cac ttc ttt Val Cys Ile Thr Val Leu Ser Phe Ile Val Trp Leu His His Phe Phe 325 330 335			1008
acg atg ggt gcg ggc gcg aac gta aac gcc ttc ttt ggt atc acc aca Thr Met Gly Ala Gly Ala Asn Val Asn Ala Phe Phe Gly Ile Thr Thr 340 345 350			1056
atg att atc gcc atc ccg acc ggg gtg aag atc ttc aac tgg ctg ttc Met Ile Ile Ala Ile Pro Thr Gly Val Lys Ile Phe Asn Trp Leu Phe 355 360 365			1104
acc atg tat cag ggc cgc atc gtg ttc cat tct gcg atg ctg tgg acc Thr Met Tyr Gln Gly Arg Ile Val Phe His Ser Ala Met Leu Trp Thr			1152

370	375	380	
atc ggt ttt atc gtc acc ttc tcg gtg ggc ggg atg act ggc gtg ctg Ile Gly Phe Ile Val Thr Phe Ser Val Gly Gly Met Thr Gly Val Leu 385 390 395 400			1200
ctg gcc gta ccg ggc gcg gac ttc gtt ctg cat aac agc ctg ttc ctg Leu Ala Val Pro Gly Ala Asp Phe Val Leu His Asn Ser Leu Phe Leu 405 410 415			1248
att gcg cac ttc cat aac gtg atc atc ggc ggc gtg gtc ttc ggc tgc Ile Ala His Phe His Asn Val Ile Ile Gly Gly Val Val Phe Gly Cys 420 425 430			1296
ttc gca ggg atg acc tac tgg tgg cct aaa gcg ttc ggt ttc aaa ctg Phe Ala Gly Met Thr Tyr Trp Trp Pro Lys Ala Phe Gly Phe Lys Leu 435 440 445			1344
aac gaa acc tgg ggt aaa cgc gcg ttc tgg ttc tgg atc atc ggc ttc Asn Glu Thr Trp Gly Lys Arg Ala Phe Trp Phe Trp Ile Ile Gly Phe 450 455 460			1392
ttc gtt gcc ttt atg cca ctg tat gcg ctg ggc ttc atg ggc atg acc Phe Val Ala Phe Met Pro Leu Tyr Ala Leu Gly Phe Met Gly Met Thr 465 470 475 480			1440
cgt cgt ttg agc cag cag att gac ccg cag ttc cac acc atg ctg atg Arg Arg Leu Ser Gln Gln Ile Asp Pro Gln Phe His Thr Met Leu Met 485 490 495			1488
att gca gcc agc ggt gca gta ctg att gcg ctg ggt att ctc tgc ctc Ile Ala Ala Ser Gly Ala Val Leu Ile Ala Leu Gly Ile Leu Cys Leu 500 505 510			1536
gtt att cag atg tac gtt tct att cgc gac cgc gac cag aac cgt gac Val Ile Gln Met Tyr Val Ser Ile Arg Asp Arg Asp Gln Asn Arg Asp 515 520 525			1584
ctg act ggc gac ccg tgg ggt ggc cgt acg ctg gag tgg gca acc tct Leu Thr Gly Asp Pro Trp Gly Gly Arg Thr Leu Glu Trp Ala Thr Ser 530 535 540			1632
tcc ccg cct ccg ttc tat aac ttt gcc gta gtg ccg cac gtt cac gaa Ser Pro Pro Pro Phe Tyr Asn Phe Ala Val Val Pro His Val His Glu 545 550 555 560			1680
cgt gat gca ttc tgg gaa atg aaa gag aaa ggc gaa gcg tat aaa aag Arg Asp Ala Phe Trp Glu Met Lys Glu Lys Gly Glu Ala Tyr Lys Lys 565 570 575			1728
cct gac cac tat gaa gaa att cat atg ccg aaa aac agc ggt gca ggt Pro Asp His Tyr Glu Glu Ile His Met Pro Lys Asn Ser Gly Ala Gly 580 585 590			1776
atc gtc att gca gct ttc tcc acc atc ttc ggt ttc gcc atg atc tgg Ile Val Ile Ala Ala Phe Ser Thr Ile Phe Gly Phe Ala Met Ile Trp 595 600 605			1824
cat atc tgg tgg ctg gcg att gtt ggc ttc gca ggc atg atc atc acc His Ile Trp Trp Leu Ala Ile Val Gly Phe Ala Gly Met Ile Ile Thr 610 615 620			1872

610	615	620	
tggtg atc gtg aaa agc ttc gac gag gac gtg gat tac tac gtg ccg gtg			1920
Trp Ile Val Lys Ser Phe Asp Glu Asp Val Asp Tyr Tyr Val Pro Val			
625	630	635	640
gca gaa atc gaa aaa ctg gaa aac cag cat ttc gat gag att act aag			1968
Ala Glu Ile Glu Lys Leu Glu Asn Gln His Phe Asp Glu Ile Thr Lys			
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gca ggg ctg aaa aat ggc aac tga			1992
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1	5	10	15
ggg cac cac gat gca ggc gga acc aaa atc ttc gga ttt tgg atc tac			96
Gly His His Asp Ala Gly Gly Thr Lys Ile Phe Gly Phe Trp Ile Tyr			
	20	25	30
ctg atg agc gac tgc att ctg ttc tct atc ttg ttt gct acc tat gcc			144
Leu Met Ser Asp Cys Ile Leu Phe Ser Ile Leu Phe Ala Thr Tyr Ala			
	35	40	45
gtt ctg gtg aac ggc acc gca ggc ggc ccg aca ggt aag gac att ttc			192
Val Leu Val Asn Gly Thr Ala Gly Gly Pro Thr Gly Lys Asp Ile Phe			
	50	55	60
gaa ctg ccg ttc gtt ctg gtt gaa act ttc ttg ctg ttg ttc agc tcc			240
Glu Leu Pro Phe Val Leu Val Glu Thr Phe Leu Leu Leu Phe Ser Ser			
	65	70	75
atc acc tac ggc atg gcg gct atc gcc atg tac aaa aac aac aaa agc			288
Ile Thr Tyr Gly Met Ala Ala Ile Ala Met Tyr Lys Asn Asn Lys Ser			
	85	90	95
cag gtt atc tcc tgg ctg gcg ttg acc tgg ttg ttt ggt gcc gga ttt			336
Gln Val Ile Ser Trp Leu Ala Leu Thr Trp Leu Phe Gly Ala Gly Phe			
	100	105	110
atc ggg atg gaa atc tat gaa ttc cat cac ctg att gtt aac ggc atg			384
Ile Gly Met Glu Ile Tyr Glu Phe His His Leu Ile Val Asn Gly Met			
	115	120	125
ggt ccg gat cgc agc ggc ttc ctg tca gcg ttc ttt gcg ctg gtc ggc			432
Gly Pro Asp Arg Ser Gly Phe Leu Ser Ala Phe Phe Ala Leu Val Gly			
	130	135	140

acg cac ggt ctg cac gtc act tct ggt ctt atc tgg atg gcg gtg ctg 480
 Thr His Gly Leu His Val Thr Ser Gly Leu Ile Trp Met Ala Val Leu
 145 150 155 160

atg gtg caa atc gcc cgt cgc ggc ctg acc agc act aac cgt acc cgc 528
 Met Val Gln Ile Ala Arg Arg Gly Leu Thr Ser Thr Asn Arg Thr Arg
 165 170 175

atc atg tgc ctg agc ctg ttc tgg cac ttc ctg gat gtg gtt tgg atc 576
 Ile Met Cys Leu Ser Leu Phe Trp His Phe Leu Asp Val Val Trp Ile
 180 185 190

tgt gtg ttc act gtt gtt tat ctg atg ggg gcg atg taa 615
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<211> 330

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<213> Escherichia coli

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 1 5 10 15

acc tac atg aca ggc ttt atc ctg tgc atc att ctg acg gtg att ccg 96
 Thr Tyr Met Thr Gly Phe Ile Leu Ser Ile Ile Leu Thr Val Ile Pro
 20 25 30

ttc tgg atg gtg atg aca gga gct gcc tct ccg gcc gta att ctg gga 144
 Phe Trp Met Val Met Thr Gly Ala Ala Ser Pro Ala Val Ile Leu Gly
 35 40 45

aca atc ctg gca atg gca gtg gta cag gtt ctg gtg cat ctg gtg tgc 192
 Thr Ile Leu Ala Met Ala Val Val Gln Val Leu Val His Leu Val Cys
 50 55 60

ttc ctg cac atg aat acc aaa tca gat gaa ggc tgg aac atg acg gcg 240
 Phe Leu His Met Asn Thr Lys Ser Asp Glu Gly Trp Asn Met Thr Ala
 65 70 75 80

ttt gtc ttc acc gtg cta atc atc gct atc ctg gtt gta ggc tcc atc 288
 Phe Val Phe Thr Val Leu Ile Ile Ala Ile Leu Val Val Gly Ser Ile
 85 90 95

tgg att atg tgg aac ctc aac tac aac atg atg atg cac taa 330
 Trp Ile Met Trp Asn Leu Asn Tyr Asn Met Met Met His *
 100 105

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<212> DNA

<213> Escherichia coli

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1				5					10					15		

acg	ccc	gac	gag	gcg	ctg	gcg	cat	gtt	ggc	gcg	gtg	att	gac	gcc	ggg	96
Thr	Pro	Asp	Glu	Ala	Leu	Ala	His	Val	Gly	Ala	Val	Ile	Asp	Ala	Gly	
			20					25					30			

ttc	gac	gcg	gtt	gaa	atc	ccg	ctg	aat	tcc	cca	caa	tgg	gag	caa	agc	144
Phe	Asp	Ala	Val	Glu	Ile	Pro	Leu	Asn	Ser	Pro	Gln	Trp	Glu	Gln	Ser	
			35				40					45				

att	ccc	gcc	atc	gtt	gat	gcg	tac	ggc	gac	aag	gcg	ttg	att	ggc	gca	192
Ile	Pro	Ala	Ile	Val	Asp	Ala	Tyr	Gly	Asp	Lys	Ala	Leu	Ile	Gly	Ala	
	50					55					60					

ggt	acg	gta	ctg	aaa	cct	gaa	cag	gtc	gat	gcg	ctc	gcc	agg	atg	ggc	240
Gly	Thr	Val	Leu	Lys	Pro	Glu	Gln	Val	Asp	Ala	Leu	Ala	Arg	Met	Gly	
65					70				75						80	

tgt	cag	ctc	atc	gtt	acg	ccc	aat	atc	cat	agt	gaa	gtg	atc	cgc	cgt	288
Cys	Gln	Leu	Ile	Val	Thr	Pro	Asn	Ile	His	Ser	Glu	Val	Ile	Arg	Arg	
				85					90					95		

gcg	gtg	ggc	tac	ggc	atg	acc	gtc	tgc	ccc	ggc	tgc	gcg	acg	gcg	acc	336
Ala	Val	Gly	Tyr	Gly	Met	Thr	Val	Cys	Pro	Gly	Cys	Ala	Thr	Ala	Thr	
			100					105					110			

gaa	gcc	ttt	acc	gcg	ctc	gaa	gcg	ggc	gcc	gca	ggc	gct	gaa	aat	att	384
Glu	Ala	Phe	Thr	Ala	Leu	Glu	Ala	Gly	Ala	Ala	Gly	Ala	Glu	Asn	Ile	
		115					120					125				

tcc	gtc	atc	ggc	ttt	tgg	tcc	gca	ata	cat	caa	agc	gtt	aaa	agc	ggt	432
Ser	Val	Ile	Gly	Phe	Trp	Ser	Ala	Ile	His	Gln	Ser	Val	Lys	Ser	Gly	
	130					135					140					

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Ile	Ala	Ile	Gly	His	Arg	Ser	Leu	Cys	Arg	Trp	Arg	Arg	Asp	Ala	Glu	
145					150				155					160		

aac	ctg	gcg	cag	tgg	ata	gac	gca	ggt	tgt	gca	ggg	gcg	ggc	tta	ggc	528
Asn	Leu	Ala	Gln	Trp	Ile	Asp	Ala	Gly	Cys	Ala	Gly	Ala	Gly	Leu	Gly	
			165					170						175		

agc	gat	ctc	tat	cgc	gcc	ggg	caa	tcc	gta	gag	cgc	acc	gcg	cag	cag	576
Ser	Asp	Leu	Tyr	Arg	Ala	Gly	Gln	Ser	Val	Glu	Arg	Thr	Ala	Gln	Gln	
			180					185					190			

gca	gca	gca	ttt	gtt	aag	gcg	tat	cga	gag	gca	ggt	gca	atg	aaa	atc	624
Ala	Ala	Ala	Phe	Val	Lys	Ala	Tyr	Arg	Glu	Ala	Gly	Ala	Met	Lys	Ile	
		195					200					205				

acc	aaa	att	acc	acg	tat	cgt	tta	cct	ccc	cgc	tgg	atg	ttc	ctg	aaa	672
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Thr	Lys	Ile	Thr	Thr	Tyr	Arg	Leu	Pro	Pro	Arg	Trp	Met	Phe	Leu	Lys		
210						215					220						
att	gaa	acc	gat	gaa	ggc	gtg	gtc	ggt	tgg	ggc	gag	ccc	gtg	atc	gaa	720	
Ile	Glu	Thr	Asp	Glu	Gly	Val	Val	Gly	Trp	Gly	Glu	Pro	Val	Ile	Glu		
225					230					235					240		
ggc	cgc	gcc	cgt	acg	gtg	gaa	gcg	gca	gtt	cac	gag	ctg	ggt	gac	tat	768	
Gly	Arg	Ala	Arg	Thr	Val	Glu	Ala	Ala	Val	His	Glu	Leu	Gly	Asp	Tyr		
				245					250					255			
ttg	att	ggt	cag	gat	cca	tcg	cgc	atc	aat	gac	tta	tgg	caa	gtg	atg	816	
Leu	Ile	Gly	Gln	Asp	Pro	Ser	Arg	Ile	Asn	Asp	Leu	Trp	Gln	Val	Met		
			260					265					270				
tat	cgc	gcc	gga	ttc	tat	cgc	ggc	ggt	ccg	atc	ctg	atg	agc	gcc	atc	864	
Tyr	Arg	Ala	Gly	Phe	Tyr	Arg	Gly	Gly	Pro	Ile	Leu	Met	Ser	Ala	Ile		
		275					280					285					
gcc	ggg	att	gac	cag	gcg	tta	tgg	gat	atc	aaa	ggt	aaa	gtg	ctg	aat	912	
Ala	Gly	Ile	Asp	Gln	Ala	Leu	Trp	Asp	Ile	Lys	Gly	Lys	Val	Leu	Asn		
	290					295					300						
gcg	ccg	gtc	tgg	caa	ctg	atg	ggc	ggc	ctg	gtt	cgc	gac	aaa	att	aaa	960	
Ala	Pro	Val	Trp	Gln	Leu	Met	Gly	Gly	Leu	Val	Arg	Asp	Lys	Ile	Lys		
305					310					315					320		
gcc	tac	agt	tgg	gtt	ggc	ggc	gat	cgt	ccg	gcg	gat	gtt	atc	gac	ggc	1008	
Ala	Tyr	Ser	Trp	Val	Gly	Gly	Asp	Arg	Pro	Ala	Asp	Val	Ile	Asp	Gly		
				325					330					335			
att	aaa	acg	cta	cgc	gaa	atc	ggc	ttc	gat	acc	ttc	aaa	ctg	aac	ggt	1056	
Ile	Lys	Thr	Leu	Arg	Glu	Ile	Gly	Phe	Asp	Thr	Phe	Lys	Leu	Asn	Gly		
			340					345					350				
tgt	gaa	gaa	ctg	ggg	cta	att	gat	aac	tcc	cgc	gcg	gta	gat	gcg	gcg	1104	
Cys	Glu	Glu	Leu	Gly	Leu	Ile	Asp	Asn	Ser	Arg	Ala	Val	Asp	Ala	Ala		
		355					360					365					
gtt	aac	acc	gtg	gca	caa	att	cgt	gaa	gct	ttt	ggc	aat	cag	att	gag	1152	
Val	Asn	Thr	Val	Ala	Gln	Ile	Arg	Glu	Ala	Phe	Gly	Asn	Gln	Ile	Glu		
	370					375					380						
ttt	ggt	ctt	gat	ttc	cac	ggt	cgc	gtc	agc	gcg	ccg	atg	gcg	aaa	gtg	1200	
Phe	Gly	Leu	Asp	Phe	His	Gly	Arg	Val	Ser	Ala	Pro	Met	Ala	Lys	Val		
385					390					395					400		
ctg	att	aaa	gaa	ctg	gag	ccg	tat	cgc	ccg	ctg	ttt	att	gag	gag	ccg	1248	
Leu	Ile	Lys	Glu	Leu	Glu	Pro	Tyr	Arg	Pro	Leu	Phe	Ile	Glu	Glu	Pro		
				405					410					415			
gtg	ctg	gcg	gaa	caa	gcc	gaa	tac	tac	ccg	aaa	ctg	gcg	gca	caa	acg	1296	
Val	Leu	Ala	Glu	Gln	Ala	Glu	Tyr	Tyr	Pro	Lys	Leu	Ala	Ala	Gln	Thr		
			420					425					430				
cat	att	cca	ctg	gcg	gcg	ggt	gaa	cgc	atg	ttc	tca	cgc	ttc	gat	ttt	1344	
His	Ile	Pro	Leu	Ala	Ala	Gly	Glu	Arg	Met	Phe	Ser	Arg	Phe	Asp	Phe		
		435					440					445					
aaa	cgc	gtg	ctg	gag	gca	ggt	ggt	att	tcg	att	ctg	caa	ccg	gat	ctc	1392	

Lys	Arg	Val	Leu	Glu	Ala	Gly	Gly	Ile	Ser	Ile	Leu	Gln	Pro	Asp	Leu	
450						455					460					
tcc	cac	gcg	ggc	ggt	att	acc	gaa	tgc	tac	aaa	atc	gcc	gga	atg	gca	1440
Ser	His	Ala	Gly	Gly	Ile	Thr	Glu	Cys	Tyr	Lys	Ile	Ala	Gly	Met	Ala	
465					470					475					480	
gaa	gcc	tat	gac	gtg	acc	ctt	gcg	ccg	cac	tgt	ccg	ctc	gga	ccg	att	1488
Glu	Ala	Tyr	Asp	Val	Thr	Leu	Ala	Pro	His	Cys	Pro	Leu	Gly	Pro	Ile	
				485					490					495		
gca	ctg	gcg	gct	tgc	ctg	cat	atc	gac	ttt	gtt	tcc	tat	aac	gcc	gta	1536
Ala	Leu	Ala	Ala	Cys	Leu	His	Ile	Asp	Phe	Val	Ser	Tyr	Asn	Ala	Val	
			500					505					510			
ctt	cag	gaa	caa	agt	atg	gga	att	cat	tac	aac	aaa	ggc	gcg	gag	tta	1584
Leu	Gln	Glu	Gln	Ser	Met	Gly	Ile	His	Tyr	Asn	Lys	Gly	Ala	Glu	Leu	
		515				520						525				
ctc	gac	ttt	gtg	aaa	aac	aaa	gaa	gac	ttc	agc	atg	gtc	ggc	ggc	ttc	1632
Leu	Asp	Phe	Val	Lys	Asn	Lys	Glu	Asp	Phe	Ser	Met	Val	Gly	Gly	Phe	
	530					535					540					
ttt	aaa	ccg	tta	acg	aaa	ccg	ggc	tta	ggc	gtg	gaa	atc	gac	gaa	gct	1680
Phe	Lys	Pro	Leu	Thr	Lys	Pro	Gly	Leu	Gly	Val	Glu	Ile	Asp	Glu	Ala	
545					550					555					560	
aaa	gtg	att	gag	ttc	agt	aaa	aat	gcc	ccg	gac	tgg	cgt	aat	ccg	ctc	1728
Lys	Val	Ile	Glu	Phe	Ser	Lys	Asn	Ala	Pro	Asp	Trp	Arg	Asn	Pro	Leu	
				565				570						575		
tgg	cgt	cat	gaa	gat	aac	agc	gta	gca	gag	tgg	taa					1764
Trp	Arg	His	Glu	Asp	Asn	Ser	Val	Ala	Glu	Trp	*					
			580					585								
<210> 165																
<211> 879																
<212> DNA																
<213> Escherichia coli																
<220>																
<221> CDS																
<222> (1)...(879)																
<400> 165																
atg	aca	gct	cgc	tac	atc	gca	att	gac	tgg	gga	tcg	acc	aat	ctg	cgc	48
Met	Thr	Ala	Arg	Tyr	Ile	Ala	Ile	Asp	Trp	Gly	Ser	Thr	Asn	Leu	Arg	
1				5				10						15		
gcc	tgg	ctt	tat	cag	ggc	gac	cac	tgc	ctg	gag	agc	agg	caa	tca	gaa	96
Ala	Trp	Leu	Tyr	Gln	Gly	Asp	His	Cys	Leu	Glu	Ser	Arg	Gln	Ser	Glu	
			20					25					30			
gca	ggc	gtc	acg	cgc	ctg	aac	gga	aaa	tct	ccg	gct	gcg	gtg	tta	gca	144
Ala	Gly	Val	Thr	Arg	Leu	Asn	Gly	Lys	Ser	Pro	Ala	Ala	Val	Leu	Ala	
		35					40					45				
gaa	gtc	acg	acc	gac	tgg	cgt	gaa	gag	aaa	acg	cca	gtg	gta	atg	gca	192
Glu	Val	Thr	Thr	Asp	Trp	Arg	Glu	Glu	Lys	Thr	Pro	Val	Val	Met	Ala	

50	55	60	
gga atg gtt ggc agc aac gtc ggc tgg aaa gtt gca ccg tat tta tct Gly Met Val Gly Ser Asn Val Gly Trp Lys Val Ala Pro Tyr Leu Ser 65 70 75 80			240
gtt cct gcc tgt ttt tcg tct att ggc gaa caa tta acg tca gtt ggc Val Pro Ala Cys Phe Ser Ser Ile Gly Glu Gln Leu Thr Ser Val Gly 85 90 95			288
gac aat atc tgg att att ccc gga tta tgt gtc tct cat gac gat aac Asp Asn Ile Trp Ile Ile Pro Gly Leu Cys Val Ser His Asp Asp Asn 100 105 110			336
cac aat gtg atg cgc ggc gaa gaa aca caa ttg atc ggc gcg cga gct His Asn Val Met Arg Gly Glu Glu Thr Gln Leu Ile Gly Ala Arg Ala 115 120 125			384
ctg gct cct tcc tct ctt tat gtc atg ccc gga acc cat tgc aaa tgg Leu Ala Pro Ser Ser Leu Tyr Val Met Pro Gly Thr His Cys Lys Trp 130 135 140			432
gtg cag gcc gat agc cag caa atc aac gat ttt cgc acc gtg atg acc Val Gln Ala Asp Ser Gln Gln Ile Asn Asp Phe Arg Thr Val Met Thr 145 150 155 160			480
ggg gaa tta cat cat tta ctg tta aat cac tca ttg att ggc gca ggt Gly Glu Leu His His Leu Leu Asn His Ser Leu Ile Gly Ala Gly 165 170 175			528
ttg ccg ccg cag gaa aac tct gcc gat gcc ttc aca gct ggc ctt gag Leu Pro Pro Gln Glu Asn Ser Ala Asp Ala Phe Thr Ala Gly Leu Glu 180 185 190			576
cgt ggt ctt aat acg ccc gcc ata ttg ccg cag ctt ttt gaa gtt cgc Arg Gly Leu Asn Thr Pro Ala Ile Leu Pro Gln Leu Phe Glu Val Arg 195 200 205			624
gcc tcg cat gtg ctg gga aca ctt ccc cgc gaa cag gtc agc gaa ttt Ala Ser His Val Leu Gly Thr Leu Pro Arg Glu Gln Val Ser Glu Phe 210 215 220			672
ctc tct ggt ttg ttg att ggc gca gag gtc gcc agt atg cgc gac tat Leu Ser Gly Leu Leu Ile Gly Ala Glu Val Ala Ser Met Arg Asp Tyr 225 230 235 240			720
gtg gcc cat caa cac gcc atc acc ctt gtc gcc gga aca tcg ctg acc Val Ala His Gln His Ala Ile Thr Leu Val Ala Gly Thr Ser Leu Thr 245 250 255			768
gcg cgc tac cag caa gcc ttt cag gcg atg ggt tgc gac gtg acg gcg Ala Arg Tyr Gln Gln Ala Phe Gln Ala Met Gly Cys Asp Val Thr Ala 260 265 270			816
gtg gcg gcc gac acg gca ttt cag gct ggt ata agg agc atc gct cat Val Ala Gly Asp Thr Ala Phe Gln Ala Gly Ile Arg Ser Ile Ala His 275 280 285			864
gca gtg gca aac taa Ala Val Ala Asn *			879

290

<210> 166

<211> 387

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(387)

<400> 166

atg	act	ctc	aat	aaa	acc	gat	cgc	att	gtc	att	acg	ctg	ggt	aaa	cag	48
Met	Thr	Leu	Asn	Lys	Thr	Asp	Arg	Ile	Val	Ile	Thr	Leu	Gly	Lys	Gln	
1				5					10					15		

atc	gtt	cac	ggc	aaa	tac	gtg	cca	ggc	tcg	ccg	ctt	ccg	gct	gag	gcg	96
Ile	Val	His	Gly	Lys	Tyr	Val	Pro	Gly	Ser	Pro	Leu	Pro	Ala	Glu	Ala	
			20					25					30			

gaa	ctc	tgt	gag	gag	ttt	gca	acc	tcg	cgc	aac	atc	atc	cgt	gag	gtg	144
Glu	Leu	Cys	Glu	Glu	Phe	Ala	Thr	Ser	Arg	Asn	Ile	Ile	Arg	Glu	Val	
		35					40					45				

ttc	cgt	tcg	ctg	atg	gcg	aag	cgg	ctg	att	gaa	atg	aaa	cgt	tat	cgc	192
Phe	Arg	Ser	Leu	Met	Ala	Lys	Arg	Leu	Ile	Glu	Met	Lys	Arg	Tyr	Arg	
	50					55					60					

ggg	gcg	ttt	gtg	gca	ccg	cgt	aac	cag	tgg	aat	tac	ctc	gac	act	gac	240
Gly	Ala	Phe	Val	Ala	Pro	Arg	Asn	Gln	Trp	Asn	Tyr	Leu	Asp	Thr	Asp	
65				70						75				80		

gta	ctg	caa	tgg	gtg	ctg	gaa	aat	gac	tac	gac	cca	cgg	ctt	atc	agt	288
Val	Leu	Gln	Trp	Val	Leu	Glu	Asn	Asp	Tyr	Asp	Pro	Arg	Leu	Ile	Ser	
			85					90						95		

gcc	atg	agc	gaa	gtg	cga	aat	ctg	gtg	gaa	ccg	gcg	att	gcc	cgt	tgg	336
Ala	Met	Ser	Glu	Val	Arg	Asn	Leu	Val	Glu	Pro	Ala	Ile	Ala	Arg	Trp	
			100				105						110			

gag	cag	agc	gcg	cga	ctt	cca	gcg	atc	tgg	cgc	aga	ttg	aat	cgg	cg	384
Glu	Gln	Ser	Ala	Arg	Leu	Pro	Ala	Ile	Trp	Arg	Arg	Leu	Asn	Arg	Arg	
		115				120						125				

tga																387
*																

<210> 167

<211> 297

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(297)

<400> 167

atg att gcc aac aat cag gac cgc gaa gcg ttt aac gaa gcg gat att 48
 Met Ile Ala Asn Asn Gln Asp Arg Glu Ala Phe Asn Glu Ala Asp Ile
 1 5 10 15
 cgc tac cac gag gcg gtg ctg cag tcg gtg cat aac ccg gtg tta cag 96
 Arg Tyr His Glu Ala Val Leu Gln Ser Val His Asn Pro Val Leu Gln
 20 25 30
 caa ctt agc att gcg atc agt tcg ctg cag cgg gcg gtt ttt gaa cga 144
 Gln Leu Ser Ile Ala Ile Ser Ser Leu Gln Arg Ala Val Phe Glu Arg
 35 40 45
 acc tgg atg ggc gat gag gcc aac atg ccg caa acg ctc cag gaa cat 192
 Thr Trp Met Gly Asp Glu Ala Asn Met Pro Gln Thr Leu Gln Glu His
 50 55 60
 aag gcg ctg ttc gat gcg ata cga cat cag gac ggc gat gcg gca gag 240
 Lys Ala Leu Phe Asp Ala Ile Arg His Gln Asp Gly Asp Ala Ala Glu
 65 70 75 80
 cag gcg gcg ctt acc atg atc gcc agc tcg aca cga agg tta aag gaa 288
 Gln Ala Ala Leu Thr Met Ile Ala Ser Ser Thr Arg Arg Leu Lys Glu
 85 90 95
 atc aca tga 297
 Ile Thr *

<210> 168
 <211> 357
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(357)

<400> 168
 atg gct cgc gta aaa cgt ggt gtt att gca cgt gca cgt cac aag aaa 48
 Met Ala Arg Val Lys Arg Gly Val Ile Ala Arg Ala Arg His Lys Lys
 1 5 10 15
 att ttg aaa caa gct aaa ggc tac tac ggt gcg cgt tct cgc gta tac 96
 Ile Leu Lys Gln Ala Lys Gly Tyr Tyr Gly Ala Arg Ser Arg Val Tyr
 20 25 30
 cgc gtt gcc ttc cag gct gtt atc aaa gct ggt cag tat gct tac cgt 144
 Arg Val Ala Phe Gln Ala Val Ile Lys Ala Gly Gln Tyr Ala Tyr Arg
 35 40 45
 gac cgt cgt caa cgt aag cgt cag ttc cgt caa ctg tgg att gcg cgt 192
 Asp Arg Arg Gln Arg Lys Arg Gln Phe Arg Gln Leu Trp Ile Ala Arg
 50 55 60
 atc aac gca gca gca cgt cag aac ggt att tct tac agc aaa ttc atc 240
 Ile Asn Ala Ala Ala Arg Gln Asn Gly Ile Ser Tyr Ser Lys Phe Ile
 65 70 75 80
 aat ggc ctg aaa aaa gcc tct gtt gaa atc gac cgt aag atc ctg gct 288

Asn	Gly	Leu	Lys	Lys	Ala	Ser	Val	Glu	Ile	Asp	Arg	Lys	Ile	Leu	Ala		
				85					90					95			
gat	atc	gca	gta	ttc	gac	aaa	gta	gcg	ttc	acc	gct	ctg	gtt	gaa	aaa	336	
Asp	Ile	Ala	Val	Phe	Asp	Lys	Val	Ala	Phe	Thr	Ala	Leu	Val	Glu	Lys		
			100					105					110				
gcg	aaa	gca	gct	ctg	gca	taa										357	
Ala	Lys	Ala	Ala	Leu	Ala	*											
			115														

<210> 169
 <211> 198
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(198)

<400> 169																	
atg	cca	aaa	att	aag	acc	gta	cgc	ggt	gct	gct	aag	cgc	ttc	aaa	aaa	48	
Met	Pro	Lys	Ile	Lys	Thr	Val	Arg	Gly	Ala	Ala	Lys	Arg	Phe	Lys	Lys		
1				5					10					15			
acc	ggt	aaa	ggt	ggt	ttt	aag	cac	aag	cac	gct	aac	ctg	cgt	cac	att	96	
Thr	Gly	Lys	Gly	Gly	Phe	Lys	His	Lys	His	Ala	Asn	Leu	Arg	His	Ile		
			20					25					30				
ctg	acc	aaa	aaa	gcg	acc	aaa	cgt	aaa	cgt	cac	ctg	cgt	ccg	aaa	gcc	144	
Leu	Thr	Lys	Lys	Ala	Thr	Lys	Arg	Lys	Arg	His	Leu	Arg	Pro	Lys	Ala		
			35				40					45					
atg	gtt	tcc	aaa	ggc	gat	ctg	ggc	ctg	gta	atc	gcg	tgc	ctg	ccg	tac	192	
Met	Val	Ser	Lys	Gly	Asp	Leu	Gly	Leu	Val	Ile	Ala	Cys	Leu	Pro	Tyr		
	50					55				60							
gca	taa															198	
Ala	*																
	65																

<210> 170
 <211> 543
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(543)

<400> 170																	
atg	aaa	ggc	gga	aaa	cga	gtt	caa	acg	gcg	cgc	cct	aac	cgt	atc	aat	48	
Met	Lys	Gly	Gly	Lys	Arg	Val	Gln	Thr	Ala	Arg	Pro	Asn	Arg	Ile	Asn		
1				5					10					15			
ggc	gaa	att	cgc	gcc	cag	gaa	gtt	cgc	tta	aca	ggt	ctg	gaa	ggc	gag	96	
Gly	Glu	Ile	Arg	Ala	Gln	Glu	Val	Arg	Leu	Thr	Gly	Leu	Glu	Gly	Glu		
			20					25					30				

cag ctt ggt att gtg agt ctg aga gaa gct ctg gag aaa gca gaa gaa 144
 Gln Leu Gly Ile Val Ser Leu Arg Glu Ala Leu Glu Lys Ala Glu Glu
 35 40 45

 gcc gga gta gac tta gtc gag atc agc cct aac gcc gag ccg ccg gtt 192
 Ala Gly Val Asp Leu Val Glu Ile Ser Pro Asn Ala Glu Pro Pro Val
 50 55 60

 tgt cgt ata atg gat tac ggc aaa ttc ctc tat gaa aag agc aag tct 240
 Cys Arg Ile Met Asp Tyr Gly Lys Phe Leu Tyr Glu Lys Ser Lys Ser
 65 70 75 80

 tct aag gaa cag aag aaa aag caa aaa gtt atc cag gtt aag gaa att 288
 Ser Lys Glu Gln Lys Lys Lys Gln Lys Val Ile Gln Val Lys Glu Ile
 85 90 95

 aaa ttc cgt cct ggt aca gat gaa ggc gac tat cag gta aaa ctc cgc 336
 Lys Phe Arg Pro Gly Thr Asp Glu Gly Asp Tyr Gln Val Lys Leu Arg
 100 105 110

 agc ctg att cgc ttt ctc gaa gag ggt gat aaa gcc aaa atc acg ctg 384
 Ser Leu Ile Arg Phe Leu Glu Glu Gly Asp Lys Ala Lys Ile Thr Leu
 115 120 125

 cgt ttc cgc ggt cgt gag atg gcg cac cag caa atc ggt atg gaa gtg 432
 Arg Phe Arg Gly Arg Glu Met Ala His Gln Gln Ile Gly Met Glu Val
 130 135 140

 ctt aat cgc gtg aaa gac gat ttg caa gaa ctg gca gtg gtc gaa tcc 480
 Leu Asn Arg Val Lys Asp Asp Leu Gln Glu Leu Ala Val Val Glu Ser
 145 150 155 160

 ttc cca acg aag atc gaa ggc cgc cag atg atc atg gtg ctc gct cct 528
 Phe Pro Thr Lys Ile Glu Gly Arg Gln Met Ile Met Val Leu Ala Pro
 165 170 175

 aag aag aaa cag taa 543
 Lys Lys Lys Gln *
 180

<210> 171
 <211> 1929
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1929)

<400> 171
 atg cct gtt ata act ctt cct gat ggc agc caa cgc cat tac gat cac 48
 Met Pro Val Ile Thr Leu Pro Asp Gly Ser Gln Arg His Tyr Asp His
 1 5 10 15

 gct gta agc ccc atg gat gtt gcg ctg gac att ggt cca ggt ctg gcg 96
 Ala Val Ser Pro Met Asp Val Ala Leu Asp Ile Gly Pro Gly Leu Ala
 20 25 30

aaa gcc tgt atc gca ggg cgc gtt aat ggc gaa ctg gtt gat gct tgc	144
Lys Ala Cys Ile Ala Gly Arg Val Asn Gly Glu Leu Val Asp Ala Cys	
35 40 45	
gat ctg att gaa aac gac gca caa ctg tcg atc att acc gcc aaa gac	192
Asp Leu Ile Glu Asn Asp Ala Gln Leu Ser Ile Ile Thr Ala Lys Asp	
50 55 60	
gaa gaa ggt ctg gag atc att cgt cac tcc tgt gcg cac ctg tta ggg	240
Glu Glu Gly Leu Glu Ile Ile Arg His Ser Cys Ala His Leu Leu Gly	
65 70 75 80	
cac gcg att aaa caa ctt tgg ccg cat acc aaa atg gca atc ggc ccg	288
His Ala Ile Lys Gln Leu Trp Pro His Thr Lys Met Ala Ile Gly Pro	
85 90 95	
gtt att gac aac ggt ttt tat tac gac gtt gat ctt gac cgc acg tta	336
Val Ile Asp Asn Gly Phe Tyr Tyr Asp Val Asp Leu Asp Arg Thr Leu	
100 105 110	
acc cag gaa gat gtc gaa gca ctc gag aag cgg atg cat gag ctt gct	384
Thr Gln Glu Asp Val Glu Ala Leu Glu Lys Arg Met His Glu Leu Ala	
115 120 125	
gag aaa aac tac gac gtc att aag aag aaa gtc agc tgg cac gaa gcg	432
Glu Lys Asn Tyr Asp Val Ile Lys Lys Lys Val Ser Trp His Glu Ala	
130 135 140	
cgt gaa act ttc gcc aac cgt ggg gag agc tac aaa gtc tcc att ctt	480
Arg Glu Thr Phe Ala Asn Arg Gly Glu Ser Tyr Lys Val Ser Ile Leu	
145 150 155 160	
gac gaa aac atc gcc cat gat gac aag cca ggt ctg tac ttc cat gaa	528
Asp Glu Asn Ile Ala His Asp Asp Lys Pro Gly Leu Tyr Phe His Glu	
165 170 175	
gaa tat gtc gat atg tgc cgc ggt ccg cac gta ccg aac atg cgt ttc	576
Glu Tyr Val Asp Met Cys Arg Gly Pro His Val Pro Asn Met Arg Phe	
180 185 190	
tgc cat cat ttc aaa cta atg aaa acg gca ggg gct tac tgg cgt ggc	624
Cys His His Phe Lys Leu Met Lys Thr Ala Gly Ala Tyr Trp Arg Gly	
195 200 205	
gac agc aac aac aaa atg ttg caa cgt att tac ggt acg gcg tgg gca	672
Asp Ser Asn Asn Lys Met Leu Gln Arg Ile Tyr Gly Thr Ala Trp Ala	
210 215 220	
gac aaa aaa gca ctt aac gct tac ctg cag cgc ctg gaa gaa gcc gcg	720
Asp Lys Lys Ala Leu Asn Ala Tyr Leu Gln Arg Leu Glu Glu Ala Ala	
225 230 235 240	
aaa cgc gac cac cgt aaa atc ggt aaa cag ctc gac ctg tac cat atg	768
Lys Arg Asp His Arg Lys Ile Gly Lys Gln Leu Asp Leu Tyr His Met	
245 250 255	
cag gaa gaa gcg ccg ggt atg gta ttc tgg cac aac gac ggc tgg acc	816
Gln Glu Glu Ala Pro Gly Met Val Phe Trp His Asn Asp Gly Trp Thr	
260 265 270	

atc ttc cgt gaa ctg gaa gtg ttt gtt cgt tct aaa ctg aaa gag tac Ile Phe Arg Glu Leu Glu Val Phe Val Arg Ser Lys Leu Lys Glu Tyr 275 280 285	864
cag tat cag gaa gtt aaa ggt ccg ttc atg atg gac cgt gtc ctg tgg Gln Tyr Gln Glu Val Lys Gly Pro Phe Met Met Asp Arg Val Leu Trp 290 295 300	912
gaa aaa acc ggt cac tgg gac aac tac aaa gat gca atg ttc acc aca Glu Lys Thr Gly His Trp Asp Asn Tyr Lys Asp Ala Met Phe Thr Thr 305 310 315 320	960
tct tct gag aac cgt gaa tac tgc att aag ccg atg aac tgc ccg ggt Ser Ser Glu Asn Arg Glu Tyr Cys Ile Lys Pro Met Asn Cys Pro Gly 325 330 335	1008
cac gta caa att ttc aac cag ggg ctg aag tct tat cgc gat ctg ccg His Val Gln Ile Phe Asn Gln Gly Leu Lys Ser Tyr Arg Asp Leu Pro 340 345 350	1056
ctg cgt atg gcc gag ttt ggt agc tgc cac cgt aac gag ccg tca ggt Leu Arg Met Ala Glu Phe Gly Ser Cys His Arg Asn Glu Pro Ser Gly 355 360 365	1104
tcg ctg cat ggc ctg atg cgc gtg cgt gga ttt acc cag gat gac gcg Ser Leu His Gly Leu Met Arg Val Arg Gly Phe Thr Gln Asp Asp Ala 370 375 380	1152
cat atc ttc tgt act gaa gaa caa att cgc gat gaa gtt aac gga tgt His Ile Phe Cys Thr Glu Glu Gln Ile Arg Asp Glu Val Asn Gly Cys 385 390 395 400	1200
atc cgt tta gtc tat gat atg tac agc act ttt ggc ttc gag aag atc Ile Arg Leu Val Tyr Asp Met Tyr Ser Thr Phe Gly Phe Glu Lys Ile 405 410 415	1248
gtc gtc aaa ctc tcc act cgt cct gaa aaa cgt att ggc agc gac gaa Val Val Lys Leu Ser Thr Arg Pro Glu Lys Arg Ile Gly Ser Asp Glu 420 425 430	1296
atg tgg gat cgt gct gag gcg gac ctg gcg gtt gcg ctg gaa gaa aac Met Trp Asp Arg Ala Glu Ala Asp Leu Ala Val Ala Leu Glu Glu Asn 435 440 445	1344
aac atc ccg ttt gaa tat caa ctg ggt gaa ggc gct ttc tac ggt ccg Asn Ile Pro Phe Glu Tyr Gln Leu Gly Glu Gly Ala Phe Tyr Gly Pro 450 455 460	1392
aaa att gaa ttt acc ctg tat gac tgc ctc gat cgt gca tgg cag tgc Lys Ile Glu Phe Thr Leu Tyr Asp Cys Leu Asp Arg Ala Trp Gln Cys 465 470 475 480	1440
ggt aca gta cag ctg gac ttc tct ttg ccg tct cgt ctg agc gct tct Gly Thr Val Gln Leu Asp Phe Ser Leu Pro Ser Arg Leu Ser Ala Ser 485 490 495	1488
tat gta ggc gaa gac aat gaa cgt aaa gta ccg gta atg att cac cgc Tyr Val Gly Glu Asp Asn Glu Arg Lys Val Pro Val Met Ile His Arg 500 505 510	1536

gca att ctg ggg tcg atg gaa cgt ttc atc ggt atc ctg acc gaa gag 1584
 Ala Ile Leu Gly Ser Met Glu Arg Phe Ile Gly Ile Leu Thr Glu Glu
 515 520 525

ttc gct ggt ttc ttc ccg acc tgg ctt gcg ccg gtt cag gtt gtt atc 1632
 Phe Ala Gly Phe Phe Pro Thr Trp Leu Ala Pro Val Gln Val Val Ile
 530 535 540

atg aat att acc gat tca cag tct gaa tac gtt aac gaa ttg acg caa 1680
 Met Asn Ile Thr Asp Ser Gln Ser Glu Tyr Val Asn Glu Leu Thr Gln
 545 550 555 560

aaa cta tca aat gcg ggc att cgt gtt aaa gca gac ttg aga aat gag 1728
 Lys Leu Ser Asn Ala Gly Ile Arg Val Lys Ala Asp Leu Arg Asn Glu
 565 570 575

aag att ggc ttt aaa atc cgc gag cac act ttg cgt cgc gtc cca tat 1776
 Lys Ile Gly Phe Lys Ile Arg Glu His Thr Leu Arg Arg Val Pro Tyr
 580 585 590

atg ctg gtc tgt ggt gat aaa gag gtg gaa tca ggc aaa gtt gcc gtt 1824
 Met Leu Val Cys Gly Asp Lys Glu Val Glu Ser Gly Lys Val Ala Val
 595 600 605

cgc acc cgc cgt ggt aaa gac ctg gga agc atg gac gta aat gaa gtg 1872
 Arg Thr Arg Arg Gly Lys Asp Leu Gly Ser Met Asp Val Asn Glu Val
 610 615 620

atc gag aag ctg caa caa gag att cgc agc cgc agt ctt aaa caa ttg 1920
 Ile Glu Lys Leu Gln Gln Glu Ile Arg Ser Arg Ser Leu Lys Gln Leu
 625 630 635 640

gag gaa taa 1929
 Glu Glu *

<210> 172
 <211> 993
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(993)

<400> 172
 atg aaa ata aag aac att cta ctc acc ctt tgc acc tca ctc ctg ctt 48
 Met Lys Ile Lys Asn Ile Leu Leu Thr Leu Cys Thr Ser Leu Leu Leu
 1 5 10 15

acc aac gtt gct gca cac gcc aaa gaa gtc aaa ata ggt atg gcg att 96
 Thr Asn Val Ala Ala His Ala Lys Glu Val Lys Ile Gly Met Ala Ile
 20 25 30

gat gat ctc cgt ctt gaa cgc tgg caa aaa gat cga gat atc ttt gtg 144
 Asp Asp Leu Arg Leu Glu Arg Trp Gln Lys Asp Arg Asp Ile Phe Val
 35 40 45

aaa aag gca gaa tct ctc ggc gcg aaa gta ttt gta cag tct gca aat 192

Lys	Lys	Ala	Glu	Ser	Leu	Gly	Ala	Lys	Val	Phe	Val	Gln	Ser	Ala	Asn		
50						55					60						
ggc	aat	gaa	gaa	aca	caa	atg	tcg	cag	att	gaa	aac	atg	ata	aac	cgg	240	
Gly	Asn	Glu	Glu	Thr	Gln	Met	Ser	Gln	Ile	Glu	Asn	Met	Ile	Asn	Arg		
65					70				75						80		
ggg	gtc	gat	gtt	ctt	gtc	att	att	ccg	tat	aac	ggg	cag	gta	tta	agt	288	
Gly	Val	Asp	Val	Leu	Val	Ile	Ile	Pro	Tyr	Asn	Gly	Gln	Val	Leu	Ser		
				85				90						95			
aac	gtt	gta	aaa	gaa	gcc	aaa	caa	gaa	ggc	att	aaa	gta	tta	gct	tac	336	
Asn	Val	Val	Lys	Glu	Ala	Lys	Gln	Glu	Gly	Ile	Lys	Val	Leu	Ala	Tyr		
			100					105					110				
gac	cgt	atg	att	aac	gat	gcg	gat	atc	gat	ttt	tat	att	tct	ttc	gat	384	
Asp	Arg	Met	Ile	Asn	Asp	Ala	Asp	Ile	Asp	Phe	Tyr	Ile	Ser	Phe	Asp		
	115					120						125					
aac	gaa	aaa	gtc	ggg	gaa	ctg	cag	gca	aaa	gcc	ctg	gtc	gat	att	gtt	432	
Asn	Glu	Lys	Val	Gly	Glu	Leu	Gln	Ala	Lys	Ala	Leu	Val	Asp	Ile	Val		
	130					135					140						
ccg	caa	ggg	aat	tac	ttc	ctg	atg	ggc	ggc	tcg	ccg	gta	gat	aac	aac	480	
Pro	Gln	Gly	Asn	Tyr	Phe	Leu	Met	Gly	Gly	Ser	Pro	Val	Asp	Asn	Asn		
145					150					155					160		
gcc	aag	ctg	ttc	cgc	gcc	gga	caa	atg	aaa	gtg	tta	aaa	cct	tac	gtt	528	
Ala	Lys	Leu	Phe	Arg	Ala	Gly	Gln	Met	Lys	Val	Leu	Lys	Pro	Tyr	Val		
				165					170					175			
gat	tcc	gga	aaa	att	aaa	gtc	gtt	ggg	gac	caa	tgg	gtt	gat	ggc	tgg	576	
Asp	Ser	Gly	Lys	Ile	Lys	Val	Val	Gly	Asp	Gln	Trp	Val	Asp	Gly	Trp		
			180					185					190				
tta	ccg	gaa	aac	gca	ttg	aaa	att	atg	gaa	aac	gcg	cta	acc	gcc	aat	624	
Leu	Pro	Glu	Asn	Ala	Leu	Lys	Ile	Met	Glu	Asn	Ala	Leu	Thr	Ala	Asn		
			195				200					205					
aat	aac	aaa	att	gat	gct	gta	gtt	gcc	tca	aac	gat	gcc	acc	gca	ggg	672	
Asn	Asn	Lys	Ile	Asp	Ala	Val	Val	Ala	Ser	Asn	Asp	Ala	Thr	Ala	Gly		
			210			215					220						
ggg	gca	att	cag	gca	tta	agc	gcg	caa	ggg	tta	tca	ggg	aaa	gta	gca	720	
Gly	Ala	Ile	Gln	Ala	Leu	Ser	Ala	Gln	Gly	Leu	Ser	Gly	Lys	Val	Ala		
225					230				235					240			
atc	tcc	ggc	cag	gat	gcg	gat	ctc	gca	ggg	att	aaa	cgt	att	gct	gcc	768	
Ile	Ser	Gly	Gln	Asp	Ala	Asp	Leu	Ala	Gly	Ile	Lys	Arg	Ile	Ala	Ala		
				245					250					255			
ggg	acg	caa	act	atg	acg	gtg	tat	aaa	cct	att	acg	ttg	ttg	gca	aat	816	
Gly	Thr	Gln	Thr	Met	Thr	Val	Tyr	Lys	Pro	Ile	Thr	Leu	Leu	Ala	Asn		
			260					265					270				
act	gcc	gca	gaa	att	gcc	gtt	gag	ttg	ggc	aat	ggg	cag	gaa	cca	aaa	864	
Thr	Ala	Ala	Glu	Ile	Ala	Val	Glu	Leu	Gly	Asn	Gly	Gln	Glu	Pro	Lys		
			275				280					285					
gca	gat	acc	aca	ctg	aat	aat	ggc	ctg	aaa	gat	gtc	ccc	tcc	cgc	ctc	912	

Ala	Asp	Thr	Thr	Leu	Asn	Asn	Gly	Leu	Lys	Asp	Val	Pro	Ser	Arg	Leu		
290						295					300						
ctg	aca	ccg	atc	gat	gtg	aat	aaa	aac	aac	atc	aaa	gat	acg	gta	att	960	
Leu	Thr	Pro	Ile	Asp	Val	Asn	Lys	Asn	Asn	Ile	Lys	Asp	Thr	Val	Ile		
305					310					315					320		
aaa	gac	gga	ttc	cac	aaa	gag	agc	gag	ctg	taa						993	
Lys	Asp	Gly	Phe	His	Lys	Glu	Ser	Glu	Leu	*							
				325						330							

<210> 173
 <211> 168
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(168)

<400> 173																	
atg	aac	aaa	ttt	att	aaa	gtt	gca	ctg	gta	ggt	gca	gta	ctg	gct	acg	48	
Met	Asn	Lys	Phe	Ile	Lys	Val	Ala	Leu	Val	Gly	Ala	Val	Leu	Ala	Thr		
1				5					10					15			
tta	act	gca	tgt	act	ggt	cat	att	gaa	aac	cgt	gat	aag	aac	tgc	tct	96	
Leu	Thr	Ala	Cys	Thr	Gly	His	Ile	Glu	Asn	Arg	Asp	Lys	Asn	Cys	Ser		
			20					25					30				
tac	gac	tac	ctg	ctg	cac	ccg	gca	att	tct	att	tct	aaa	atc	att	ggc	144	
Tyr	Asp	Tyr	Leu	Leu	His	Pro	Ala	Ile	Ser	Ile	Ser	Lys	Ile	Ile	Gly		
		35					40					45					
ggt	tgc	ggt	cct	act	gca	cag	taa									168	
Gly	Cys	Gly	Pro	Thr	Ala	Gln	*										
	50					55											

<210> 174
 <211> 1389
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1389)

<400> 174																	
atg	act	gca	aac	tct	ccc	cta	caa	cgt	att	gga	caa	gaa	aaa	ggt	atc	48	
Met	Thr	Ala	Asn	Ser	Pro	Leu	Gln	Arg	Ile	Gly	Gln	Glu	Lys	Gly	Ile		
1				5					10					15			
gct	atg	gga	agc	cag	gaa	ctc	caa	cgc	aag	ctc	gga	ttt	tgg	gcc	gtt	96	
Ala	Met	Gly	Ser	Gln	Glu	Leu	Gln	Arg	Lys	Leu	Gly	Phe	Trp	Ala	Val		
			20					25					30				
ctt	gca	atc	gcc	gtc	ggg	aca	acc	gtc	ggc	tcc	ggt	att	ttt	gta	tct	144	
Leu	Ala	Ile	Ala	Val	Gly	Thr	Thr	Val	Gly	Ser	Gly	Ile	Phe	Val	Ser		
		35					40					45					

gtg ggt gaa gtg gca aaa gca gcg ggc acg ccg tgg ctt acg gtg ctc Val Gly Glu Val Ala Lys Ala Ala Gly Thr Pro Trp Leu Thr Val Leu 50 55 60	192
gcg ttt gtc att ggc ggg tta att gtg atc ccg caa atg tgc gtc tat Ala Phe Val Ile Gly Gly Leu Ile Val Ile Pro Gln Met Cys Val Tyr 65 70 75 80	240
gcg gaa cta tcc acc gct tat ccg gaa aat ggc gca gat tat gtt tat Ala Glu Leu Ser Thr Ala Tyr Pro Glu Asn Gly Ala Asp Tyr Val Tyr 85 90 95	288
ctg aaa aat gcc gga agc cga ccg ctg gct ttc ctc tcc ggc tgg gcc Leu Lys Asn Ala Gly Ser Arg Pro Leu Ala Phe Leu Ser Gly Trp Ala 100 105 110	336
agc ttc tgg gcc aac gat gcg ccg tca ttg tcg att atg gcg ctg gcg Ser Phe Trp Ala Asn Asp Ala Pro Ser Leu Ser Ile Met Ala Leu Ala 115 120 125	384
att gtc agc aat ctt ggc ttt tta acg cct atc gat ccg ttg ctc ggt Ile Val Ser Asn Leu Gly Phe Leu Thr Pro Ile Asp Pro Leu Leu Gly 130 135 140	432
aaa ttt atc gcc gcc gga tta att atc gcc ttt atg ttg cta cac ctg Lys Phe Ile Ala Ala Gly Leu Ile Ile Ala Phe Met Leu Leu His Leu 145 150 155 160	480
cgc tcc gtt gaa ggc ggc gca gcg ttt cag acg cta att acc atc gcc Arg Ser Val Glu Gly Gly Ala Ala Phe Gln Thr Leu Ile Thr Ile Ala 165 170 175	528
aaa att atc ccg ttc act atc gtc att ggc ctt ggg atc ttc tgg ttt Lys Ile Ile Pro Phe Thr Ile Val Ile Gly Leu Gly Ile Phe Trp Phe 180 185 190	576
aaa gcg gag aat ttt gcc gcc cct acc acc act gcg att ggc gca acg Lys Ala Glu Asn Phe Ala Ala Pro Thr Thr Thr Ala Ile Gly Ala Thr 195 200 205	624
ggc agc ttt atg gcg ctg ctg gcg ggg atc tct gcc acc agt tgg tcg Gly Ser Phe Met Ala Leu Leu Ala Gly Ile Ser Ala Thr Ser Trp Ser 210 215 220	672
tat acc ggc atg gcc tct atc tgt tat atg acc ggc gaa att aaa aac Tyr Thr Gly Met Ala Ser Ile Cys Tyr Met Thr Gly Glu Ile Lys Asn 225 230 235 240	720
ccc gga aaa acc atg cca cga gcg ctg att ggt tcc tgt ctg ctg gtt Pro Gly Lys Thr Met Pro Arg Ala Leu Ile Gly Ser Cys Leu Leu Val 245 250 255	768
ctg gtg ctc tac acc ctg ctg gcg ctg gtg att tcc ggc ctg atg ccc Leu Val Leu Tyr Thr Leu Leu Ala Leu Val Ile Ser Gly Leu Met Pro 260 265 270	816
ttc gac aaa ctc gcc aat tct gaa acg ccg att tcc gac gcc ctg acc Phe Asp Lys Leu Ala Asn Ser Glu Thr Pro Ile Ser Asp Ala Leu Thr 275 280 285	864

tgg atc ccc gca ctc ggc agc acc gct ggg atc ttt gtt gcc atc acg	912
Trp Ile Pro Ala Leu Gly Ser Thr Ala Gly Ile Phe Val Ala Ile Thr	
290 295 300	
gcg atg atc gtc att ctt ggt tgc ctt tcc agc tgc gtg atg tac cag	960
Ala Met Ile Val Ile Leu Gly Ser Leu Ser Ser Cys Val Met Tyr Gln	
305 310 315 320	
ccg cgg ctg gaa tac gcg atg gcg aaa gac aac ctg ttc ttt aaa tgc	1008
Pro Arg Leu Glu Tyr Ala Met Ala Lys Asp Asn Leu Phe Phe Lys Cys	
325 330 335	
ttc ggc cat gtg cat ccg aaa tac aac acg ccg gat gtc tcc atc atc	1056
Phe Gly His Val His Pro Lys Tyr Asn Thr Pro Asp Val Ser Ile Ile	
340 345 350	
ctg caa ggg gcg ctg ggg atc ttc ttc atc ttc gtt tcc gat ctc acc	1104
Leu Gln Gly Ala Leu Gly Ile Phe Phe Ile Phe Val Ser Asp Leu Thr	
355 360 365	
agc ctg ctg ggt tat ttc acc ctg gtg atg tgt ttc aaa aat acc ctc	1152
Ser Leu Leu Gly Tyr Phe Thr Leu Val Met Cys Phe Lys Asn Thr Leu	
370 375 380	
acc ttc ggc tcc atc atc tgg tgt cgt aaa cgc gac gat tac aaa ccg	1200
Thr Phe Gly Ser Ile Ile Trp Cys Arg Lys Arg Asp Asp Tyr Lys Pro	
385 390 395 400	
ctg tgg cgt act ccg gct ttc ggg ctg atg acc acc ctc gcc att gcg	1248
Leu Trp Arg Thr Pro Ala Phe Gly Leu Met Thr Thr Leu Ala Ile Ala	
405 410 415	
tca agc ctc att ctg gtc gcc tca acc ttt gtc tgg gca ccg att ccc	1296
Ser Ser Leu Ile Leu Val Ala Ser Thr Phe Val Trp Ala Pro Ile Pro	
420 425 430	
ggc ctt atc tgc gcc gtc atc gtt att gct act ggt ctg cct gct tac	1344
Gly Leu Ile Cys Ala Val Ile Val Ile Ala Thr Gly Leu Pro Ala Tyr	
435 440 445	
gcc ttc tgg gcg aag cgt agc cgc cag ctc aac gct ttg tgc taa	1389
Ala Phe Trp Ala Lys Arg Ser Arg Gln Leu Asn Ala Leu Ser *	
450 455 460	

<210> 175

<211> 1044

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1044)

<400> 175

atg tta tct gga gaa aat aaa atg ttg gat att gat aaa agc acc gtg	48
Met Leu Ser Gly Glu Asn Lys Met Leu Asp Ile Asp Lys Ser Thr Val	
1 5 10 15	

gac ttt ctg gtc acc gaa aat atg gtt cag gaa gtg gaa aaa gtt ctc Asp Phe Leu Val Thr Glu Asn Met Val Gln Glu Val Glu Lys Val Leu 20 25 30	96
agc cat gac gtt ccg ctg gtg cac gcc atc gtg gaa gag atg gtg aag Ser His Asp Val Pro Leu Val His Ala Ile Val Glu Glu Met Val Lys 35 40 45	144
cgc gac att gat cgt att tat ttc gtt gcc tgc gga tgc cca ctc aac Arg Asp Ile Asp Arg Ile Tyr Phe Val Ala Cys Gly Ser Pro Leu Asn 50 55 60	192
gcg gcg caa acg gcg aaa cat ctg gcg gat cgc ttt tcc gat ctt cag Ala Ala Gln Thr Ala Lys His Leu Ala Asp Arg Phe Ser Asp Leu Gln 65 70 75 80	240
gtc tac gcc att tcc ggc tgg gag ttc tgc gat aac acc ccg tat cgc Val Tyr Ala Ile Ser Gly Trp Glu Phe Cys Asp Asn Thr Pro Tyr Arg 85 90 95	288
ctc gac gat cgt tgc gca gta att ggc gtt tct gac tac ggt aaa acc Leu Asp Asp Arg Cys Ala Val Ile Gly Val Ser Asp Tyr Gly Lys Thr 100 105 110	336
gaa gag gta atc aaa gcg ctg gag ctg ggc cgg gcc tgc ggc gca ctc Glu Glu Val Ile Lys Ala Leu Glu Leu Gly Arg Ala Cys Gly Ala Leu 115 120 125	384
act gcg gcg ttc acc aaa cgc gcg gat agc ccg att acc tgc gcg gcg Thr Ala Ala Phe Thr Lys Arg Ala Asp Ser Pro Ile Thr Ser Ala Ala 130 135 140	432
gaa ttt agc att gat tat cag gcc gac tgt atc tgg gaa att cac ctg Glu Phe Ser Ile Asp Tyr Gln Ala Asp Cys Ile Trp Glu Ile His Leu 145 150 155 160	480
ctg ctc tgc tac agc gtg gtg ctg gag atg atc acc cgc ctc gcg ccg Leu Leu Cys Tyr Ser Val Val Leu Glu Met Ile Thr Arg Leu Ala Pro 165 170 175	528
aac gcg gaa atc ggc aag atc aaa aac gat ctc aag cag ttg ccg aat Asn Ala Glu Ile Gly Lys Ile Lys Asn Asp Leu Lys Gln Leu Pro Asn 180 185 190	576
gcg ctc ggt cat ctg gta cgc acc tgg gaa gaa aaa ggc cgc cag ctt Ala Leu Gly His Leu Val Arg Thr Trp Glu Glu Lys Gly Arg Gln Leu 195 200 205	624
ggt gaa ctg gcc agc cag tgg ccg atg att tat acc gtt gct gcg ggt Gly Glu Leu Ala Ser Gln Trp Pro Met Ile Tyr Thr Val Ala Ala Gly 210 215 220	672
ccg ctg cgt ccg ctg ggt tac aaa gaa ggc att gta acg ctg atg gaa Pro Leu Arg Pro Leu Gly Tyr Lys Glu Gly Ile Val Thr Leu Met Glu 225 230 235 240	720
ttt acc tgg acg cac ggc tgc gtg att gag agc gga gag ttc cgc cat Phe Thr Trp Thr His Gly Cys Val Ile Glu Ser Gly Glu Phe Arg His 245 250 255	768

ggc ccg ctg gag att gtc gaa ccg ggc gtt ccg ttc ctg ttc ctg ctc 816
 Gly Pro Leu Glu Ile Val Glu Pro Gly Val Pro Phe Leu Phe Leu Leu
 260 265 270

ggc aat gat gaa agt cgc cac acc acc gaa cgc gcc att aac ttt gtt 864
 Gly Asn Asp Glu Ser Arg His Thr Thr Glu Arg Ala Ile Asn Phe Val
 275 280 285

aaa cag cgt act gac aac gtg atc gtc atc gat tac gcc gaa att tcg 912
 Lys Gln Arg Thr Asp Asn Val Ile Val Ile Asp Tyr Ala Glu Ile Ser
 290 295 300

caa ggg ctg cac ccg tgg ctg gca ccg ttc ctg atg ttc gtg cca atg 960
 Gln Gly Leu His Pro Trp Leu Ala Pro Phe Leu Met Phe Val Pro Met
 305 310 315 320

gag tgg ctc tgc tac tac ctg tct att tac aaa gat cac aac ccg gat 1008
 Glu Trp Leu Cys Tyr Tyr Leu Ser Ile Tyr Lys Asp His Asn Pro Asp
 325 330 335

gaa cgc cgc tat tac ggt ggt ctg gtg gaa tat taa 1044
 Glu Arg Arg Tyr Tyr Gly Gly Leu Val Glu Tyr *
 340 345

<210> 176
 <211> 450
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(450)

<400> 176

atg aac gcc gct att acg gtg gtc tgg tgg aat att aat ccc tct ccc 48
 Met Asn Ala Ala Ile Thr Val Val Trp Trp Asn Ile Asn Pro Ser Pro
 1 5 10 15

ggc ccg gca acg ggc cgg att tac gca agg agt tac ccg atg aaa aca 96
 Gly Pro Ala Thr Gly Arg Ile Tyr Ala Arg Ser Tyr Pro Met Lys Thr
 20 25 30

ggt atg ttt acc tgc ggc cac cag cgg ctg cct att gaa cac gca ttt 144
 Gly Met Phe Thr Cys Gly His Gln Arg Leu Pro Ile Glu His Ala Phe
 35 40 45

cgt gat gca agc gag ctg ggt tac gac ggc atc gaa att tgg ggc ggt 192
 Arg Asp Ala Ser Glu Leu Gly Tyr Asp Gly Ile Glu Ile Trp Gly Gly
 50 55 60

cgc ccg cac gcg ttc gcg ccg gac tta aaa gcg ggc ggc atc aaa caa 240
 Arg Pro His Ala Phe Ala Pro Asp Leu Lys Ala Gly Gly Ile Lys Gln
 65 70 75 80

atc aag gcg ctg gcg cag acg tat cag atg ccg att atc ggc tat acg 288
 Ile Lys Ala Leu Ala Gln Thr Tyr Gln Met Pro Ile Ile Gly Tyr Thr
 85 90 95

cca gaa acc aac ggc tat ccg tat aac atg atg ctg ggc gat gaa cat 336

Pro Glu Thr Asn Gly Tyr Pro Tyr Asn Met Met Leu Gly Asp Glu His
 100 105 110

atg cgt cgc gaa agc ctc gac atg atc aag ctg gcg atg gat atg gca 384
 Met Arg Arg Glu Ser Leu Asp Met Ile Lys Leu Ala Met Asp Met Ala
 115 120 125

aaa gag atg aac gcg ggt tat acg ctg att tcc gcc ggc cca cgc ggg 432
 Lys Glu Met Asn Ala Gly Tyr Thr Leu Ile Ser Ala Gly Pro Arg Gly
 130 135 140

cta tct cac gcc acc taa 450
 Leu Ser His Ala Thr *
 145

<210> 177
 <211> 384
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(384)

<400> 177

atg cgt gat att cag atg gtt ctt gag cgt tgg gga gcg tgg gcg gct 48
 Met Arg Asp Ile Gln Met Val Leu Glu Arg Trp Gly Ala Trp Ala Ala
 1 5 10 15

aat aat cat gaa gat gtg acc tgg tgc tcc att gcc gcc ggt ttt aag 96
 Asn Asn His Glu Asp Val Thr Trp Ser Ser Ile Ala Ala Gly Phe Lys
 20 25 30

gga tta att act tca aaa gta aaa tct cgc ccg caa tgt tgt gac gat 144
 Gly Leu Ile Thr Ser Lys Val Lys Ser Arg Pro Gln Cys Cys Asp Asp
 35 40 45

gac gcg atg atc att tgc ggg tgc atg gcc cgt ctg aaa aag aac aac 192
 Asp Ala Met Ile Ile Cys Gly Cys Met Ala Arg Leu Lys Lys Asn Asn
 50 55 60

agc gat ttg cac gat tta tta gta gat tat tat gta gtc ggt atg aca 240
 Ser Asp Leu His Asp Leu Leu Val Asp Tyr Tyr Val Val Gly Met Thr
 65 70 75 80

ttc atg tca ctg gca ggt aag cat tgc tgc tct gat ggt tat atc ggg 288
 Phe Met Ser Leu Ala Gly Lys His Cys Cys Ser Asp Gly Tyr Ile Gly
 85 90 95

aaa agg tta cag aag gct gag ggc ata att gaa ggg atg tta atg gca 336
 Lys Arg Leu Gln Lys Ala Glu Gly Ile Ile Glu Gly Met Leu Met Ala
 100 105 110

tta gat atc cgg tta gag atg gat atc gtt gtt aat aac tct aat taa 384
 Leu Asp Ile Arg Leu Glu Met Asp Ile Val Val Asn Asn Ser Asn *
 115 120 125

<210> 178

<211> 1362

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1362)

<400> 178

atg	ttt	gat	aat	tta	acc	gat	cgt	ttg	tcg	cgc	acg	ctg	cgc	aat	atc	48
Met	Phe	Asp	Asn	Leu	Thr	Asp	Arg	Leu	Ser	Arg	Thr	Leu	Arg	Asn	Ile	
1				5					10					15		

agt	ggc	cgt	gga	cgc	ctc	act	gaa	gac	aac	gta	aaa	gat	acg	ctg	cgc	96
Ser	Gly	Arg	Gly	Arg	Leu	Thr	Glu	Asp	Asn	Val	Lys	Asp	Thr	Leu	Arg	
			20					25					30			

gaa	gtg	cgc	atg	gcg	ctg	ctg	gag	gcg	gac	gta	gct	ctg	ccg	gta	gtg	144
Glu	Val	Arg	Met	Ala	Leu	Leu	Glu	Ala	Asp	Val	Ala	Leu	Pro	Val	Val	
		35					40					45				

cgt	gag	ttt	atc	aat	cgc	gta	aaa	gag	aaa	gcg	gtt	ggt	cat	gaa	gtt	192
Arg	Glu	Phe	Ile	Asn	Arg	Val	Lys	Glu	Lys	Ala	Val	Gly	His	Glu	Val	
	50					55					60					

aat	aag	agc	ctg	acg	ccg	ggg	cag	gag	ttc	gtc	aaa	ata	gtc	cgt	aac	240
Asn	Lys	Ser	Leu	Thr	Pro	Gly	Gln	Glu	Phe	Val	Lys	Ile	Val	Arg	Asn	
65					70				75						80	

gaa	ctg	gtt	gcg	gcg	atg	ggc	gaa	gag	aac	cag	acc	ctg	aac	ctg	gct	288
Glu	Leu	Val	Ala	Ala	Met	Gly	Glu	Glu	Asn	Gln	Thr	Leu	Asn	Leu	Ala	
			85						90					95		

gcg	caa	ccg	cct	gcg	gtc	gta	ctg	atg	gcg	ggc	ctg	caa	ggt	gcc	ggt	336
Ala	Gln	Pro	Pro	Ala	Val	Val	Leu	Met	Ala	Gly	Leu	Gln	Gly	Ala	Gly	
			100				105						110			

aaa	aca	acc	agc	gtt	ggt	aaa	ctc	ggt	aag	ttc	ctg	cgc	gag	aag	cac	384
Lys	Thr	Thr	Ser	Val	Gly	Lys	Leu	Gly	Lys	Phe	Leu	Arg	Glu	Lys	His	
		115				120						125				

aag	aag	aaa	gtg	ctg	gtg	gtt	tct	gcc	gac	gtt	tat	cgc	ccg	gcg	gca	432
Lys	Lys	Lys	Val	Leu	Val	Val	Ser	Ala	Asp	Val	Tyr	Arg	Pro	Ala	Ala	
	130					135					140					

atc	aaa	cag	ctt	gag	acg	ctg	gca	gag	cag	gtg	ggc	gtt	gat	ttc	ttc	480
Ile	Lys	Gln	Leu	Glu	Thr	Leu	Ala	Glu	Gln	Val	Gly	Val	Asp	Phe	Phe	
145					150				155						160	

cct	tct	gat	gtt	ggt	cag	aag	ccg	gta	gat	atc	gtt	aac	gcg	gcg	ctg	528
Pro	Ser	Asp	Val	Gly	Gln	Lys	Pro	Val	Asp	Ile	Val	Asn	Ala	Ala	Leu	
				165					170					175		

aaa	gaa	gcc	aaa	ctg	aaa	ttc	tac	gac	gtg	ctg	ctg	gtg	gat	acc	gct	576
Lys	Glu	Ala	Lys	Leu	Lys	Phe	Tyr	Asp	Val	Leu	Leu	Val	Asp	Thr	Ala	
			180					185					190			

ggt	cgt	ctg	cac	gtt	gac	gaa	gcg	atg	atg	gac	gag	atc	aaa	caa	gtc	624
Gly	Arg	Leu	His	Val	Asp	Glu	Ala	Met	Met	Asp	Glu	Ile	Lys	Gln	Val	
		195				200						205				

cat gcg tcg att aac ccg gtt gaa acc ctg ttt gtg gtt gac gcc atg His Ala Ser Ile Asn Pro Val Glu Thr Leu Phe Val Val Asp Ala Met 210 215 220	672
acc ggt cag gat gcg gcc aat acg gca aaa gca ttc aat gaa gcg tta Thr Gly Gln Asp Ala Ala Asn Thr Ala Lys Ala Phe Asn Glu Ala Leu 225 230 235 240	720
ccg ctt acc ggc gta gtg ttg acc aaa gtg gac ggc gat gcc cgc ggc Pro Leu Thr Gly Val Val Leu Thr Lys Val Asp Gly Asp Ala Arg Gly 245 250 255	768
ggg gcg gcg ctc tct att cgt cac atc act ggc aaa ccg atc aag ttc Gly Ala Ala Leu Ser Ile Arg His Ile Thr Gly Lys Pro Ile Lys Phe 260 265 270	816
ctc ggt gtt ggc gag aaa act gag gcg ctg gag ccg ttc cat ccg gac Leu Gly Val Gly Glu Lys Thr Glu Ala Leu Glu Pro Phe His Pro Asp 275 280 285	864
cgc atc gcg tcg cgt att ctc ggc atg ggc gac gta ctg tcg ctg atc Arg Ile Ala Ser Arg Ile Leu Gly Met Gly Asp Val Leu Ser Leu Ile 290 295 300	912
gaa gat atc gaa agc aaa gtt gac cgc gcg cag gca gag aaa tta gcc Glu Asp Ile Glu Ser Lys Val Asp Arg Ala Gln Ala Glu Lys Leu Ala 305 310 315 320	960
agc aag ctg aaa aaa ggt gac ggc ttc gat ctc aac gac ttt ctt gag Ser Lys Leu Lys Lys Gly Asp Gly Phe Asp Leu Asn Asp Phe Leu Glu 325 330 335	1008
cag ctg cgc cag atg aaa aat atg ggc ggc atg gct agt ctg atg ggc Gln Leu Arg Gln Met Lys Asn Met Gly Gly Met Ala Ser Leu Met Gly 340 345 350	1056
aag ctg ccg ggc atg ggg cag atc ccg gat aac gtc aag tca cag atg Lys Leu Pro Gly Met Gly Gln Ile Pro Asp Asn Val Lys Ser Gln Met 355 360 365	1104
gac gat aaa gtg ctg gtg cgt atg gaa gcc atc atc aac tcg atg acg Asp Asp Lys Val Leu Val Arg Met Glu Ala Ile Ile Asn Ser Met Thr 370 375 380	1152
atg aaa gag cgc gct aag cca gaa atc atc aaa ggt tcg cgt aaa cgc Met Lys Glu Arg Ala Lys Pro Glu Ile Ile Lys Gly Ser Arg Lys Arg 385 390 395 400	1200
cgt att gct gcc ggt tgc ggt atg cag gtg cag gac gtt aac cgt ctt Arg Ile Ala Ala Gly Cys Gly Met Gln Val Gln Asp Val Asn Arg Leu 405 410 415	1248
ctg aaa cag ttc gac gac atg cag cgc atg atg aag aaa atg aag aag Leu Lys Gln Phe Asp Asp Met Gln Arg Met Met Lys Lys Met Lys Lys 420 425 430	1296
ggc gga atg gcg aag atg atg aga agc atg aag ggt atg atg ccc cca Gly Gly Met Ala Lys Met Met Arg Ser Met Lys Gly Met Met Pro Pro 435 440 445	1344

ggc ttc cct ggt cgc taa
Gly Phe Pro Gly Arg *
450

1362

<210> 179
<211> 1734
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(1734)

<400> 179
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Met Lys Gln Gln Ile Gln Leu Arg Arg Arg Glu Val Asp Glu Thr Ala
1 5 10 15
gac ttg ccc gct gaa ttg cct ccc ttg ctg cgc cgt tta tac gcc agc 96
Asp Leu Pro Ala Glu Leu Pro Pro Leu Arg Arg Leu Tyr Ala Ser
20 25 30
cgg gga gta cgc agt gcg caa gaa ctg gaa cgc agt gtt aaa ggt atg 144
Arg Gly Val Arg Ser Ala Gln Glu Leu Glu Arg Ser Val Lys Gly Met
35 40 45
ctg ccc tgg cag caa ctg agc ggc gtc gaa aag gcc gtt gag atc ctt 192
Leu Pro Trp Gln Gln Leu Ser Gly Val Glu Lys Ala Val Glu Ile Leu
50 55 60
tac aac gct ttt cgc gaa gga acg cgg att att gtg gtc ggt gat ttc 240
Tyr Asn Ala Phe Arg Glu Gly Thr Arg Ile Ile Val Val Gly Asp Phe
65 70 75 80
gac gcc gac ggc gcg acc agc acg gct cta agc gtg ctg gcg atg cgc 288
Asp Ala Asp Gly Ala Thr Ser Thr Ala Leu Ser Val Leu Ala Met Arg
85 90 95
tcg ctt ggt tgc agc aat atc gac tac ctg gta cca aac cgt ttc gaa 336
Ser Leu Gly Cys Ser Asn Ile Asp Tyr Leu Val Pro Asn Arg Phe Glu
100 105 110
gac ggt tac ggc tta agc ccg gaa gtg gtc gat cag gcc cat gcc cgt 384
Asp Gly Tyr Gly Leu Ser Pro Glu Val Val Asp Gln Ala His Ala Arg
115 120 125
ggc gcg cag tta att gtc acg gtg gat aac ggt att tcc tcc cat gcg 432
Gly Ala Gln Leu Ile Val Thr Val Asp Asn Gly Ile Ser Ser His Ala
130 135 140
ggg gtt gag cac gct cgc tcg ttg ggc atc ccg gtt att gtt acc gat 480
Gly Val Glu His Ala Arg Ser Leu Gly Ile Pro Val Ile Val Thr Asp
145 150 155 160
cac cat ttg cca ggc gac aca tta ccc gca gcg gaa gcg atc att aac 528
His His Leu Pro Gly Asp Thr Leu Pro Ala Ala Glu Ala Ile Ile Asn
165 170 175

cct aac ttg cgc gac tgt aat ttc ccg tcg aaa tca ctg gca ggc gtg Pro Asn Leu Arg Asp Cys Asn Phe Pro Ser Lys Ser Leu Ala Gly Val 180 185 190	576
ggg gtg gcg ttt tat ctg atg ctg gcg ctg cgc acc ttt ttg cgc gat Gly Val Ala Phe Tyr Leu Met Leu Ala Leu Arg Thr Phe Leu Arg Asp 195 200 205	624
cag ggc tgg ttt gat gag cgt aac atc gca att cct aac ctg gca gaa Gln Gly Trp Phe Asp Glu Arg Asn Ile Ala Ile Pro Asn Leu Ala Glu 210 215 220	672
ctg ctg gat ctg gtc gcg ctg ggg aca gtg gcg gac gtc gtg ccg ctg Leu Leu Asp Leu Val Ala Leu Gly Thr Val Ala Asp Val Val Pro Leu 225 230 235 240	720
gac gct aat aat cgc att ctg acc tgg cag ggg atg agt cgc atc cga Asp Ala Asn Asn Arg Ile Leu Thr Trp Gln Gly Met Ser Arg Ile Arg 245 250 255	768
gcc gga aag tgc cgt ccg ggg att aaa gcg ctg ctt gaa gtg gca aac Ala Gly Lys Cys Arg Pro Gly Ile Lys Ala Leu Leu Glu Val Ala Asn 260 265 270	816
cgt gat gca caa aaa ctc gcc gcc agc gat tta ggt ttt gcg ctg ggg Arg Asp Ala Gln Lys Leu Ala Ala Ser Asp Leu Gly Phe Ala Leu Gly 275 280 285	864
cca cgt ctc aat gct gcc gga cga ctg gac gat atg tcc gtc ggt gtg Pro Arg Leu Asn Ala Ala Gly Arg Leu Asp Asp Met Ser Val Gly Val 290 295 300	912
gcg ctg ttg ttg tgc gac aac atc ggc gaa gcg cgc gtg ctg gca aat Ala Leu Leu Leu Cys Asp Asn Ile Gly Glu Ala Arg Val Leu Ala Asn 305 310 315 320	960
gaa ctc gat gcg cta aac cag acg cga aaa gag atc gaa caa gga atg Glu Leu Asp Ala Leu Asn Gln Thr Arg Lys Glu Ile Glu Gln Gly Met 325 330 335	1008
caa att gaa gcc ctg acc ctg tgc gag aaa ctg gag cgc agc cgt gac Gln Ile Glu Ala Leu Thr Leu Cys Glu Lys Leu Glu Arg Ser Arg Asp 340 345 350	1056
acg cta ccc ggc ggg ctg gca atg tat cac ccc gaa tgg cat cag ggc Thr Leu Pro Gly Gly Leu Ala Met Tyr His Pro Glu Trp His Gln Gly 355 360 365	1104
gtt gtc ggt att ctg gct tcg cgc atc aaa gag cgt ttt cac cgt ccg Val Val Gly Ile Leu Ala Ser Arg Ile Lys Glu Arg Phe His Arg Pro 370 375 380	1152
gtt atc gcg ttt gcg cca gca ggt gac ggt acg ctg aaa ggt tcc ggt Val Ile Ala Phe Ala Pro Ala Gly Asp Gly Thr Leu Lys Gly Ser Gly 385 390 395 400	1200
cgc tcc att cag ggg ctg cat atg cgt gat gcg ctg gag cga tta gac Arg Ser Ile Gln Gly Leu His Met Arg Asp Ala Leu Glu Arg Leu Asp 405 410 415	1248

aca ctc tac cct ggc atg atg ctg aag ttt ggc ggt cat gcg atg gcg Thr Leu Tyr Pro Gly Met Met Leu Lys Phe Gly Gly His Ala Met Ala 420 425 430	1296
gcg ggt ttg tcg ctg gaa gag gat aaa ttc aaa ctc ttt caa caa cgg Ala Gly Leu Ser Leu Glu Glu Asp Lys Phe Lys Leu Phe Gln Gln Arg 435 440 445	1344
ttt ggc gaa ctg gtt act gag tgg ctg gac cct tcg cta ttg caa ggc Phe Gly Glu Leu Val Thr Glu Trp Leu Asp Pro Ser Leu Leu Gln Gly 450 455 460	1392
gaa gtg gta tca gac ggt ccg tta agc ccg gcc gaa atg acc atg gaa Glu Val Val Ser Asp Gly Pro Leu Ser Pro Ala Glu Met Thr Met Glu 465 470 475 480	1440
gtg gcg cag ctg ctg cgc gat gct ggc ccg tgg ggg cag atg ttc ccg Val Ala Gln Leu Leu Arg Asp Ala Gly Pro Trp Gly Gln Met Phe Pro 485 490 495	1488
gag ccg ctg ttt gac ggt cat ttc cgt ctg ctg caa cag cgg ctg gtg Glu Pro Leu Phe Asp Gly His Phe Arg Leu Leu Gln Gln Arg Leu Val 500 505 510	1536
ggc gaa cgt cat ttg aag gtg atg gtc gaa ccg gtc ggc ggc ggt cca Gly Glu Arg His Leu Lys Val Met Val Glu Pro Val Gly Gly Gly Pro 515 520 525	1584
ctg ctg gat ggt att gct ttt aat gtc gat acc gcc ctc tgg ccg gat Leu Leu Asp Gly Ile Ala Phe Asn Val Asp Thr Ala Leu Trp Pro Asp 530 535 540	1632
aac ggc gtg cgc gaa gtg caa ctg gct tat aag ctc gat atc aac gag Asn Gly Val Arg Glu Val Gln Leu Ala Tyr Lys Leu Asp Ile Asn Glu 545 550 555 560	1680
ttt cgc ggc aac cgc agc ctg caa att atc atc gac aat atc tgg cca Phe Arg Gly Asn Arg Ser Leu Gln Ile Ile Ile Asp Asn Ile Trp Pro 565 570 575	1728
att tag Ile *	1734

<210> 180

<211> 711

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(711)

<400> 180

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---	----

ttt gct cag gct gat gac gcg gca att caa caa acg tta gcc aaa atg	96
---	----

Phe	Ala	Gln	Ala	Asp	Asp	Ala	Ala	Ile	Gln	Gln	Thr	Leu	Ala	Lys	Met		
		20						25					30				
ggc	atc	aaa	agc	agc	gat	att	cag	ccc	gcg	cct	gta	gct	ggc	atg	aag	144	
Gly	Ile	Lys	Ser	Ser	Asp	Ile	Gln	Pro	Ala	Pro	Val	Ala	Gly	Met	Lys		
		35					40					45					
aca	gtt	ctg	act	aac	agc	ggc	gtg	ttg	tac	atc	acc	gat	gat	ggg	aaa	192	
Thr	Val	Leu	Thr	Asn	Ser	Gly	Val	Leu	Tyr	Ile	Thr	Asp	Asp	Gly	Lys		
		50				55					60						
cat	atc	att	cag	ggg	cca	atg	tat	gac	gtt	agt	ggc	acg	gct	ccg	gtc	240	
His	Ile	Ile	Gln	Gly	Pro	Met	Tyr	Asp	Val	Ser	Gly	Thr	Ala	Pro	Val		
	65				70				75						80		
aat	gtc	acc	aat	aag	atg	ctg	tta	aag	cag	ttg	aat	gcg	ctt	gaa	aaa	288	
Asn	Val	Thr	Asn	Lys	Met	Leu	Leu	Lys	Gln	Leu	Asn	Ala	Leu	Glu	Lys		
			85					90						95			
gag	atg	atc	gtt	tat	aaa	gcg	ccg	cag	gaa	aaa	cac	gtc	atc	acc	gtg	336	
Glu	Met	Ile	Val	Tyr	Lys	Ala	Pro	Gln	Glu	Lys	His	Val	Ile	Thr	Val		
			100					105					110				
ttt	act	gat	att	acc	tgt	ggg	tac	tgc	cac	aaa	ctg	cat	gag	caa	atg	384	
Phe	Thr	Asp	Ile	Thr	Cys	Gly	Tyr	Cys	His	Lys	Leu	His	Glu	Gln	Met		
		115				120						125					
gca	gac	tac	aac	gcg	ctg	ggg	atc	acc	gtg	cgt	tat	ctt	gct	ttc	ccg	432	
Ala	Asp	Tyr	Asn	Ala	Leu	Gly	Ile	Thr	Val	Arg	Tyr	Leu	Ala	Phe	Pro		
		130				135					140						
cgc	cag	ggg	ctg	gac	agc	gat	gca	gag	aaa	gaa	atg	aaa	gct	atc	tgg	480	
Arg	Gln	Gly	Leu	Asp	Ser	Asp	Ala	Glu	Lys	Glu	Met	Lys	Ala	Ile	Trp		
	145				150				155					160			
tgt	gcg	aaa	gat	aaa	aac	aaa	gcg	ttt	gat	gat	gtg	atg	gca	ggg	aaa	528	
Cys	Ala	Lys	Asp	Lys	Asn	Lys	Ala	Phe	Asp	Asp	Val	Met	Ala	Gly	Lys		
			165					170						175			
agc	gtc	gca	cca	gcc	agt	tgc	gac	gtg	gat	att	gcc	gac	cat	tac	gca	576	
Ser	Val	Ala	Pro	Ala	Ser	Cys	Asp	Val	Asp	Ile	Ala	Asp	His	Tyr	Ala		
			180					185					190				
ctt	ggc	gtc	cag	ctt	ggc	gtt	agc	ggg	act	ccg	gca	gtt	gtg	ctg	agc	624	
Leu	Gly	Val	Gln	Leu	Gly	Val	Ser	Gly	Thr	Pro	Ala	Val	Val	Leu	Ser		
		195					200					205					
aat	ggc	aca	ctt	gtt	ccg	ggg	tac	cag	ccg	ccg	aaa	gag	atg	aaa	gaa	672	
Asn	Gly	Thr	Leu	Val	Pro	Gly	Tyr	Gln	Pro	Pro	Lys	Glu	Met	Lys	Glu		
		210				215					220						
ttc	ctc	gac	gaa	cac	caa	aaa	atg	acc	acc	ggg	aaa	taa				711	
Phe	Leu	Asp	Glu	His	Gln	Lys	Met	Thr	Ser	Gly	Lys	*					
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<210> 181

<211> 897

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(897)

<400> 181

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Met	Lys	Gln	Asp	Leu	Ala	Arg	Ile	Glu	Gln	Phe	Leu	Asp	Ala	Leu	Trp	
1				5				10						15		

ctg	gaa	aaa	aat	ctg	gct	gaa	aat	acg	ttg	aac	gct	tac	cgt	cgc	gat	96
Leu	Glu	Lys	Asn	Leu	Ala	Glu	Asn	Thr	Leu	Asn	Ala	Tyr	Arg	Arg	Asp	
			20					25					30			

ctg	tca	atg	atg	gtg	gag	tgg	ttg	cat	cac	cgc	ggg	ttg	acg	ctg	gcg	144
Leu	Ser	Met	Met	Val	Glu	Trp	Leu	His	His	Arg	Gly	Leu	Thr	Leu	Ala	
		35					40						45			

acg	gcg	caa	agt	gac	gat	ttg	cag	gca	tta	ctg	gca	gaa	cgg	ctg	gag	192
Thr	Ala	Gln	Ser	Asp	Asp	Leu	Gln	Ala	Leu	Leu	Ala	Glu	Arg	Leu	Glu	
	50					55					60					

ggc	ggg	tat	aaa	gcc	acc	agc	tca	gcg	cgt	ttg	ctg	agt	gca	gtg	cgc	240
Gly	Gly	Tyr	Lys	Ala	Thr	Ser	Ser	Ala	Arg	Leu	Leu	Ser	Ala	Val	Arg	
65				70						75					80	

cga	ttg	ttc	cag	tat	ctt	tat	cgc	gaa	aag	ttt	cgt	gaa	gac	gat	ccc	288
Arg	Leu	Phe	Gln	Tyr	Leu	Tyr	Arg	Glu	Lys	Phe	Arg	Glu	Asp	Asp	Pro	
			85						90					95		

agt	gcg	cat	ctc	gct	tca	ccg	aaa	ttg	ccc	cag	cgt	ttg	cca	aaa	gat	336
Ser	Ala	His	Leu	Ala	Ser	Pro	Lys	Leu	Pro	Gln	Arg	Leu	Pro	Lys	Asp	
			100					105					110			

tta	agc	gaa	gcg	cag	gtc	gaa	cgt	tta	tta	cag	gca	cca	tta	atc	gat	384
Leu	Ser	Glu	Ala	Gln	Val	Glu	Arg	Leu	Leu	Gln	Ala	Pro	Leu	Ile	Asp	
		115					120					125				

cag	cca	ctg	gag	cta	cgc	gat	aaa	gcc	atg	ctt	gaa	gtg	ttg	tat	gct	432
Gln	Pro	Leu	Glu	Leu	Arg	Asp	Lys	Ala	Met	Leu	Glu	Val	Leu	Tyr	Ala	
	130					135					140					

acc	ggg	ctg	cgt	gtc	tct	gaa	ctg	gtc	gga	ctg	aca	atg	agt	gat	atc	480
Thr	Gly	Leu	Arg	Val	Ser	Glu	Leu	Val	Gly	Leu	Thr	Met	Ser	Asp	Ile	
145				150					155						160	

agc	ctg	cgt	cag	ggc	gtg	gta	cgg	gtc	att	ggg	aaa	ggc	aac	aaa	gag	528
Ser	Leu	Arg	Gln	Gly	Val	Val	Arg	Val	Ile	Gly	Lys	Gly	Asn	Lys	Glu	
			165					170						175		

cgt	ctg	gtg	ccg	tta	ggg	gaa	gag	gcg	gtt	tac	tgg	ctg	gaa	acc	tat	576
Arg	Leu	Val	Pro	Leu	Gly	Glu	Glu	Ala	Val	Tyr	Trp	Leu	Glu	Thr	Tyr	
			180					185					190			

ctg	gaa	cat	ggg	cgt	ccg	tgg	ctg	ctg	aat	ggg	gtg	tca	att	gac	gtg	624
Leu	Glu	His	Gly	Arg	Pro	Trp	Leu	Leu	Asn	Gly	Val	Ser	Ile	Asp	Val	
		195				200						205				

ttg	ttt	ccc	agc	cag	cgt	gcg	cag	cag	atg	acg	cga	cag	acc	ttc	tgg	672
Leu	Phe	Pro	Ser	Gln	Arg	Ala	Gln	Gln	Met	Thr	Arg	Gln	Thr	Phe	Trp	

210	215	220	
cac cgt att aaa cat tat gct gtg ctg gcg ggt atc gac agc gaa aag			720
His Arg Ile Lys His Tyr Ala Val Leu Ala Gly Ile Asp Ser Glu Lys			
225	230	235	240
ctg tca ccg cat gtg ttg cgt cac gct ttt gcc act cat tta tta aat			768
Leu Ser Pro His Val Leu Arg His Ala Phe Ala Thr His Leu Leu Asn			
	245	250	255
cat ggt gcg gat tta cgc gtg gtg cag atg cta ctg ggc cac agc gat			816
His Gly Ala Asp Leu Arg Val Val Gln Met Leu Leu Gly His Ser Asp			
	260	265	270
ctc tcc acc acg caa att tat acg cat gtc gct acc gag cgt ctg cgg			864
Leu Ser Thr Thr Gln Ile Tyr Thr His Val Ala Thr Glu Arg Leu Arg			
	275	280	285
caa ctt cat caa cag cat cac ccg cgg gcg tga			897
Gln Leu His Gln Gln His His Pro Arg Ala *			
	290	295	
<210> 182			
<211> 741			
<212> DNA			
<213> Escherichia coli			
<220>			
<221> CDS			
<222> (1)...(741)			
<400> 182			
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Met Phe Phe Asn Thr Lys His Thr Thr Ala Leu Cys Phe Val Thr Cys			
1	5	10	15
atg gct ttt agt tca tgc tct att gcg gac att gtc att tgc ggt act			96
Met Ala Phe Ser Ser Ser Ser Ile Ala Asp Ile Val Ile Ser Gly Thr			
	20	25	30
cgc gta ata tat aaa agc gat caa aaa agt gtc aac gta cgt ctg gaa			144
Arg Val Ile Tyr Lys Ser Asp Gln Lys Ser Val Asn Val Arg Leu Glu			
	35	40	45
aat aaa ggg aat aac ccg ttg ctt gtc cag agt tgg tta gat act ggc			192
Asn Lys Gly Asn Asn Pro Leu Leu Val Gln Ser Trp Leu Asp Thr Gly			
	50	55	60
gat gac aac gct gag cct ggc agt att aca gtc cct ttt act gct acg			240
Asp Asp Asn Ala Glu Pro Gly Ser Ile Thr Val Pro Phe Thr Ala Thr			
	65	70	75
ccg cca gta tgc cgt att gat gcc aaa cgt ggg caa aca atc aaa tta			288
Pro Pro Val Ser Arg Ile Asp Ala Lys Arg Gly Gln Thr Ile Lys Leu			
	85	90	95
atg tac aca gcc agc acc tca ctg cct aaa gac aga gag agc gtg ttc			336
Met Tyr Thr Ala Ser Thr Ser Leu Pro Lys Asp Arg Glu Ser Val Phe			
	100	105	110

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Trp Phe Asn Val Leu Glu Val Pro Pro Lys Pro Asp Ala Glu Lys Val	
115 120 125	
gcg aat caa agc ctg ctg caa ctg gca ttt cgc aca cgt ata aaa ctt	432
Ala Asn Gln Ser Leu Leu Gln Leu Ala Phe Arg Thr Arg Ile Lys Leu	
130 135 140	
ttc tat cgc ccg gat gga ttg aag gga aat ccc tct gaa gcc ccg tta	480
Phe Tyr Arg Pro Asp Gly Leu Lys Gly Asn Pro Ser Glu Ala Pro Leu	
145 150 155 160	
gcc ctg aag tgg ttc tgg tca ggt tca gaa ggt aag gcg tca tta cga	528
Ala Leu Lys Trp Phe Trp Ser Gly Ser Glu Gly Lys Ala Ser Leu Arg	
165 170 175	
gtg acc aat cca acc cct tac tac gtc tct ttt agc agt ggt gat tta	576
Val Thr Asn Pro Thr Pro Tyr Tyr Val Ser Phe Ser Ser Gly Asp Leu	
180 185 190	
gaa gct agc ggt aaa cgc tat ccg att gat gtg aaa atg att gca cca	624
Glu Ala Ser Gly Lys Arg Tyr Pro Ile Asp Val Lys Met Ile Ala Pro	
195 200 205	
ttt agt gat gag gtc atg aaa gtc aat ggc ctt aat ggc aaa gcg aat	672
Phe Ser Asp Glu Val Met Lys Val Asn Gly Leu Asn Gly Lys Ala Asn	
210 215 220	
tct gca aaa gtg cat ttt tac gcc att aat gac ttt ggt ggc gca att	720
Ser Ala Lys Val His Phe Tyr Ala Ile Asn Asp Phe Gly Gly Ala Ile	
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Thr Phe Cys Ala Leu Leu Tyr Cys Asn Thr Ala Phe Ser Ala Glu Leu	
20 25 30	
gtt gaa tat gac cat acc ttc ctg atg ggg cag aat gca tct aat att	144
Val Glu Tyr Asp His Thr Phe Leu Met Gly Gln Asn Ala Ser Asn Ile	
35 40 45	

gat ctc agc cgg tac agt gaa ggt aac ccc gct ata ccg ggt gtt tac Asp Leu Ser Arg Tyr Ser Glu Gly Asn Pro Ala Ile Pro Gly Val Tyr 50 55 60	192
gac gtc agt gtt tat gta aac gac caa cca atc att aac caa agt att Asp Val Ser Val Tyr Val Asn Asp Gln Pro Ile Ile Asn Gln Ser Ile 65 70 75 80	240
aca ttt gtc gca att gaa gga aaa aag aac gcc cag gct tgt atc aca Thr Phe Val Ala Ile Glu Gly Lys Lys Asn Ala Gln Ala Cys Ile Thr 85 90 95	288
tta aag aat tta ttg cag ttt cat att aat tct ccc gat ata aat aac Leu Lys Asn Leu Leu Gln Phe His Ile Asn Ser Pro Asp Ile Asn Asn 100 105 110	336
gaa aaa gcc gtt ctg ctt gcc agg gat gaa acg ctc ggc aat tgc ctc Glu Lys Ala Val Leu Leu Ala Arg Asp Glu Thr Leu Gly Asn Cys Leu 115 120 125	384
aat ttg acg gaa att atc cct cag gct tct gtt cgt tat gac gtt aac Asn Leu Thr Glu Ile Ile Pro Gln Ala Ser Val Arg Tyr Asp Val Asn 130 135 140	432
gat caa cgt ctg gat ata gac gtt cct caa gcc tgg gta atg aaa aat Asp Gln Arg Leu Asp Ile Asp Val Pro Gln Ala Trp Val Met Lys Asn 145 150 155 160	480
tac caa aac tat gtt gat cca tcg tta tgg gaa aac ggc att aat gcg Tyr Gln Asn Tyr Val Asp Pro Ser Leu Trp Glu Asn Gly Ile Asn Ala 165 170 175	528
gcc atg ttg tca tac aac ctc aac gga tat cat agt gaa acc cct ggt Ala Met Leu Ser Tyr Asn Leu Asn Gly Tyr His Ser Glu Thr Pro Gly 180 185 190	576
cga aaa aat gaa agc att tat gct gca ttt aac ggt ggg atg aat tta Arg Lys Asn Glu Ser Ile Tyr Ala Ala Phe Asn Gly Gly Met Asn Leu 195 200 205	624
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ctg agt ccg tca ggg tac ggc agc gat ctt att gtt acc atc gaa gaa Leu Ser Pro Ser Gly Tyr Gly Ser Asp Leu Ile Val Thr Ile Glu Glu 325 330 335	1008
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tac tac tac ggc ctg aat aac tat ctg acg ggt tat acc ggt att cag Tyr Tyr Tyr Gly Leu Asn Asn Tyr Leu Thr Gly Tyr Thr Gly Ile Gln 385 390 395 400	1200
ata acc gat aat aac tat acc gct ggt ttg tta ggt ctt ggt ctg aat Ile Thr Asp Asn Asn Tyr Thr Ala Gly Leu Leu Gly Leu Gly Leu Asn 405 410 415	1248
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cgc tat tcg aca cag aat tac ctt ggt ctt aat gat gca cta act cta Arg Tyr Ser Thr Gln Asn Tyr Leu Gly Leu Asn Asp Ala Leu Thr Leu 465 470 475 480	1440
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cag cgt tca tgg aat gaa gac ggc gac act gac gat agc gtt tat ctt Gln Arg Ser Trp Asn Glu Asp Gly Asp Thr Asp Asp Ser Val Tyr Leu 565 570 575	1728
agc ttc acc att cca att gaa aaa tta ctt ggc act gaa caa cgt act Ser Phe Thr Ile Pro Ile Glu Lys Leu Leu Gly Thr Glu Gln Arg Thr 580 585 590	1776
tca ggt ttc cag agt att gat act caa ata agc agt gac ttt aag ggt Ser Gly Phe Gln Ser Ile Asp Thr Gln Ile Ser Ser Asp Phe Lys Gly 595 600 605	1824
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ttc agt aat gat agt ttt agc gac tcc gat aca ctg gcg gta gtt cag Phe Ser Asn Asp Ser Phe Ser Asp Ser Asp Thr Leu Ala Val Val Gln 690 695 700	2112
gct cca ggt gct caa gga gcg cga ata aat tat ggc aac agt act atc Ala Pro Gly Ala Gln Gly Ala Arg Ile Asn Tyr Gly Asn Ser Thr Ile 705 710 715 720	2160
gat cga tgg ggt tat ggt gtc acc agc gct ctt tct cct tat cat gaa Asp Arg Trp Gly Tyr Gly Val Thr Ser Ala Leu Ser Pro Tyr His Glu 725 730 735	2208
aac cgt atc gcg ctg gat atc aac gat ctt gag aac gat gtt gaa tta Asn Arg Ile Ala Leu Asp Ile Asn Asp Leu Glu Asn Asp Val Glu Leu 740 745 750	2256
aaa agt acc agt gca gta gct gta ccg cgt cag ggt tca gtc gtc ttt Lys Ser Thr Ser Ala Val Ala Val Pro Arg Gln Gly Ser Val Val Phe 755 760 765	2304

gct gat ttt gaa acc gtg caa ggg caa tca gcc att atg aac atc aca Ala Asp Phe Glu Thr Val Gln Gly Gln Ser Ala Ile Met Asn Ile Thr 770 775 780	2352
cga agt gat ggt aaa aat att cca ttt gct gca gat att tat gat gag Arg Ser Asp Gly Lys Asn Ile Pro Phe Ala Ala Asp Ile Tyr Asp Glu 785 790 795 800	2400
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cgt ggt att gag cag cag gga aat atc agc att aaa tgg ctc gaa caa Arg Gly Ile Glu Gln Gln Gly Asn Ile Ser Ile Lys Trp Leu Glu Gln 820 825 830	2496
agt aaa ccc gta agt tgt ctt gcg cat tat caa caa agc cca gaa gca Ser Lys Pro Val Ser Cys Leu Ala His Tyr Gln Gln Ser Pro Glu Ala 835 840 845	2544
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tct acc acc gaa acc aca gaa cct gat cgt aca ttg cag tta tct gcc Ser Thr Thr Glu Thr Thr Glu Pro Asp Arg Thr Leu Gln Leu Ser Ala 35 40 45	144
gaa cag gct gct cgc atc agg gaa atg acg gtc atc acc tcc agc ctg Glu Gln Ala Ala Arg Ile Arg Glu Met Thr Val Ile Thr Ser Ser Leu 50 55 60	192
atg atg agt ctg acc gtc gat gaa agc gat ctt tct gtg cat ctg gta Met Met Ser Leu Thr Val Asp Glu Ser Asp Leu Ser Val His Leu Val 65 70 75 80	240
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Gly Arg Lys Ile Asn Lys Arg Glu Trp Ala Gly Asn Ala Ser Ala Trp	
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cat gac aca ccg gcg gtt gct cgt gat tta tca cac ggg ctt tcc ttt	336
His Asp Thr Pro Ala Val Ala Arg Asp Leu Ser His Gly Leu Ser Phe	
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Ala Glu Gln Val Val Ser Glu Ala His Ser Ala Ile Val Ile Leu Asp	
115 120 125	
agc cgg ggg aat atc caa cgc ttc aat cgg tta tgt gaa gat tac aca	432
Ser Arg Gly Asn Ile Gln Arg Phe Asn Arg Leu Cys Glu Asp Tyr Thr	
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Gly Leu Lys Glu His Asp Val Ile Gly Gln Ser Val Phe Lys Leu Phe	
145 150 155 160	
atg agc cgt cgt gaa gct gcg gca tcc agg cgc aat aac cgt gta ttt	528
Met Ser Arg Arg Glu Ala Ala Ala Ser Arg Arg Asn Asn Arg Val Phe	
165 170 175	
ttt cga agc ggc aat gca tat gaa gtc gaa ctg tgg ata cca aca tgt	576
Phe Arg Ser Gly Asn Ala Tyr Glu Val Glu Leu Trp Ile Pro Thr Cys	
180 185 190	
aaa ggc cag cgg ctg ttt ctg ttt cgc aat aaa ttt gtc cac agc ggc	624
Lys Gly Gln Arg Leu Phe Leu Phe Arg Asn Lys Phe Val His Ser Gly	
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Ser Gly Lys Asn Glu Ile Phe Leu Ile Cys Ser Gly Thr Asp Ile Thr	
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Glu Glu Arg Arg Ala Gln Glu Arg Leu Arg Ile Leu Ala Asn Thr Asp	
225 230 235 240	
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Ser Ile Thr Gly Leu Pro Asn Arg Asn Ala Met Gln Asp Leu Ile Asp	
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cac gct att aat cat gca gat aac aat aaa gtt ggg gtt gtg tat ctt	816
His Ala Ile Asn His Ala Asp Asn Asn Lys Val Gly Val Val Tyr Leu	
260 265 270	
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Asp Leu Asp Asn Phe Lys Lys Val Asn Asp Ala Tyr Gly His Leu Phe	
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Gly Asp Gln Leu Leu Arg Asp Val Ser Leu Ala Ile Leu Ser Cys Leu	
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Glu His Asp Gln Val Leu Ala Arg Pro Gly Gly Asp Glu Phe Leu Val	
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Ile Leu Thr Arg Leu Arg Leu Pro Phe Arg Ile Gly Leu Ile Glu Val	
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Tyr Thr Ser Cys Ser Val Gly Ile Ala Leu Ser Pro Glu His Gly Ser	
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Asp Ser Thr Ala Ile Ile Arg His Ala Asp Thr Ala Met Tyr Thr Ala	
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Ser Gly Leu Ile Val Pro Leu Gly Arg Trp Val Ile Leu Asp Val Val	
465 470 475 480	
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485 490 495	
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Val Asn Ile Ser Ala Arg Gln Leu Ala Asp Gln Thr Ile Phe Thr Ala	
500 505 510	
ctg aaa cag gtt ctc cag gaa ctc aat ttt gaa tac tgc cct ata gat	1584
Leu Lys Gln Val Leu Gln Glu Leu Asn Phe Glu Tyr Cys Pro Ile Asp	
515 520 525	
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Val Glu Leu Thr Glu Ser Cys Leu Ile Glu Asn Asp Glu Leu Ala Leu	
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Ser Val Ile Gln Gln Phe Ser Gln Leu Gly Ala Gln Val His Leu Asp	
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Asp Phe Gly Thr Gly Tyr Ser Ser Leu Ser Gln Leu Ala Arg Phe Pro
 565 570 575
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 Ile Asp Ala Ile Lys Leu Asp Gln Val Phe Val Arg Asp Ile His Lys
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 Gln Pro Val Ser Gln Ser Leu Val Arg Ala Ile Val Ala Val Ala Gln
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 610 615 620
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 Ile Ser Ala Ser Ala His Ala Ala Gly Gly Ile Ala Leu Gly Ala Thr
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 Asn Ser His Thr Asn Glu Arg Phe Leu Val Asn Ser Trp Ile Glu Asn
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Thr Ile Pro Ser Val Asp Lys Asn Ala Leu Asn Gly Arg Asn Val Leu			
115	120	125	
caa ctg gcg att tta tcg cgc atg aaa tta ttt ctc cgt cca att caa			432
Gln Leu Ala Ile Leu Ser Arg Met Lys Leu Phe Leu Arg Pro Ile Gln			
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Ala Pro Arg Val Asn Ser Gln Ile Pro Leu Pro Ser Gly Val Gln Gly			
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35	40	45	

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tcg cag gat atc gta ttt gaa tcg aca aca gaa aat aca ggt gat aaa Ser Gln Asp Ile Val Phe Glu Ser Thr Thr Glu Asn Thr Gly Asp Lys 85 90 95	288
tca ggt ggg tta atg ccc tgt ttt aac cag gta ctt ctt gaa cga att Ser Gly Gly Leu Met Pro Cys Phe Asn Gln Val Leu Leu Glu Arg Ile 100 105 110	336
ggc ctt aat agc agt gca ttt ccc gag tta gcc cag cag caa aac aat Gly Leu Asn Ser Ser Ala Phe Pro Glu Leu Ala Gln Gln Gln Asn Asn 115 120 125	384
aaa tgc atc aat tta ctg aaa gct gta cct gat gcc aca att aac ttt Lys Cys Ile Asn Leu Leu Lys Ala Val Pro Asp Ala Thr Ile Asn Phe 130 135 140	432
gat ttt gca gcg atg cgc ctg aac atc act att cct cag ata gcg ttg Asp Phe Ala Ala Met Arg Leu Asn Ile Thr Ile Pro Gln Ile Ala Leu 145 150 155 160	480
ttg agt agc gct cac ggt tac att ccg cct gaa gag tgg gat gaa ggt Leu Ser Ser Ala His Gly Tyr Ile Pro Pro Glu Glu Trp Asp Glu Gly 165 170 175	528
att cct gct tta ctc ctg aat tat aat ttc acc ggt aac aga ggt aat Ile Pro Ala Leu Leu Leu Asn Tyr Asn Phe Thr Gly Asn Arg Gly Asn 180 185 190	576
ggc aac gat agc tat ttt ttt agt gag ctc agc ggg att aat att ggc Gly Asn Asp Ser Tyr Phe Phe Ser Glu Leu Ser Gly Ile Asn Ile Gly 195 200 205	624
ccg tgg cgt tta cgc aac aat ggt tcc tgg aac tat ttt cgc gga aat Pro Trp Arg Leu Arg Asn Asn Gly Ser Trp Asn Tyr Phe Arg Gly Asn 210 215 220	672
gga tat cat tca gaa cag tgg aat aat att ggc acc tgg gta cag cgc Gly Tyr His Ser Glu Gln Trp Asn Asn Ile Gly Thr Trp Val Gln Arg 225 230 235 240	720
gcc att att ccg ctg aaa agt gaa ctg gta atg gga gac ggc aat aca Ala Ile Ile Pro Leu Lys Ser Glu Leu Val Met Gly Asp Gly Asn Thr 245 250 255	768
gga agt gat att ttc gat ggc gtt gga ttt cgt ggt gta cgg ctt tat Gly Ser Asp Ile Phe Asp Gly Val Gly Phe Arg Gly Val Arg Leu Tyr 260 265 270	816
tct tct gat aat atg tat cct gat agc cag caa ggg ttt gcc cca acg Ser Ser Asp Asn Met Tyr Pro Asp Ser Gln Gln Gly Phe Ala Pro Thr 275 280 285	864

gta cgt ggg att gcc cgt acg gcg gcc cag cta acg att cgg caa aat Val Arg Gly Ile Ala Arg Thr Ala Ala Gln Leu Thr Ile Arg Gln Asn 290 295 300	912
ggc ttt att atc tat caa agc tat gtt tcc ccc ggc gct ttt gaa att Gly Phe Ile Ile Tyr Gln Ser Tyr Val Ser Pro Gly Ala Phe Glu Ile 305 310 315 320	960
aca gat ttg cac ccg aca tct tca aat ggc gat ctg gac gtc acc atc Thr Asp Leu His Pro Thr Ser Ser Asn Gly Asp Leu Asp Val Thr Ile 325 330 335	1008
gac gag cgc gat ggc aat cag cag aat tac aca att ccg tat tca aca Asp Glu Arg Asp Gly Asn Gln Gln Asn Tyr Thr Ile Pro Tyr Ser Thr 340 345 350	1056
gtg cca att tta caa cgc gaa ggg cgt ttc aaa ttt gac ctg acg gcg Val Pro Ile Leu Gln Arg Glu Gly Arg Phe Lys Phe Asp Leu Thr Ala 355 360 365	1104
ggc gat ttt cgt agc ggt aat agt cag caa tca tcg cct ttc ttt ttt Gly Asp Phe Arg Ser Gly Asn Ser Gln Gln Ser Ser Pro Phe Phe Phe 370 375 380	1152
cag ggt acg gca ctc ggc ggt tta cca cag gaa ttt act gcc tac ggc Gln Gly Thr Ala Leu Gly Gly Leu Pro Gln Glu Phe Thr Ala Tyr Gly 385 390 395 400	1200
ggg acg caa tta tct gcc aat tac acc gcc ttt tta tta ggg ctg ggg Gly Thr Gln Leu Ser Ala Asn Tyr Thr Ala Phe Leu Leu Gly Leu Gly 405 410 415	1248
cgc aat ctc ggg aac tgg ggc gca gtg tcg ctg gat gta acg cat gcg Arg Asn Leu Gly Asn Trp Gly Ala Val Ser Leu Asp Val Thr His Ala 420 425 430	1296
cgc agt cag tta gcc gac gcc agt cgt cat gag ggg gat tct att cgc Arg Ser Gln Leu Ala Asp Ala Ser Arg His Glu Gly Asp Ser Ile Arg 435 440 445	1344
ttc ctc tat gcg aaa tcg atg aac acc ttc ggc acc aat ttt cag tta Phe Leu Tyr Ala Lys Ser Met Asn Thr Phe Gly Thr Asn Phe Gln Leu 450 455 460	1392
atg ggt tac cgc tat tcg aca caa ggt ttt tat acc ctt gat gat gtt Met Gly Tyr Arg Tyr Ser Thr Gln Gly Phe Tyr Thr Leu Asp Asp Val 465 470 475 480	1440
gcg tat cgt cga atg gag ggg tac gaa tat gat tac gac ggt gag cat Ala Tyr Arg Arg Met Glu Gly Tyr Glu Tyr Asp Tyr Asp Gly Glu His 485 490 495	1488
cgc gat gaa ccg ata atc gtg aat tac cac aat tta cgc ttt agc cgt Arg Asp Glu Pro Ile Ile Val Asn Tyr His Asn Leu Arg Phe Ser Arg 500 505 510	1536
aaa gac cgt ttg cag tta aat gtt tca caa tca ctt aat gac ttt ggc Lys Asp Arg Leu Gln Leu Asn Val Ser Gln Ser Leu Asn Asp Phe Gly 515 520 525	1584

tcg ctt tat att tct ggt acc cat caa aaa tac tgg aat act tcg gat	1632
Ser Leu Tyr Ile Ser Gly Thr His Gln Lys Tyr Trp Asn Thr Ser Asp	
530 535 540	
tca gat acg tgg tat cag gtg ggg tat acc agc agc tgg gtt ggc atc	1680
Ser Asp Thr Trp Tyr Gln Val Gly Tyr Thr Ser Ser Trp Val Gly Ile	
545 550 555 560	
agt tat tcg ctc tca ttt tcg tgg aat gaa tct gta ggg atc ccc gat	1728
Ser Tyr Ser Leu Ser Phe Ser Trp Asn Glu Ser Val Gly Ile Pro Asp	
565 570 575	
aac gaa cgt att gtc gga ctt aat gtt tca gtg cct ttc aat gtt ttg	1776
Asn Glu Arg Ile Val Gly Leu Asn Val Ser Val Pro Phe Asn Val Leu	
580 585 590	
acc aaa cgt cgc tac acc cgg gaa aat gcg ctc gac cgc gct tat gcc	1824
Thr Lys Arg Arg Tyr Thr Arg Glu Asn Ala Leu Asp Arg Ala Tyr Ala	
595 600 605	
tcc ttt aac gcc aac cgt aac agc aac ggg caa aat agc tgg ctg gca	1872
Ser Phe Asn Ala Asn Arg Asn Ser Asn Gly Gln Asn Ser Trp Leu Ala	
610 615 620	
ggt gta ggt ggg acc tta ctg gaa ggc cac aac ctg agt tat cac gta	1920
Gly Val Gly Gly Thr Leu Leu Glu Gly His Asn Leu Ser Tyr His Val	
625 630 635 640	
agc cag ggt gat acc tcg aat aat ggg tac acg ggc agc gcc acg gca	1968
Ser Gln Gly Asp Thr Ser Asn Asn Gly Tyr Thr Gly Ser Ala Thr Ala	
645 650 655	
aac tgg cag gcc gct tac ggt acg ctg ggg ggc ggg tat aac tac gac	2016
Asn Trp Gln Ala Ala Tyr Gly Thr Leu Gly Gly Gly Tyr Asn Tyr Asp	
660 665 670	
cgc gat caa cat gac gtt aac tgg cag ctg tct ggc ggt gtg gtc ggg	2064
Arg Asp Gln His Asp Val Asn Trp Gln Leu Ser Gly Gly Val Val Gly	
675 680 685	
cat gaa aat ggc ata acg ctg agc cag cct tta ggg gat acc aat gtt	2112
His Glu Asn Gly Ile Thr Leu Ser Gln Pro Leu Gly Asp Thr Asn Val	
690 695 700	
ttg att aaa gcg cct ggc gca ggc ggt gta cgc att gaa aat caa act	2160
Leu Ile Lys Ala Pro Gly Ala Gly Gly Val Arg Ile Glu Asn Gln Thr	
705 710 715 720	
ggc att tta acc gac tgg cgc ggc tat gcg gtg atg ctg tat gcc acg	2208
Gly Ile Leu Thr Asp Trp Arg Gly Tyr Ala Val Met Leu Tyr Ala Thr	
725 730 735	
gtt tat cgg tat aac cgt atc gcg ctt gat acc aat acg atg ggg aat	2256
Val Tyr Arg Tyr Asn Arg Ile Ala Leu Asp Thr Asn Thr Met Gly Asn	
740 745 750	
tcc atc gat gtt gaa aaa aat att agc agc gtt gtg ccg acg caa ggc	2304
Ser Ile Asp Val Glu Lys Asn Ile Ser Ser Val Val Pro Thr Gln Gly	
755 760 765	

gcg ttg gtt cgt gcc aat ttt gat acc cgc ata ggc gtg cgg gcg ctc Ala Leu Val Arg Ala Asn Phe Asp Thr Arg Ile Gly Val Arg Ala Leu 770 775 780	2352
att acc gtt acc cag ggc gga aaa ccg gtg ccg ttt gga tca ctg gta Ile Thr Val Thr Gln Gly Gly Lys Pro Val Pro Phe Gly Ser Leu Val 785 790 795 800	2400
cgg gaa aac agt acc gga ata acc agt atg gtg ggt gat gac ggg caa Arg Glu Asn Ser Thr Gly Ile Thr Ser Met Val Gly Asp Asp Gly Gln 805 810 815	2448
gtt tat tta agt ggt gcg cca ttg tct ggt gaa tta ctg gtt cag tgg Val Tyr Leu Ser Gly Ala Pro Leu Ser Gly Glu Leu Val Gln Trp 820 825 830	2496
gga gac ggc gcg aac tca cgc tgc att gcg cac tat gta ttg ccg aag Gly Asp Gly Ala Asn Ser Arg Cys Ile Ala His Tyr Val Leu Pro Lys 835 840 845	2544
caa agc tta cag caa gcc gtc act gtt att tcg gca gtt tgc aca cat Gln Ser Leu Gln Gln Ala Val Thr Val Ile Ser Ala Val Cys Thr His 850 855 860	2592
cct ggc tca taa Pro Gly Ser *	2604
865	
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<220>	
<221> CDS	
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aat agt act ggc gta gca gaa gat gaa cac tat gat ctc tca aat atc Asn Ser Thr Gly Val Ala Glu Asp Glu His Tyr Asp Leu Ser Asn Ile 20 25 30	96
ttt aat agc acc aat aac cag cca ggg cag att gtt gtt tta ccg gaa Phe Asn Ser Thr Asn Asn Gln Pro Gly Gln Ile Val Val Leu Pro Glu 35 40 45	144
aaa tcc ggc tgg gta ggt gtc tca gca att tgt cca ccc ggt acg ctg Lys Ser Gly Trp Val Gly Val Ser Ala Ile Cys Pro Pro Gly Thr Leu 50 55 60	192
gtg aat tat aca tac cgt agt tat gtc acc aac ttt att gtt cag gaa Val Asn Tyr Thr Tyr Arg Ser Tyr Val Thr Asn Phe Ile Val Gln Glu 65 70 75 80	240

act atc gat aat tat aaa tat atg caa tta cat gat tat cta tta ggt Thr Ile Asp Asn Tyr Lys Tyr Met Gln Leu His Asp Tyr Leu Leu Gly 85 90 95	288
gcg atg agt ctg gtt gat agt gtg atg gat att cag ttc ccc ccg caa Ala Met Ser Leu Val Asp Ser Val Met Asp Ile Gln Phe Pro Pro Gln 100 105 110	336
aat tat att cgg atg gga aca gat cct aac gtt tcg caa aac ctt cca Asn Tyr Ile Arg Met Gly Thr Asp Pro Asn Val Ser Gln Asn Leu Pro 115 120 125	384
ttc ggg gtg atg gat tct cgt tta ata ttt cgt tta aag gtt att cgt Phe Gly Val Met Asp Ser Arg Leu Ile Phe Arg Leu Lys Val Ile Arg 130 135 140	432
ccc ttt att aac atg gtg gag atc ccc aga cag gtg atg ttt acc gtg Pro Phe Ile Asn Met Val Glu Ile Pro Arg Gln Val Met Phe Thr Val 145 150 155 160	480
tat gtg aca tca acg cct tac gat ccg ttg gtt aca cct gtt tat acc Tyr Val Thr Ser Thr Pro Tyr Asp Pro Leu Val Thr Pro Val Tyr Thr 165 170 175	528
att agt ttt ggt ggc cgg gtt gaa gta ccg caa aac tgc gaa tta aat Ile Ser Phe Gly Gly Arg Val Glu Val Pro Gln Asn Cys Glu Leu Asn 180 185 190	576
gcc ggg cag att gtt gaa ttt gat ttt ggt gat atc ggc gca tcg tta Ala Gly Gln Ile Val Glu Phe Asp Phe Gly Asp Ile Gly Ala Ser Leu 195 200 205	624
ttt agt gcg gca ggg ccg ggt aat cga cct gct ggt gtc atg ccg caa Phe Ser Ala Ala Gly Pro Gly Asn Arg Pro Ala Gly Val Met Pro Gln 210 215 220	672
acc aag agc att gcg gtc aaa tgt acg aat gtt gct gcg cag gct tat Thr Lys Ser Ile Ala Val Lys Cys Thr Asn Val Ala Ala Gln Ala Tyr 225 230 235 240	720
tta aca atg cgt ctg gaa gcc agt gcc gtt tct ggt cag gcg atg gtg Leu Thr Met Arg Leu Glu Ala Ser Ala Val Ser Gly Gln Ala Met Val 245 250 255	768
tcg gac aat cag gat tta ggt ttt att gtc gcc gat cag aac gat acg Ser Asp Asn Gln Asp Leu Gly Phe Ile Val Ala Asp Gln Asn Asp Thr 260 265 270	816
ccg atc acg cct aac gat ctc aat agc gtt att cct ttc cgt ctg gat Pro Ile Thr Pro Asn Asp Leu Asn Ser Val Ile Pro Phe Arg Leu Asp 275 280 285	864
gca gct gcg gca gcc aat gtc aca ctt cgc gcc tgg cct atc agt att Ala Ala Ala Ala Asn Val Thr Leu Arg Ala Trp Pro Ile Ser Ile 290 295 300	912
acc ggt caa aaa ccg acc gaa ggg ccg ttt agc gcg ctg ggg tat tta Thr Gly Gln Lys Pro Thr Glu Gly Pro Phe Ser Ala Leu Gly Tyr Leu 305 310 315 320	960

cgc gtc gat tat caa tga
 Arg Val Asp Tyr Gln *
 325

978

<210> 189
 <211> 516
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(516)

<400> 188
 atg aga aga gta ctc ttt agc tgt ttc tgc ggg cta ctg tgg agt tcc 48
 Met Arg Arg Val Leu Phe Ser Cys Phe Cys Gly Leu Leu Trp Ser Ser
 1 5 10 15

agt gga tgg gca gtt gac cct tta gga acg att aat atc aat ttg cac 96
 Ser Gly Trp Ala Val Asp Pro Leu Gly Thr Ile Asn Ile Asn Leu His
 20 25 30

ggt aac gtt gtt gat ttc tcc tgt acc gta aac aca gcg gat att gat 144
 Gly Asn Val Val Asp Phe Ser Cys Thr Val Asn Thr Ala Asp Ile Asp
 35 40 45

aag acg gta gat tta ggc aga tgg cct acg aca caa cta ctg aac gct 192
 Lys Thr Val Asp Leu Gly Arg Trp Pro Thr Thr Gln Leu Leu Asn Ala
 50 55 60

ggc gat acc acg gca ctc gtc cct ttt agc ctg cgg ctg gag gga tgt 240
 Gly Asp Thr Thr Ala Leu Val Pro Phe Ser Leu Arg Leu Glu Gly Cys
 65 70 75 80

cct ccg ggt tca gtt gcg att tta ttt acg gga acg ccg gca tcc gat 288
 Pro Pro Gly Ser Val Ala Ile Leu Phe Thr Gly Thr Pro Ala Ser Asp
 85 90 95

acc aac ctg ctg gct ctg gat gat ccc gca atg gca caa acc gtc gcc 336
 Thr Asn Leu Leu Ala Leu Asp Asp Pro Ala Met Ala Gln Thr Val Ala
 100 105 110

atc gaa tta cgt aat agc gat cgc tcc cgg ctc gca ctg ggg gag gcg 384
 Ile Glu Leu Arg Asn Ser Asp Arg Ser Arg Leu Ala Leu Gly Glu Ala
 115 120 125

agc ccg act gag gaa gta gat gca aat ggc aat gtc aca cta aac ttt 432
 Ser Pro Thr Glu Glu Val Asp Ala Asn Gly Asn Val Thr Leu Asn Phe
 130 135 140

ttt gcc aat tat cga gcg tta gcc agc ggt gtt cgg cca ggt gtg gcg 480
 Phe Ala Asn Tyr Arg Ala Leu Ala Ser Gly Val Arg Pro Gly Val Ala
 145 150 155 160

aaa gcg gat gcg ata ttt atg atc aat tat aat taa 516
 Lys Ala Asp Ala Ile Phe Met Ile Asn Tyr Asn *
 165 170

<210> 189
 <211> 585
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(585)

<400> 189
 atg ttt ggc tat cgc agt aac gtg cca aaa gtg cgc tta acc aca gac 48
 Met Phe Gly Tyr Arg Ser Asn Val Pro Lys Val Arg Leu Thr Thr Asp
 1 5 10 15

cga ctg gtc gtg cgt ctg gtg cat gat cgt gat gcc tgg cgt ctt gcg 96
 Arg Leu Val Val Arg Leu Val His Asp Arg Asp Ala Trp Arg Leu Ala
 20 25 30

gat tat tac gca gag aat cgc cat ttc ctc aag ccc tgg gag cca gtg 144
 Asp Tyr Tyr Ala Glu Asn Arg His Phe Leu Lys Pro Trp Glu Pro Val
 35 40 45

cgc gac gaa agc cac tgt tat cca tca ggc tgg cag gcc agg ctg ggg 192
 Arg Asp Glu Ser His Cys Tyr Pro Ser Gly Trp Gln Ala Arg Leu Gly
 50 55 60

atg att aac gaa ttt cat aaa caa ggt tca gct ttc tac ttt ggc tta 240
 Met Ile Asn Glu Phe His Lys Gln Gly Ser Ala Phe Tyr Phe Gly Leu
 65 70 75 80

ttc gac ccg gac gaa aaa gag att att ggc gtt gcc aat ttt tcc aat 288
 Phe Asp Pro Asp Glu Lys Glu Ile Ile Gly Val Ala Asn Phe Ser Asn
 85 90 95

gtt gtt cgt ggc tct ttt cat gcc tgc tat ctc ggt tat tcg att ggg 336
 Val Val Arg Gly Ser Phe His Ala Cys Tyr Leu Gly Tyr Ser Ile Gly
 100 105 110

caa aaa tgg cag ggc aaa gga ctc atg ttt gaa gcc ctg acc gca gcc 384
 Gln Lys Trp Gln Gly Lys Gly Leu Met Phe Glu Ala Leu Thr Ala Ala
 115 120 125

att cgt tat atg cag cgc acc caa cat att cat cgc att atg gct aat 432
 Ile Arg Tyr Met Gln Arg Thr Gln His Ile His Arg Ile Met Ala Asn
 130 135 140

tat atg ccg cac aat aaa cgc agc ggt gat tta ctg gcg cga ctg ggt 480
 Tyr Met Pro His Asn Lys Arg Ser Gly Asp Leu Leu Ala Arg Leu Gly
 145 150 155 160

ttt gaa aaa gaa ggc tat gcg aaa gac tat ctg ttg att gat gga caa 528
 Phe Glu Lys Glu Gly Tyr Ala Lys Asp Tyr Leu Leu Ile Asp Gly Gln
 165 170 175

tgg cgc gat cac gta ctg acg gca tta act acc cca gac tgg acg ccc 576
 Trp Arg Asp His Val Leu Thr Ala Leu Thr Thr Pro Asp Trp Thr Pro
 180 185 190

ggc cgc taa 585
 Gly Arg *

<210> 190
 <211> 648
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(648)

<400> 190
 atg aaa tat caa ctt act gcc ctt gaa gct cgc gtg att ggt tgc ttg 48
 Met Lys Tyr Gln Leu Thr Ala Leu Glu Ala Arg Val Ile Gly Cys Leu
 1 5 10 15
 ctg gaa aag cag gtg acc acg ccg gag caa tac ccg ctc tca gtc aat 96
 Leu Glu Lys Gln Val Thr Thr Pro Glu Gln Tyr Pro Leu Ser Val Asn
 20 25 30
 ggt gta gtc acg gcc tgt aat cag aaa acg aac cgt gaa ccg gtc atg 144
 Gly Val Val Thr Ala Cys Asn Gln Lys Thr Asn Arg Glu Pro Val Met
 35 40 45
 aat ctg agt gaa tcc gaa gtg cag gaa cag ctg gat aat ctg gtc aaa 192
 Asn Leu Ser Glu Ser Glu Val Gln Glu Gln Leu Asp Asn Leu Val Lys
 50 55 60
 cgt cat tat cta cgc aca gtg agc ggt ttt ggt aat cgg gtc acc aaa 240
 Arg His Tyr Leu Arg Thr Val Ser Gly Phe Gly Asn Arg Val Thr Lys
 65 70 75 80
 tat gag caa cgt ttt tgt aat tca gaa ttt ggc gat ctg aaa ctg agc 288
 Tyr Glu Gln Arg Phe Cys Asn Ser Glu Phe Gly Asp Leu Lys Leu Ser
 85 90 95
 gca gcg gaa gtg gcg tta atc acc acg ttg tta ttg cgt ggt gcc cag 336
 Ala Ala Glu Val Ala Leu Ile Thr Thr Leu Leu Leu Arg Gly Ala Gln
 100 105 110
 acg cca ggt gaa ctg cgc agc cgc gcc gcg cga atg tat gaa ttc agc 384
 Thr Pro Gly Glu Leu Arg Ser Arg Ala Ala Arg Met Tyr Glu Phe Ser
 115 120 125
 gat atg gcg gaa gtg gag tcg acg ctg gaa caa ctg gca aat cgc gaa 432
 Asp Met Ala Glu Val Glu Ser Thr Leu Glu Gln Leu Ala Asn Arg Glu
 130 135 140
 gat ggt cct ttt gtg gtg cgt ctg gcc cgc gaa ccg ggt aaa cgc gaa 480
 Asp Gly Pro Phe Val Val Arg Leu Ala Arg Glu Pro Gly Lys Arg Glu
 145 150 155 160
 aac cgc tac atg cat ctt ttc agt ggt gag gtt gaa gat cag ccg gcg 528
 Asn Arg Tyr Met His Leu Phe Ser Gly Glu Val Glu Asp Gln Pro Ala
 165 170 175
 gtg acg gat atg tcg aac gcg gtt gac ggt gat tta cag gcc cgc gtc 576
 Val Thr Asp Met Ser Asn Ala Val Asp Gly Asp Leu Gln Ala Arg Val
 180 185 190

gaa gcc ctg gaa atc gaa gtg gca gaa ctg aaa cag cgt ctt gat tcg 624
 Glu Ala Leu Glu Ile Glu Val Ala Glu Leu Lys Gln Arg Leu Asp Ser
 195 200 205

ttg ctg gcc cat ctg gga gat taa 648
 Leu Leu Ala His Leu Gly Asp *
 210 215

<210> 191
 <211> 924
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(924)

<400> 191

gtg aaa aaa tta cgt atc ggc gta gtg gga tta ggt ggc att gcg caa 48
 Val Lys Lys Leu Arg Ile Gly Val Val Gly Leu Gly Gly Ile Ala Gln
 1 5 10 15

aaa gcg tgg tta ccg gtg ctg gcg gca gcg tct gac tgg acg tta caa 96
 Lys Ala Trp Leu Pro Val Leu Ala Ala Ser Asp Trp Thr Leu Gln
 20 25 30

gga gcc tgg tcg cct acg cgc gcg aaa gcc ctg cca att tgt gaa agc 144
 Gly Ala Trp Ser Pro Thr Arg Ala Lys Ala Leu Pro Ile Cys Glu Ser
 35 40 45

tgg cgc att cct tat gcc gat tcg tta tcc agc ctt gcc gcc agt tgc 192
 Trp Arg Ile Pro Tyr Ala Asp Ser Leu Ser Ser Leu Ala Ala Ser Cys
 50 55 60

gat gcg gtt ttt gtg cat tcc agc acc gcc agc cac ttt gac gtg gtc 240
 Asp Ala Val Phe Val His Ser Ser Thr Ala Ser His Phe Asp Val Val
 65 70 75 80

agt acg tta ctc aat gcg ggg gta cat gtc tgt gtc gat aaa ccg ctg 288
 Ser Thr Leu Leu Asn Ala Gly Val His Val Cys Val Asp Lys Pro Leu
 85 90 95

gca gaa aat ctg cgc gat gct gaa cgg ctg gtg gaa ctg gcg gcg cgg 336
 Ala Glu Asn Leu Arg Asp Ala Glu Arg Leu Val Glu Leu Ala Ala Arg
 100 105 110

aaa aaa ctg acg ttg atg gtc ggt ttt aac cgt cgt ttc gca cca ctc 384
 Lys Lys Leu Thr Leu Met Val Gly Phe Asn Arg Arg Phe Ala Pro Leu
 115 120 125

tac ggt gag tta aaa acg caa ctc gcc acc gca gcc tcg cta aga atg 432
 Tyr Gly Glu Leu Lys Thr Gln Leu Ala Thr Ala Ala Ser Leu Arg Met
 130 135 140

gat aaa cat cgt agc aat agc gtc ggg cca cac gat ctt tat ttc acg 480
 Asp Lys His Arg Ser Asn Ser Val Gly Pro His Asp Leu Tyr Phe Thr
 145 150 155 160

ttg ctg gat gat tat ctg cat gtg gtg gat acc gcg ctg tgg ttg tcg 528
 Leu Leu Asp Asp Tyr Leu His Val Val Asp Thr Ala Leu Trp Leu Ser
 165 170 175

 ggc ggc aaa gcc tct ctg gat ggc ggt acg cta ctg act aac gac gct 576
 Gly Gly Lys Ala Ser Leu Asp Gly Gly Thr Leu Leu Thr Asn Asp Ala
 180 185 190

 ggc gaa atg ctg ttt gcc gag cac cat ttt tcg gct ggt cct ttg cag 624
 Gly Glu Met Leu Phe Ala Glu His His Phe Ser Ala Gly Pro Leu Gln
 195 200 205

 atc acc acc tgt atg cat cgc cgt gcc gga agt cag cgt gaa acc gtg 672
 Ile Thr Thr Cys Met His Arg Arg Ala Gly Ser Gln Arg Glu Thr Val
 210 215 220

 cag gcc gtg act gac ggt gcg ctc atc gac att acg gat atg cgc gaa 720
 Gln Ala Val Thr Asp Gly Ala Leu Ile Asp Ile Thr Asp Met Arg Glu
 225 230 235 240

 tgg cgt gag gag cgc ggg cag ggc gta gtg cat aaa ccg att cct ggt 768
 Trp Arg Glu Glu Arg Gly Gln Gly Val Val His Lys Pro Ile Pro Gly
 245 250 255

 tgg cag agt acg ctt gag caa cgt ggg ttt gtc ggc tgt gcg cgg cac 816
 Trp Gln Ser Thr Leu Glu Gln Arg Gly Phe Val Gly Cys Ala Arg His
 260 265 270

 ttc att gaa tgt gtg caa aac cag aca gtt ccg caa acc gcc ggc gaa 864
 Phe Ile Glu Cys Val Gln Asn Gln Thr Val Pro Gln Thr Ala Gly Glu
 275 280 285

 cag gcc gtg ctg gcg caa cgt atc gtt gac aag atc tgg cgc gat gcg 912
 Gln Ala Val Leu Ala Gln Arg Ile Val Asp Lys Ile Trp Arg Asp Ala
 290 295 300

 atg agt gaa taa 924
 Met Ser Glu *
 305

<210> 192

<211> 720

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(720)

<400> 192

atg tta aag cgc gtg ttc ctc agc ctg tta gtc ctg atc ggc ttg ctg 48
 Met Leu Lys Arg Val Phe Leu Ser Leu Leu Val Leu Ile Gly Leu Leu
 1 5 10 15

ctg ttg act gtg ctc ggc ctc gat cgc tgg atg agc tgg aaa acc gcg 96
 Leu Leu Thr Val Leu Gly Leu Asp Arg Trp Met Ser Trp Lys Thr Ala
 20 25 30

cct tat atc tac gac gaa ttg cag gat ctc ccc tac cgc cag gtc ggt 144

Pro	Tyr	Ile	Tyr	Asp	Glu	Leu	Gln	Asp	Leu	Pro	Tyr	Arg	Gln	Val	Gly		
	35						40					45					
gtg	gtg	ctc	gga	aca	gca	aaa	tat	tat	cgt	act	ggc	gta	att	aat	cag	192	
Val	Val	Leu	Gly	Thr	Ala	Lys	Tyr	Tyr	Arg	Thr	Gly	Val	Ile	Asn	Gln		
	50					55					60						
tat	tat	cgc	tac	cgc	att	caa	gga	gcg	att	aat	gcc	tat	aac	agc	ggc	240	
Tyr	Tyr	Arg	Tyr	Arg	Ile	Gln	Gly	Ala	Ile	Asn	Ala	Tyr	Asn	Ser	Gly		
	65				70					75					80		
aag	gta	aat	tat	cta	tta	ctg	agc	ggc	gat	aac	gca	ttg	caa	agt	tat	288	
Lys	Val	Asn	Tyr	Leu	Leu	Leu	Ser	Gly	Asp	Asn	Ala	Leu	Gln	Ser	Tyr		
			85						90					95			
aat	gag	ccg	atg	acc	atg	cgc	aaa	gat	tta	atc	gct	gct	ggc	gtc	gac	336	
Asn	Glu	Pro	Met	Thr	Met	Arg	Lys	Asp	Leu	Ile	Ala	Ala	Gly	Val	Asp		
		100						105					110				
cca	tca	gat	att	gtt	ctc	gat	tac	gca	ggc	ttt	cgt	acg	ctg	gat	tcc	384	
Pro	Ser	Asp	Ile	Val	Leu	Asp	Tyr	Ala	Gly	Phe	Arg	Thr	Leu	Asp	Ser		
		115						120				125					
atc	gtg	cgt	aca	cgc	aaa	gtt	ttc	gat	act	aat	gat	ttc	att	att	atc	432	
Ile	Val	Arg	Thr	Arg	Lys	Val	Phe	Asp	Thr	Asn	Asp	Phe	Ile	Ile	Ile		
	130					135					140						
acc	caa	cgt	ttc	cac	tgt	gag	cga	gca	tta	ttt	att	gcg	ctg	cat	atg	480	
Thr	Gln	Arg	Phe	His	Cys	Glu	Arg	Ala	Leu	Phe	Ile	Ala	Leu	His	Met		
	145				150					155					160		
ggg	att	cag	gct	cag	tgt	tat	gcc	gta	ccg	tca	ccg	aaa	gat	atg	ctg	528	
Gly	Ile	Gln	Ala	Gln	Cys	Tyr	Ala	Val	Pro	Ser	Pro	Lys	Asp	Met	Leu		
				165					170					175			
tca	gta	cgt	att	cgt	gaa	ttt	gcc	gcc	cgt	ttc	ggc	gcg	ctg	gct	gac	576	
Ser	Val	Arg	Ile	Arg	Glu	Phe	Ala	Ala	Arg	Phe	Gly	Ala	Leu	Ala	Asp		
			180					185					190				
ctt	tat	att	ttt	aaa	cgt	gaa	ccg	cgt	ttt	tta	ggg	ccg	ctg	gtc	cct	624	
Leu	Tyr	Ile	Phe	Lys	Arg	Glu	Pro	Arg	Phe	Leu	Gly	Pro	Leu	Val	Pro		
		195						200					205				
att	ccg	gct	atg	cac	cag	gta	ccg	gaa	gat	gcg	cag	ggg	tat	ccc	gcc	672	
Ile	Pro	Ala	Met	His	Gln	Val	Pro	Glu	Asp	Ala	Gln	Gly	Tyr	Pro	Ala		
		210				215					220						
gtc	aca	ccc	gaa	cag	tta	ctt	gaa	tta	caa	aag	aaa	caa	gga	aag	tag	720	
Val	Thr	Pro	Glu	Gln	Leu	Leu	Glu	Leu	Gln	Lys	Lys	Gln	Gly	Lys	*		
	225				230					235							

<210> 193

<211> 240

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(240)

<400> 193

atg	gat	gta	cag	cag	ttt	ttt	gtc	gtt	gcc	gtt	ttt	ttc	ctt	atc	ccg	48
Met	Asp	Val	Gln	Gln	Phe	Phe	Val	Val	Ala	Val	Phe	Phe	Leu	Ile	Pro	
1			5						10					15		

ata	ttt	tgt	ttc	cgc	gaa	gca	tgg	aaa	ggc	tgg	cgc	gca	ggc	gcg	att	96
Ile	Phe	Cys	Phe	Arg	Glu	Ala	Trp	Lys	Gly	Trp	Arg	Ala	Gly	Ala	Ile	
			20					25					30			

gat	aaa	cgg	gtt	aaa	aat	gca	ccg	gaa	ccg	gtg	tat	gtc	tgg	cga	gca	144
Asp	Lys	Arg	Val	Lys	Asn	Ala	Pro	Glu	Pro	Val	Tyr	Val	Trp	Arg	Ala	
		35					40					45				

aaa	aat	ccc	gga	ctc	ttt	ttc	gct	tat	atg	gtg	gca	tat	atc	ggc	ttc	192
Lys	Asn	Pro	Gly	Leu	Phe	Phe	Ala	Tyr	Met	Val	Ala	Tyr	Ile	Gly	Phe	
	50					55				60						

gga	att	tta	tct	atc	ggc	atg	att	gtt	tat	ctt	att	ttc	tat	cgt	taa	240
Gly	Ile	Leu	Ser	Ile	Gly	Met	Ile	Val	Tyr	Leu	Ile	Phe	Tyr	Arg	*	
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<210> 194

<211> 1533

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1533)

<400> 194

atg	gcg	acg	atc	gat	tct	atg	aat	aag	gac	acc	aca	cgt	ttg	agc	gat	48
Met	Ala	Thr	Ile	Asp	Ser	Met	Asn	Lys	Asp	Thr	Thr	Arg	Leu	Ser	Asp	
1				5					10					15		

gga	ccc	gac	tgg	acg	ttc	gac	ctg	ctg	gat	gtt	tat	ctg	gca	gag	ata	96
Gly	Pro	Asp	Trp	Thr	Phe	Asp	Leu	Leu	Asp	Val	Tyr	Leu	Ala	Glu	Ile	
			20					25					30			

gac	cgg	gtg	gcg	aaa	ctc	tac	cgg	ctg	gat	acc	tac	ccg	cac	cag	att	144
Asp	Arg	Val	Ala	Lys	Leu	Tyr	Arg	Leu	Asp	Thr	Tyr	Pro	His	Gln	Ile	
		35					40					45				

gaa	gtg	ata	acc	tca	gaa	cag	atg	atg	gat	gcc	tac	tcc	agc	gtc	ggc	192
Glu	Val	Ile	Thr	Ser	Glu	Gln	Met	Met	Asp	Ala	Tyr	Ser	Ser	Val	Gly	
	50					55				60						

atg	cca	att	aac	tat	ccg	cac	tgg	tca	ttc	ggg	aaa	aag	ttt	atc	gag	240
Met	Pro	Ile	Asn	Tyr	Pro	His	Trp	Ser	Phe	Gly	Lys	Lys	Phe	Ile	Glu	
65					70					75					80	

act	gaa	cgg	ctg	tat	aag	cac	ggg	cag	caa	gga	ctg	gcc	tat	gaa	atc	288
Thr	Glu	Arg	Leu	Tyr	Lys	His	Gly	Gln	Gln	Gly	Leu	Ala	Tyr	Glu	Ile	
				85					90					95		

gtc	att	aac	tct	aac	ccg	tgt	atc	gct	tac	ctg	atg	gaa	gag	aac	acc	336
Val	Ile	Asn	Ser	Asn	Pro	Cys	Ile	Ala	Tyr	Leu	Met	Glu	Glu	Asn	Thr	
			100					105						110		

att acc atg caa gcg ctg gtg atg gct cat gcc tgc tat ggg cat aac Ile Thr Met Gln Ala Leu Val Met Ala His Ala Cys Tyr Gly His Asn 115 120 125	384
tct ttc ttc aaa aac aat tac tta ttc cgt agc tgg acc gac gcc agt Ser Phe Phe Lys Asn Asn Tyr Leu Phe Arg Ser Trp Thr Asp Ala Ser 130 135 140	432
tcg att gtc gat tat ctg att ttt gcc cgt aaa tat att acc gag tgc Ser Ile Val Asp Tyr Leu Ile Phe Ala Arg Lys Tyr Ile Thr Glu Cys 145 150 155 160	480
gaa gag cgt tat ggc gtt gat gaa gta gaa cgg ctt ctg gac tcg tgc Glu Glu Arg Tyr Gly Val Asp Glu Val Glu Arg Leu Leu Asp Ser Cys 165 170 175	528
cac gcg ctg atg aac tac ggc gtg gac cgg tac aaa cgc ccg caa aaa His Ala Leu Met Asn Tyr Gly Val Asp Arg Tyr Lys Arg Pro Gln Lys 180 185 190	576
atc tcg ctg caa gaa gag aaa gcc cgg cag aaa agt cgc gaa gag tat Ile Ser Leu Gln Glu Glu Lys Ala Arg Gln Lys Ser Arg Glu Glu Tyr 195 200 205	624
ctg caa agt cag gtc aat atg ctc tgg cgt acc ctg ccg aag cgc gag Leu Gln Ser Gln Val Asn Met Leu Trp Arg Thr Leu Pro Lys Arg Glu 210 215 220	672
gaa gag aaa acg gtt gct gaa gcg cgc cgc tat ccg tcc gaa cca caa Glu Glu Lys Thr Val Ala Glu Ala Arg Arg Tyr Pro Ser Glu Pro Gln 225 230 235 240	720
gaa aac ctg ctc tat ttt atg gag aaa aat gcg cca ctg ctg gaa tca Glu Asn Leu Leu Tyr Phe Met Glu Lys Asn Ala Pro Leu Leu Glu Ser 245 250 255	768
tgg cag cgt gaa atc ctg cgt att gtg cgt aag gtg agc cag tat ttt Trp Gln Arg Glu Ile Leu Arg Ile Val Arg Lys Val Ser Gln Tyr Phe 260 265 270	816
tat ccg caa aaa cag act cag gtg atg aac gaa ggc tgg gcg acc ttc Tyr Pro Gln Lys Gln Thr Gln Val Met Asn Glu Gly Trp Ala Thr Phe 275 280 285	864
tgg cac tac acc atc ctt aac cat ctg tat gat gaa ggg aaa gta acg Trp His Tyr Thr Ile Leu Asn His Leu Tyr Asp Glu Gly Lys Val Thr 290 295 300	912
gaa cgt ttt atg ctg gag ttt ttg cac agc cac acc aat gtg gtc ttc Glu Arg Phe Met Leu Glu Phe Leu His Ser His Thr Asn Val Val Phe 305 310 315 320	960
cag ccc ccc tat aac agc ccg tgg tac agc ggc atc aac ccg tat gcc Gln Pro Pro Tyr Asn Ser Pro Trp Tyr Ser Gly Ile Asn Pro Tyr Ala 325 330 335	1008
ctc ggg ttc gcc atg ttc cag gat att aaa cgg att tgt cag tcg cca Leu Gly Phe Ala Met Phe Gln Asp Ile Lys Arg Ile Cys Gln Ser Pro 340 345 350	1056

acg gaa gaa gac aaa tac tgg ttc ccg gat atc gcc ggt tcc gac tgg 1104
 Thr Glu Glu Asp Lys Tyr Trp Phe Pro Asp Ile Ala Gly Ser Asp Trp
 355 360 365

ctg gaa acg ctg cat ttc gcg atg cgt gat ttc aaa gat gag agt ttt 1152
 Leu Glu Thr Leu His Phe Ala Met Arg Asp Phe Lys Asp Glu Ser Phe
 370 375 380

atc agc cag ttc ctg tca ccg aaa gtg atg cgt gat ttc cgc ttc ttc 1200
 Ile Ser Gln Phe Leu Ser Pro Lys Val Met Arg Asp Phe Arg Phe Phe
 385 390 395 400

acc gtg ctg gat gac gat cgg cat aat tat ctg gag att tcc gct att 1248
 Thr Val Leu Asp Asp Arg His Asn Tyr Leu Glu Ile Ser Ala Ile
 405 410 415

cat aat gaa gaa ggt tat cgg gag atc cgt aac cgg tta tcg tcg caa 1296
 His Asn Glu Glu Gly Tyr Arg Glu Ile Arg Asn Arg Leu Ser Ser Gln
 420 425 430

tat aac tta agt aat ctg gag ccg aat att cag atc tgg aac gtg gat 1344
 Tyr Asn Leu Ser Asn Leu Glu Pro Asn Ile Gln Ile Trp Asn Val Asp
 435 440 445

ttg cgc ggc gac cgt tcg ctg acg ctg cgt tat att cca cat aat cgc 1392
 Leu Arg Gly Asp Arg Ser Leu Thr Leu Arg Tyr Ile Pro His Asn Arg
 450 455 460

gca ccg ctg gat cgg ggg cgc aaa gaa gtc ctg aag cat gtg cat cgc 1440
 Ala Pro Leu Asp Arg Gly Arg Lys Glu Val Leu Lys His Val His Arg
 465 470 475 480

ctg tgg gga ttt gat gtg atg ctc gaa cag caa aac gaa gac ggc agc 1488
 Leu Trp Gly Phe Asp Val Met Leu Glu Gln Asn Glu Asp Gly Ser
 485 490 495

atc gag ttg ctg gaa cgt tgc ccg cca aga atg gga aat ctg taa 1533
 Ile Glu Leu Leu Glu Arg Cys Pro Pro Arg Met Gly Asn Leu *
 500 505 510

<210> 195

<211> 1359

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1539)

<400> 195

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 Met Lys Arg Leu Ser Ile Thr Val Arg Leu Thr Leu Leu Phe Ile Leu
 1 5 10 15

cta ctg tct gtt gct ggc gcc gga att gtc tgg act ctc tat aat ggc 96
 Leu Leu Ser Val Ala Gly Ala Gly Ile Val Trp Thr Leu Tyr Asn Gly
 20 25 30

ctg gca agt gag ttg aaa tgg cgc gat gat aca aca ctc att aac cgg	144
Leu Ala Ser Glu Leu Lys Trp Arg Asp Asp Thr Thr Leu Ile Asn Arg	
35 40 45	
aca gcg cag atc aag cag ttg tta att gat ggg gta aat cca gat acg	192
Thr Ala Gln Ile Lys Gln Leu Leu Ile Asp Gly Val Asn Pro Asp Thr	
50 55 60	
tta cct gtg tac ttt aac cgg atg atg gat gtt agt cag gat atc ttg	240
Leu Pro Val Tyr Phe Asn Arg Met Met Asp Val Ser Gln Asp Ile Leu	
65 70 75 80	
att att cat ggt gat agc atc aat aaa att gtt aac cgg aca aat gtc	288
Ile Ile His Gly Asp Ser Ile Asn Lys Ile Val Asn Arg Thr Asn Val	
85 90 95	
agt gat ggc atg tta aat aac ata cct gct agt gag aca atc agc gca	336
Ser Asp Gly Met Leu Asn Asn Ile Pro Ala Ser Glu Thr Ile Ser Ala	
100 105 110	
gct ggc att tac aga agc att att aat gat aca gag ata gat gct tta	384
Ala Gly Ile Tyr Arg Ser Ile Ile Asn Asp Thr Glu Ile Asp Ala Leu	
115 120 125	
cga att aat att gat gaa gtt tcg cca tca tta acg gtt act gtg gct	432
Arg Ile Asn Ile Asp Glu Val Ser Pro Ser Leu Thr Val Thr Val Ala	
130 135 140	
aaa ttg gct tca gcc aga cat aac atg ctt gaa cag tat aaa att aat	480
Lys Leu Ala Ser Ala Arg His Asn Met Leu Glu Gln Tyr Lys Ile Asn	
145 150 155 160	
agc att ata att tgc att gtc gcc att gta ctt tgc tca gta tta agt	528
Ser Ile Ile Ile Cys Ile Val Ala Ile Val Leu Cys Ser Val Leu Ser	
165 170 175	
ccg ctg tta atc aga acg gga tta cga gag atc aaa aag ttg agt ggt	576
Pro Leu Leu Ile Arg Thr Gly Leu Arg Glu Ile Lys Lys Leu Ser Gly	
180 185 190	
gta acg gaa gcg ctg aat tat aac gat agc cga gag cct gtt gag gtt	624
Val Thr Glu Ala Leu Asn Tyr Asn Asp Ser Arg Glu Pro Val Glu Val	
195 200 205	
agc gca tta ccg aga gaa cta aaa cct ctt ggg cag gcg ttg aat aaa	672
Ser Ala Leu Pro Arg Glu Leu Lys Pro Leu Gly Gln Ala Leu Asn Lys	
210 215 220	
atg cat cat gct tta gtc aaa gat ttt gag cgt cta agt cag ttt gct	720
Met His His Ala Leu Val Lys Asp Phe Glu Arg Leu Ser Gln Phe Ala	
225 230 235 240	
gac gat ctc gct cat gaa ctt aga acg cca att aat gca tta ctg ggt	768
Asp Asp Leu Ala His Glu Leu Arg Thr Pro Ile Asn Ala Leu Leu Gly	
245 250 255	
cag aat cag gtt acg ctc agt caa acc aga agt atc gct gaa tat caa	816
Gln Asn Gln Val Thr Leu Ser Gln Thr Arg Ser Ile Ala Glu Tyr Gln	
260 265 270	

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aaa aca att gcc gga aac att gaa gag ctg gaa aat att tcg cgg tta      864
Lys Thr Ile Ala Gly Asn Ile Glu Glu Leu Glu Asn Ile Ser Arg Leu
      275                      280                      285

aca gag aac ata ctg ttt ctt gcc agg gca gat aaa aac aat gtt ttg      912
Thr Glu Asn Ile Leu Phe Leu Ala Arg Ala Asp Lys Asn Asn Val Leu
      290                      295                      300

gtg aaa ctg gac tcg ctt tct ctc aat aag gaa gtc gaa aat ttg ttg      960
Val Lys Leu Asp Ser Leu Ser Leu Asn Lys Glu Val Glu Asn Leu Leu
      305                      310                      315                      320

gac tat ctt gaa tac ctt tca gac gag aaa gag att tgc ttt aag gtc      1008
Asp Tyr Leu Glu Tyr Leu Ser Asp Glu Lys Glu Ile Cys Phe Lys Val
      325                      330                      335

gag tgc aat cag caa atc ttt gcg gat aaa att tta cta caa cga atg      1056
Glu Cys Asn Gln Gln Ile Phe Ala Asp Lys Ile Leu Leu Gln Arg Met
      340                      345                      350

tta tcg aat ctt att gtt aat gcc att aga tat tcg cca gaa aaa tcg      1104
Leu Ser Asn Leu Ile Val Asn Ala Ile Arg Tyr Ser Pro Glu Lys Ser
      355                      360                      365

cgt att cat ata acc agt ttt ctt gat acc aac agc tat ctt aat att      1152
Arg Ile His Ile Thr Ser Phe Leu Asp Thr Asn Ser Tyr Leu Asn Ile
      370                      375                      380

gat atc gcc agc cct gga acg aaa att aat gag cct gaa aaa ctc ttc      1200
Asp Ile Ala Ser Pro Gly Thr Lys Ile Asn Glu Pro Glu Lys Leu Phe
      385                      390                      395                      400

cgt aga ttt tgg cgg gga gat aat tcg cgt cat tcc gta ggt cag gga      1248
Arg Arg Phe Trp Arg Gly Asp Asn Ser Arg His Ser Val Gly Gln Gly
      405                      410                      415

cta ggc ctt tct tta gtc aaa gcg att gcc gaa ttg cat ggg gga agt      1296
Leu Gly Leu Ser Leu Val Lys Ala Ile Ala Glu Leu His Gly Gly Ser
      420                      425                      430

gct acg tat cac tat ctc aat aag cat aat gtg ttc cgg att acg tta      1344
Ala Thr Tyr His Tyr Leu Asn Lys His Asn Val Phe Arg Ile Thr Leu
      435                      440                      445

ccg caa aga aat taa      1359
Pro Gln Arg Asn *
      450

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<210> 196
 <211> 720
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(720)

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<400> 196
atg aac cag gct gtt tct ata aca tat gat tta tgg cat att att ttc      48

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Met	Asn	Gln	Ala	Val	Ser	Ile	Thr	Tyr	Asp	Leu	Trp	His	Ile	Ile	Phe	
1				5					10					15		
atg	aag	att	cta	ctt	att	gaa	gat	aat	caa	agg	acc	cag	gaa	tgg	gta	96
Met	Lys	Ile	Leu	Leu	Ile	Glu	Asp	Asn	Gln	Arg	Thr	Gln	Glu	Trp	Val	
			20					25					30			
acg	cag	ggg	ctt	tcc	gaa	gcg	ggt	tat	gtc	atc	gat	gcc	gtt	tct	gat	144
Thr	Gln	Gly	Leu	Ser	Glu	Ala	Gly	Tyr	Val	Ile	Asp	Ala	Val	Ser	Asp	
		35					40					45				
ggc	aga	gat	ggg	ctt	tat	ctt	gcg	ctg	aag	gat	gat	tat	gca	ttg	atc	192
Gly	Arg	Asp	Gly	Leu	Tyr	Leu	Ala	Leu	Lys	Asp	Asp	Tyr	Ala	Leu	Ile	
	50					55				60						
att	ctg	gat	att	atg	ctt	ccg	ggt	atg	gat	ggc	tgg	cag	atc	tta	caa	240
Ile	Leu	Asp	Ile	Met	Leu	Pro	Gly	Met	Asp	Gly	Trp	Gln	Ile	Leu	Gln	
	65				70				75					80		
acg	tta	aga	aca	gca	aag	caa	acc	cct	gtt	att	tgc	ctt	act	gca	agg	288
Thr	Leu	Arg	Thr	Ala	Lys	Gln	Thr	Pro	Val	Ile	Cys	Leu	Thr	Ala	Arg	
			85					90					95			
gat	tct	gtc	gat	gac	aga	gtc	aga	ggg	ctg	gac	agt	ggg	gca	aat	gat	336
Asp	Ser	Val	Asp	Asp	Arg	Val	Arg	Gly	Leu	Asp	Ser	Gly	Ala	Asn	Asp	
		100						105					110			
tat	ctg	gta	aaa	cct	ttt	tca	ttt	tct	gag	ttg	ctg	gca	agg	gtt	cgg	384
Tyr	Leu	Val	Lys	Pro	Phe	Ser	Phe	Ser	Glu	Leu	Leu	Ala	Arg	Val	Arg	
	115					120						125				
gca	caa	tta	agg	caa	cat	cac	gct	ttg	aat	tca	aca	tta	gaa	atc	agc	432
Ala	Gln	Leu	Arg	Gln	His	His	Ala	Leu	Asn	Ser	Thr	Leu	Glu	Ile	Ser	
	130					135				140						
ggc	tta	aga	atg	gac	tct	gtt	agt	cat	agt	gtg	agc	agg	gac	aat	atc	480
Gly	Leu	Arg	Met	Asp	Ser	Val	Ser	His	Ser	Val	Ser	Arg	Asp	Asn	Ile	
	145				150				155					160		
agt	att	aca	ctg	acg	cgc	aag	gag	ttt	cag	tta	ctt	tgg	cta	ctg	gcc	528
Ser	Ile	Thr	Leu	Thr	Arg	Lys	Glu	Phe	Gln	Leu	Leu	Trp	Leu	Leu	Ala	
			165					170					175			
tcc	aga	gct	ggc	gaa	att	ata	ccc	aga	acg	gtt	att	gcg	agt	gaa	att	576
Ser	Arg	Ala	Gly	Glu	Ile	Ile	Pro	Arg	Thr	Val	Ile	Ala	Ser	Glu	Ile	
		180						185					190			
tgg	gga	atc	aac	ttt	gat	agt	gat	acc	aat	acg	gtg	gac	gtc	gcc	att	624
Trp	Gly	Ile	Asn	Phe	Asp	Ser	Asp	Thr	Asn	Thr	Val	Asp	Val	Ala	Ile	
		195					200					205				
cgc	agg	ctc	cgc	gca	aaa	gtt	gat	gat	cct	ttt	cct	gaa	aag	cta	att	672
Arg	Arg	Leu	Arg	Ala	Lys	Val	Asp	Asp	Pro	Phe	Pro	Glu	Lys	Leu	Ile	
	210					215					220					
gcc	aca	atc	cgg	ggg	atg	ggc	tat	tca	ttc	gta	gcg	gta	aaa	aaa	taa	720
Ala	Thr	Ile	Arg	Gly	Met	Gly	Tyr	Ser	Phe	Val	Ala	Val	Lys	Lys	*	
	225				230					235						

<210> 197
 <211> 519
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(519)

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 gct ttt agg gca tcc ttt cat tta cac ttt tta cga aat cat ggg atc 96
 Ala Phe Arg Ala Ser Phe His Leu His Phe Leu Arg Asn His Gly Ile
 20 25 30
 act aac aaa ata tcg ctt gtc agt tat att gta tgg cag gaa aga tat 144
 Thr Asn Lys Ile Ser Leu Val Ser Tyr Ile Val Trp Gln Glu Arg Tyr
 35 40 45
 gcg act gat att aca gat ccc caa agt gga gag ttt atg acc att aaa 192
 Ala Thr Asp Ile Thr Asp Pro Gln Ser Gly Glu Phe Met Thr Ile Lys
 50 55 60
 aat aag atg ttg ctg ggt gcg ctt ttg ctg gtt acc agt gcc gcc tgg 240
 Asn Lys Met Leu Leu Gly Ala Leu Leu Leu Val Thr Ser Ala Ala Trp
 65 70 75 80
 gcc gca cca gcc acc gcg ggt tcg acc aat acc tcg gga att tct aag 288
 Ala Ala Pro Ala Thr Ala Gly Ser Thr Asn Thr Ser Gly Ile Ser Lys
 85 90 95
 tat gag tta agt agt ttc att gct gac ttt aag cat ttc aaa cca ggg 336
 Tyr Glu Leu Ser Ser Phe Ile Ala Asp Phe Lys His Phe Lys Pro Gly
 100 105 110
 gac acc gta cca gaa atg tac cgt acc gat gag tac aac att aag cag 384
 Asp Thr Val Pro Glu Met Tyr Arg Thr Asp Glu Tyr Asn Ile Lys Gln
 115 120 125
 tgg cag ttg cgt aac ctg ccc gcg cct gat gcc ggg acg cac tgg acc 432
 Trp Gln Leu Arg Asn Leu Pro Ala Pro Asp Ala Gly Thr His Trp Thr
 130 135 140
 tat atg ggt ggc gcg tac gtg ttg atc agc gac acc gac ggt aaa atc 480
 Tyr Met Gly Gly Ala Tyr Val Leu Ile Ser Asp Thr Asp Gly Lys Ile
 145 150 155 160
 att aaa gcc tac gac ggt gag att ttt tat cat cgc taa 519
 Ile Lys Ala Tyr Asp Gly Glu Ile Phe Tyr His Arg *
 165 170

<210> 198
 <211> 825
 <212> DNA
 <213> Escherichia coli

<220>

<221> CDS

<222> (1)...(825)

<400> 198

atg acc gaa ttt aca act ctt ctt cag caa gga aac gcc tgg ttc ttc	48
Met Thr Glu Phe Thr Thr Leu Leu Gln Gln Gly Asn Ala Trp Phe Phe	
1 5 10 15	
atc ccc agc gcc atc tta ctt ggt gcg ctt cat ggc ctg gaa cca ggg	96
Ile Pro Ser Ala Ile Leu Leu Gly Ala Leu His Gly Leu Glu Pro Gly	
20 25 30	
cac tca aaa acg atg atg gcg gcg ttt atc atc gcc atc aaa ggc acc	144
His Ser Lys Thr Met Met Ala Ala Phe Ile Ile Ala Ile Lys Gly Thr	
35 40 45	
att aaa caa gcg gtg atg ctc gga ctg gca gca act att tcg cat acc	192
Ile Lys Gln Ala Val Met Leu Gly Leu Ala Ala Thr Ile Ser His Thr	
50 55 60	
gca gtg gtc tgg tta att gcc ttt ggc ggg atg gtg atc agc aag cgc	240
Ala Val Val Trp Leu Ile Ala Phe Gly Gly Met Val Ile Ser Lys Arg	
65 70 75 80	
ttt act gct caa tca gca gaa ccg tgg ctc cag ctg att tcc gca gtg	288
Phe Thr Ala Gln Ser Ala Glu Pro Trp Leu Gln Leu Ile Ser Ala Val	
85 90 95	
atc att att agc acc gcg ttc tgg atg ttc tgg cgt acc tgg cgc ggc	336
Ile Ile Ile Ser Thr Ala Phe Trp Met Phe Trp Arg Thr Trp Arg Gly	
100 105 110	
gaa cgc aac tgg ctg gag aat atg cac ggg cat gat tat gag cat cat	384
Glu Arg Asn Trp Leu Glu Asn Met His Gly His Asp Tyr Glu His His	
115 120 125	
cat cac gat cac gaa cat cac cac gac cat gga cat cat cac cat cac	432
His His Asp His Glu His His His Asp His Gly His His His His His	
130 135 140	
gaa cat ggc gag tat cag gat gcc cat gca cga gcc cat gcc aat gac	480
Glu His Gly Glu Tyr Gln Asp Ala His Ala Arg Ala His Ala Asn Asp	
145 150 155 160	
att aaa cga cgc ttt gat ggt aga gag gtc acc aac tgg caa att ttg	528
Ile Lys Arg Arg Phe Asp Gly Arg Glu Val Thr Asn Trp Gln Ile Leu	
165 170 175	
tta ttt ggc tta acc ggt ggc ctt atc ccc tgc ccg gca gca att acc	576
Leu Phe Gly Leu Thr Gly Gly Leu Ile Pro Cys Pro Ala Ala Ile Thr	
180 185 190	
gtg ctg ttg ata tgc att cag ttg aaa gcc ctg aca ctg ggc gca aca	624
Val Leu Leu Ile Cys Ile Gln Leu Lys Ala Leu Thr Leu Gly Ala Thr	
195 200 205	
ctg gtc gtc agt ttc agc att ggc ctg gcg tta acg ctt gtc acc gta	672
Leu Val Val Ser Phe Ser Ile Gly Leu Ala Leu Thr Leu Val Thr Val	
210 215 220	

```

ggc gtt ggc gca gca atc agc gtt cag cag gtc gca aaa cgc tgg agc      720
Gly Val Gly Ala Ala Ile Ser Val Gln Gln Val Ala Lys Arg Trp Ser
225                230                235                240

gga ttt aac act ctc gct aaa cgc gcc ccc tat ttt tcc agt ctg ttg      768
Gly Phe Asn Thr Leu Ala Lys Arg Ala Pro Tyr Phe Ser Ser Leu Leu
                245                250                255

att ggc tta gtc ggt gtg tat atg ggc gta cat ggc ttc atg ggc ata      816
Ile Gly Leu Val Gly Val Tyr Met Gly Val His Gly Phe Met Gly Ile
                260                265                270

atg cga taa      825
Met Arg *
```

```

<210> 199
<211> 249
<212> DNA
<213> Escherichia coli
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<220>
<221> CDS
<222> (1)...(249)
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```

<400> 199
atg tgt att ggc gtt cca ggc cag gtg ctg gct gtc ggt gaa gat att      48
Met Cys Ile Gly Val Pro Gly Gln Val Leu Ala Val Gly Glu Asp Ile
1                5                10                15

cac cag ctt gcg cag gtt gaa gta tgt ggt atc aag cgc gat gtg aat      96
His Gln Leu Ala Gln Val Glu Val Cys Gly Ile Lys Arg Asp Val Asn
                20                25                30

atc gcc ctg att tgt gaa ggt aac cct gcc gat cta ctg ggc cag tgg      144
Ile Ala Leu Ile Cys Glu Gly Asn Pro Ala Asp Leu Leu Gly Gln Trp
                35                40                45

gtg ctg gta cac gtc gga ttt gcc atg agc atc atc gac gaa gat gaa      192
Val Leu Val His Val Gly Phe Ala Met Ser Ile Ile Asp Glu Asp Glu
                50                55                60

gcc aaa gcc aca tta gac gca ctg cgc caa atg gat tac gac att acc      240
Ala Lys Ala Thr Leu Asp Ala Leu Arg Gln Met Asp Tyr Asp Ile Thr
                65                70                75                80

agc gcg tga      249
Ser Ala *
```

```

<210> 200
<211> 342
<212> DNA
<213> Escherichia coli
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<220>
<221> CDS
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<222> (1)...(342)

<400> 200

atg cat gag ttg tct ctt tgc cag agc gcc gtt gaa att atc caa cgg	48
Met His Glu Leu Ser Leu Cys Gln Ser Ala Val Glu Ile Ile Gln Arg	
1 5 10 15	
cag gcg gag cag cac gat gtt aag cgc gtc acc gcc gtg tgg ctg gaa	96
Gln Ala Glu Gln His Asp Val Lys Arg Val Thr Ala Val Trp Leu Glu	
20 25 30	
att ggc gcg ctc tcc tgc gtt gag gag agc gcc gtc cgt ttt agt ttt	144
Ile Gly Ala Leu Ser Cys Val Glu Glu Ser Ala Val Arg Phe Ser Phe	
35 40 45	
gaa att gtc tgc cac gga acg gtg gcg caa ggg tgc gat tta cat atc	192
Glu Ile Val Cys His Gly Thr Val Ala Gln Gly Cys Asp Leu His Ile	
50 55 60	
gtc tat aaa ccc gcc cag gct tgg tgc tgg gat tgc agc cag gtg gtg	240
Val Tyr Lys Pro Ala Gln Ala Trp Cys Trp Asp Cys Ser Gln Val Val	
65 70 75 80	
gag att cat cag cac gat gcg cag tgt ccg ctc tgt cac ggc gag cgg	288
Glu Ile His Gln His Asp Ala Gln Cys Pro Leu Cys His Gly Glu Arg	
85 90 95	
ttg cgt gtc gat acc ggc gat tcg ctg atc gtc aaa agt att gaa gtt	336
Leu Arg Val Asp Thr Gly Asp Ser Leu Ile Val Lys Ser Ile Glu Val	
100 105 110	
gaa taa	342
Glu *	

<210> 201

<211> 489

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(489)

<400> 201

atg act gaa gag ata gca ggt ttc cag acc tcc ccg aag gcg caa gta	48
Met Thr Glu Glu Ile Ala Gly Phe Gln Thr Ser Pro Lys Ala Gln Val	
1 5 10 15	
cag gca gcg ttt gaa gaa att gcc cgg cgt tcg atg cac gat ctc tct	96
Gln Ala Ala Phe Glu Glu Ile Ala Arg Arg Ser Met His Asp Leu Ser	
20 25 30	
ttt ctg cat cct tca atg ccg gtg tat gtt tct gat ttt acg ctg ttc	144
Phe Leu His Pro Ser Met Pro Val Tyr Val Ser Asp Phe Thr Leu Phe	
35 40 45	
gaa ggt cag tgg acg ggg tgt gtg atc acc ccg tgg atg ctg agt gca	192
Glu Gly Gln Trp Thr Gly Cys Val Ile Thr Pro Trp Met Leu Ser Ala	

50	55	60	
gtt atc ttc ccc ggc ccg gat caa ctc tgg ccg ctg cgc aaa gtg agt			240
Val Ile Phe Pro Gly Pro Asp Gln Leu Trp Pro Leu Arg Lys Val Ser			
65	70	75	80
gaa aaa att ggt ctg caa ctg ccg tat ggc act atg acc ttt acc gtt			288
Glu Lys Ile Gly Leu Gln Leu Pro Tyr Gly Thr Met Thr Phe Thr Val			
	85	90	95
ggc gaa ctg gac ggt gtt tcg caa tat ctc tcc tgt tcg ctg atg tcg			336
Gly Glu Leu Asp Gly Val Ser Gln Tyr Leu Ser Cys Ser Leu Met Ser			
	100	105	110
ccg ctt tcg cac agc atg tcg att gaa gag ggc caa cgc ctg acg gat			384
Pro Leu Ser His Ser Met Ser Ile Glu Glu Gly Gln Arg Leu Thr Asp			
	115	120	125
gac tgc gca cga atg atc ctt tcg ctg cca gtc acg aat ccg gat gta			432
Asp Cys Ala Arg Met Ile Leu Ser Leu Pro Val Thr Asn Pro Asp Val			
	130	135	140
cca cac gca ggg cgt cgc gcc ctg ctg ttt ggt cgc agg agt ggc gaa			480
Pro His Ala Gly Arg Arg Ala Leu Leu Phe Gly Arg Arg Ser Gly Glu			
	145	150	155
aat gca tga			489
Asn Ala *			

<210> 202

<211> 495

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(495)

<400> 202

atg cgt att tta gtc tta ggg gtc ggc aat att ttg ctg acc gat gaa	48
Met Arg Ile Leu Val Leu Gly Val Gly Asn Ile Leu Leu Thr Asp Glu	
1	5

gcc atc ggt gtg cgg att gtc gaa gcg tta gag caa cga tac att ctg	96
Ala Ile Gly Val Arg Ile Val Glu Ala Leu Glu Gln Arg Tyr Ile Leu	
	20

ccg gat tat gtt gag atc ctc gat ggc ggc acg gcg gga atg gag ctg	144
Pro Asp Tyr Val Glu Ile Leu Asp Gly Gly Thr Ala Gly Met Glu Leu	
	35

ctt ggc gac atg gca aat cgc gat cat ttg att att gcg gat gcc att	192
Leu Gly Asp Met Ala Asn Arg Asp His Leu Ile Ile Ala Asp Ala Ile	
	50

gtc tcg aaa aag aac gcg ccg gga acg atg atg atc ctg cgg gat gaa	240
Val Ser Lys Lys Asn Ala Pro Gly Thr Met Met Ile Leu Arg Asp Glu	
	65

gaa gtt ccg gcg ttg ttt acc aac aaa atc tct ccg cat cag ctt ggc 288
 Glu Val Pro Ala Leu Phe Thr Asn Lys Ile Ser Pro His Gln Leu Gly
 85 90 95

ctg gcc gac gtc ttg tcg gcc ctg cgc ttc acc ggc gag ttt ccg aaa 336
 Leu Ala Asp Val Leu Ser Ala Leu Arg Phe Thr Gly Glu Phe Pro Lys
 100 105 110

aag ctg acc ctg gtc ggc gtg atc ccg gaa tcg ctg gag cca cac atc 384
 Lys Leu Thr Leu Val Gly Val Ile Pro Glu Ser Leu Glu Pro His Ile
 115 120 125

ggc tta acg ccg acg gtt gaa gca atg att gaa cct gcg ctt gag cag 432
 Gly Leu Thr Pro Thr Val Glu Ala Met Ile Glu Pro Ala Leu Glu Gln
 130 135 140

gtt ctg gct gcg ctg cgt gaa tct ggc gtg gaa gcc atc cca cgg gag 480
 Val Leu Ala Ala Leu Arg Glu Ser Gly Val Glu Ala Ile Pro Arg Glu
 145 150 155 160

gcg att cat gac tga 495
 Ala Ile His Asp *

<210> 203
 <211> 1704
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1704)

<400> 203
 atg agc cag aga att act att gat ccg gta acc cgt att gag ggg cat 48
 Met Ser Gln Arg Ile Thr Ile Asp Pro Val Thr Arg Ile Glu Gly His
 1 5 10 15

tta cgc atc gat tgc gaa atc gaa aat ggc gtc gtt tcg aaa gca tgg 96
 Leu Arg Ile Asp Cys Glu Ile Glu Asn Gly Val Val Ser Lys Ala Trp
 20 25 30

gct tcc ggt acc atg tgg cgc ggc atg gaa gag atc gtg aaa aac cgc 144
 Ala Ser Gly Thr Met Trp Arg Gly Met Glu Glu Ile Val Lys Asn Arg
 35 40 45

gat ccg cgc gat gca tgg atg att gtg caa cgt atc tgt ggc gta tgt 192
 Asp Pro Arg Asp Ala Trp Met Ile Val Gln Arg Ile Cys Gly Val Cys
 50 55 60

act acc act cac gcg ctg tct tcc gtt cgt gcg gca gaa agt gcg ctg 240
 Thr Thr Thr His Ala Leu Ser Ser Val Arg Ala Ala Glu Ser Ala Leu
 65 70 75 80

aat atc gac gtt ccg gtt aac gcg caa tac atc cgt aac atc att ctg 288
 Asn Ile Asp Val Pro Val Asn Ala Gln Tyr Ile Arg Asn Ile Ile Leu
 85 90 95

gct gcg cac acc acg cat gac cat att gtt cat ttc tat cag ctt tcg Ala Ala His Thr His Asp His Ile Val His Phe Tyr Gln Leu Ser 100 105 110	336
gcg ctg gac tgg gtg gac atc act tct gca ctg caa gct gac cca acc Ala Leu Asp Trp Val Asp Ile Thr Ser Ala Leu Gln Ala Asp Pro Thr 115 120 125	384
aaa gcc tcc gaa atg ctg aaa ggc gtt tcg acc tgg cac ctg aac agt Lys Ala Ser Glu Met Leu Lys Gly Val Ser Thr Trp His Leu Asn Ser 130 135 140	432
ccg gaa gag ttc acc aaa gtt cag aac aag atc aaa gat ctg gtt gcc Pro Glu Glu Phe Thr Lys Val Gln Asn Lys Ile Lys Asp Leu Val Ala 145 150 155 160	480
agc ggt cag ttg ggt att ttc gct aat ggc tac tgg ggt cat ccg gcg Ser Gly Gln Leu Gly Ile Phe Ala Asn Gly Tyr Trp Gly His Pro Ala 165 170 175	528
atg aaa ctg ccg ccg gaa gtg aac ctg att gcg gta gcg cac tac ctg Met Lys Leu Pro Pro Glu Val Asn Leu Ile Ala Val Ala His Tyr Leu 180 185 190	576
caa gcg ttg gag tgc cag cgt gac gct aac cgc gtc gtg gcg ctg ctg Gln Ala Leu Glu Cys Gln Arg Asp Ala Asn Arg Val Val Ala Leu Leu 195 200 205	624
ggc ggt aaa acg ccg cac att cag aac ctg gcg gta ggt ggt gtc gcg Gly Gly Lys Thr Pro His Ile Gln Asn Leu Ala Val Gly Gly Val Ala 210 215 220	672
aac ccg atc aac ctc gac ggt ttg ggc gtg ctg aac ctt gag cgc ctg Asn Pro Ile Asn Leu Asp Gly Leu Gly Val Leu Asn Leu Glu Arg Leu 225 230 235 240	720
atg tac atc aag tct ttc atc gac aaa ctg agc gac ttt gtt gag cag Met Tyr Ile Lys Ser Phe Ile Asp Lys Leu Ser Asp Phe Val Glu Gln 245 250 255	768
gtt tat aag gtt gat acc gca gtt att gcc gcg ttc tac ccg gaa tgg Val Tyr Lys Val Asp Thr Ala Val Ile Ala Ala Phe Tyr Pro Glu Trp 260 265 270	816
ctg aca cgc ggt aaa ggt gcg gtg aac tac ctg agc gtg ccg gaa ttc Leu Thr Arg Gly Lys Gly Ala Val Asn Tyr Leu Ser Val Pro Glu Phe 275 280 285	864
ccg acc gac agt aaa aac ggc agc ttc ctg ttc ccg ggc ggc tac att Pro Thr Asp Ser Lys Asn Gly Ser Phe Leu Phe Pro Gly Gly Tyr Ile 290 295 300	912
gag aat gcg gat ctg tcc tcg tat cgt ccg atc act tct cat tcc gat Glu Asn Ala Asp Leu Ser Ser Tyr Arg Pro Ile Thr Ser His Ser Asp 305 310 315 320	960
gaa tac ctg atc aaa ggc att cag gaa agc gcg aag cac tcc tgg tat Glu Tyr Leu Ile Lys Gly Ile Gln Glu Ser Ala Lys His Ser Trp Tyr 325 330 335	1008

aaa gac gaa gcg ccg cag gca ccg tgg gaa ggc acc acc att ccg gct Lys Asp Glu Ala Pro Gln Ala Pro Trp Glu Gly Thr Thr Ile Pro Ala 340 345 350	1056
tat gat ggt tgg tct gac gac ggg aaa tat tcc tgg gtg aaa tca ccg Tyr Asp Gly Trp Ser Asp Asp Gly Lys Tyr Ser Trp Val Lys Ser Pro 355 360 365	1104
act ttc tac ggc aaa acg gta gaa gtg ggg cca ctg gct aat atg ctg Thr Phe Tyr Gly Lys Thr Val Glu Val Gly Pro Leu Ala Asn Met Leu 370 375 380	1152
gtg aaa ctg gcg gca ggt cgc gaa tct acc cag aac aaa ctg aat gaa Val Lys Leu Ala Ala Gly Arg Glu Ser Thr Gln Asn Lys Leu Asn Glu 385 390 395 400	1200
atc gtt gcg att tat cag aaa ctg act ggc aac acg ctg gaa gtg gca Ile Val Ala Ile Tyr Gln Lys Leu Thr Gly Asn Thr Leu Glu Val Ala 405 410 415	1248
cag ctg cac tcc acg ctg ggc cgt att att ggt cgt acc gtt cac tgc Gln Leu His Ser Thr Leu Gly Arg Ile Ile Gly Arg Thr Val His Cys 420 425 430	1296
tgt gaa ttg cag gat atc ctg caa aac caa tac agt gca ctg atc acc Cys Glu Leu Gln Asp Ile Leu Gln Asn Gln Tyr Ser Ala Leu Ile Thr 435 440 445	1344
aat atc ggc aaa ggc gat cac acc acc ttt gtg aag ccg aac att ccg Asn Ile Gly Lys Gly Asp His Thr Thr Phe Val Lys Pro Asn Ile Pro 450 455 460	1392
gca acg ggt gaa ttc aaa ggt gtt ggc ttc ctc gaa gcg ccg cgc ggt Ala Thr Gly Glu Phe Lys Gly Val Gly Phe Leu Glu Ala Pro Arg Gly 465 470 475 480	1440
atg ctc tct cac tgg atg gtt att aaa gac ggt atc atc agc aac tac Met Leu Ser His Trp Met Val Ile Lys Asp Gly Ile Ile Ser Asn Tyr 485 490 495	1488
cag gcg gtt gtt cca tca acc tgg aac tct ggt ccg cgt aac ttc aat Gln Ala Val Val Pro Ser Thr Trp Asn Ser Gly Pro Arg Asn Phe Asn 500 505 510	1536
gat gac gtc ggt cct tac gag cag tgc ctg gtg ggt aca ccg gtt gcc Asp Asp Val Gly Pro Tyr Glu Gln Ser Leu Val Gly Thr Pro Val Ala 515 520 525	1584
gat ccg aat aaa ccg ctg gaa gtg gtg cgt acc att cac tcc ttt gac Asp Pro Asn Lys Pro Leu Glu Val Val Arg Thr Ile His Ser Phe Asp 530 535 540	1632
ccg tgc atg gcc tgt gcg gta cac gta gtg gat gct gac ggc aac gaa Pro Cys Met Ala Cys Ala Val His Val Val Asp Ala Asp Gly Asn Glu 545 550 555 560	1680
gtg gtt tca gtg aag gtt ctg taa Val Val Ser Val Lys Val Leu *	1704
565	

<210> 204
 <211> 1179
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1179)

<400> 204
 atg agt cat gat cca caa ccg ctg ggc ggc aaa atc atc agt' aaa ccg 48
 Met Ser His Asp Pro Gln Pro Leu Gly Gly Lys Ile Ile Ser Lys Pro
 1 5 10 15

gtc atg att ttt gga ccg tta atc gtc atc tgt atg ctc ctg att gtg 96
 Val Met Ile Phe Gly Pro Leu Ile Val Ile Cys Met Leu Leu Ile Val
 20 25 30

aag cgt ctg gtg ttc ggt ctg ggc tct gtc tct gac ctg aac ggc ggc 144
 Lys Arg Leu Val Phe Gly Leu Gly Ser Val Ser Asp Leu Asn Gly Gly
 35 40 45

ttc ccg tgg ggc gtg tgg atc gcg ttt gac ctg ctg att ggc acc ggc 192
 Phe Pro Trp Gly Val Trp Ile Ala Phe Asp Leu Leu Ile Gly Thr Gly
 50 55 60

ttt gcc tgt ggc ggc tgg gcg ctg gcg tgg gcg gta tac gtc ttt aac 240
 Phe Ala Cys Gly Gly Trp Ala Leu Ala Trp Ala Val Tyr Val Phe Asn
 65 70 75 80

cgt ggg caa tac cat ccg ctg gtg cgt ccg gcg ctg ttg gcg agt ctg 288
 Arg Gly Gln Tyr His Pro Leu Val Arg Pro Ala Leu Leu Ala Ser Leu
 85 90 95

ttt ggt tac tca ctg ggt ggc ttg tcg atc act atc gac gtg ggt cgc 336
 Phe Gly Tyr Ser Leu Gly Gly Leu Ser Ile Thr Ile Asp Val Gly Arg
 100 105 110

tac tgg aac ctg ccg tac ttc tac att ccg ggt cac ttc aac gtg aac 384
 Tyr Trp Asn Leu Pro Tyr Phe Tyr Ile Pro Gly His Phe Asn Val Asn
 115 120 125

tcg gta ctg ttc gag acg gcg gtc tgt atg acc atc tat atc ggc gtg 432
 Ser Val Leu Phe Glu Thr Ala Val Cys Met Thr Ile Tyr Ile Gly Val
 130 135 140

atg gca ctg gag ttt gct ccg gca ctg ttt gaa cgt ctg ggg tgg aag 480
 Met Ala Leu Glu Phe Ala Pro Ala Leu Phe Glu Arg Leu Gly Trp Lys
 145 150 155 160

gtg tcg cta cag cga cta aac aag gtg atg ttc ttc atc atc gcg ctc 528
 Val Ser Leu Gln Arg Leu Asn Lys Val Met Phe Phe Ile Ile Ala Leu
 165 170 175

ggt gcg ctg ctg ccg acc atg cac cag tct tca atg ggg tcg ctg atg 576
 Gly Ala Leu Leu Pro Thr Met His Gln Ser Ser Met Gly Ser Leu Met
 180 185 190

atc tcg gcg ggc tac aag gtg cat ccg ttg tgg cag agc tat gaa atg 624

Ile Ser Ala Gly Tyr Lys Val His Pro Leu Trp Gln Ser Tyr Glu Met	
195 200 205	
ttg ccg ctg ttc tcg ctg ctg acg gcg ttc atc atg ggc ttc tcg att	672
Leu Pro Leu Phe Ser Leu Leu Thr Ala Phe Ile Met Gly Phe Ser Ile	
210 215 220	
gtc atc ttt gaa ggt tcg ctg gtg cag gcg ggt ctg cgt ggc aac ggt	720
Val Ile Phe Glu Gly Ser Leu Val Gln Ala Gly Leu Arg Gly Asn Gly	
225 230 235 240	
ccg gat gaa aag agt ctg ttt gtt aag ctg acc aac acc atc agt gtg	768
Pro Asp Glu Lys Ser Leu Phe Val Lys Leu Thr Asn Thr Ile Ser Val	
245 250 255	
ttg ctg gcg att ttc atc gtg ctg cgc ttt ggc gag ctt atc tat cgc	816
Leu Leu Ala Ile Phe Ile Val Leu Arg Phe Gly Glu Leu Ile Tyr Arg	
260 265 270	
gac aag ctg tcg tta gcg ttt gcc ggt gac ttc tac tcc gtg atg ttc	864
Asp Lys Leu Ser Leu Ala Phe Ala Gly Asp Phe Tyr Ser Val Met Phe	
275 280 285	
tgg att gaa gtc ctg ctg atg ctc ttc ccg ctg gtc gtt ctg cgt gtg	912
Trp Ile Glu Val Leu Leu Met Leu Phe Pro Leu Val Val Leu Arg Val	
290 295 300	
gcg aag ctg cgt aat gat tcc cgc atg ctg ttc ctg tca gca ctg agc	960
Ala Lys Leu Arg Asn Asp Ser Arg Met Leu Phe Leu Ser Ala Leu Ser	
305 310 315 320	
gca ctg tta ggt tgt gca acc tgg cgt ctg acc tat tcg ctg gtg gca	1008
Ala Leu Leu Gly Cys Ala Thr Trp Arg Leu Thr Tyr Ser Leu Val Ala	
325 330 335	
ttc aac ccg ggc ggc ggt tac gcc tac ttc ccg acc tgg gaa gaa ctg	1056
Phe Asn Pro Gly Gly Gly Tyr Ala Tyr Phe Pro Thr Trp Glu Glu Leu	
340 345 350	
ttg att tct att ggt ttt gtg gct att gag att tgc gct tac atc gta	1104
Leu Ile Ser Ile Gly Phe Val Ala Ile Glu Ile Cys Ala Tyr Ile Val	
355 360 365	
ctc att cgt cta ctg ccg ata ctt cct cct tta aaa caa aac gat cat	1152
Leu Ile Arg Leu Leu Pro Ile Leu Pro Pro Leu Lys Gln Asn Asp His	
370 375 380	
aat cgt cat gag gcg agc aaa gca tga	1179
Asn Arg His Glu Ala Ser Lys Ala *	
385 390	

<210> 205

<211> 987

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(987)

<400> 205
 gtg aac aga cgt aat ttt att aaa gca gcc tcc tgc ggg gca ttg ctg 48
 Met Asn Arg Arg Asn Phe Ile Lys Ala Ala Ser Cys Gly Ala Leu Leu
 1 5 10 15

acg ggc gcg ctg ccg tct gtc agt cat gcg gct gct gaa aac cgc ccg 96
 Thr Gly Ala Leu Pro Ser Val Ser His Ala Ala Ala Glu Asn Arg Pro
 20 25 30

cca att ccg gga tcg ctg ggg atg ttg tac gac tcg acc ttg tgc gta 144
 Pro Ile Pro Gly Ser Leu Gly Met Leu Tyr Asp Ser Thr Leu Cys Val
 35 40 45

ggc tgc cag gct tgc gtc acc aag tgt cag gat atc aat ttc cct gaa 192
 Gly Cys Gln Ala Cys Val Thr Lys Cys Gln Asp Ile Asn Phe Pro Glu
 50 55 60

cgt aac ccg caa ggg gaa cag acc tgg tcg aac aac gac aaa ctg tcg 240
 Arg Asn Pro Gln Gly Glu Gln Thr Trp Ser Asn Asn Asp Lys Leu Ser
 65 70 75 80

ccg tat acc aat aac atc att cag gtg tgg acc agc ggc aca ggg gtc 288
 Pro Tyr Thr Asn Asn Ile Ile Gln Val Trp Thr Ser Gly Thr Gly Val
 85 90 95

aac aaa gac cag gag gag aac ggc tac gcg tac att aag aaa cag tgt 336
 Asn Lys Asp Gln Glu Glu Asn Gly Tyr Ala Tyr Ile Lys Lys Gln Cys
 100 105 110

atg cac tgc gtc gat ccg aac tgt gtc tct gtg tgc ccg gtc tct gca 384
 Met His Cys Val Asp Pro Asn Cys Val Ser Val Cys Pro Val Ser Ala
 115 120 125

ctg aaa aaa gat ccg aaa acc ggc att gtc cat tac gac aaa gat gtg 432
 Leu Lys Lys Asp Pro Lys Thr Gly Ile Val His Tyr Asp Lys Asp Val
 130 135 140

tgc acc ggc tgc cgt tac tgc atg gtc gcc tgt ccg tac aac gtg ccg 480
 Cys Thr Gly Cys Arg Tyr Cys Met Val Ala Cys Pro Tyr Asn Val Pro
 145 150 155 160

aag tac gac tac aac aac ccg ttt ggt gcg ctg cat aag tgc gag ctg 528
 Lys Tyr Asp Tyr Asn Asn Pro Phe Gly Ala Leu His Lys Cys Glu Leu
 165 170 175

tgc aac cag aaa ggt gtg gaa cgt ctc gat aaa ggc ggt cta cct ggc 576
 Cys Asn Gln Lys Gly Val Glu Arg Leu Asp Lys Gly Gly Leu Pro Gly
 180 185 190

tgc gta gaa gtg tgc ccg gcg ggc gcg gtg att ttc ggt acg cgt gaa 624
 Cys Val Glu Val Cys Pro Ala Gly Ala Val Ile Phe Gly Thr Arg Glu
 195 200 205

gag ctg atg gcg gag gcg aaa aaa cgt ctg gcg ctg aag cct ggc agc 672
 Glu Leu Met Ala Glu Ala Lys Lys Arg Leu Ala Leu Lys Pro Gly Ser
 210 215 220

gaa tac cac tat ccg cgt cag acg ctg aaa tct ggc gac act tac ctg 720
 Glu Tyr His Tyr Pro Arg Gln Thr Leu Lys Ser Gly Asp Thr Tyr Leu

225	230	235	240	
cat acg gtg ccg aaa tat tat ccg cat ctg tac ggc gag aaa gag ggc				768
His Thr Val Pro Lys Tyr Tyr Pro His Leu Tyr Gly Glu Lys Glu Gly				
245		250	255	
ggc ggt act cag gtt ctg gta ctg acg ggt gtg cct tat gaa aat ctc				816
Gly Gly Thr Gln Val Leu Val Leu Thr Gly Val Pro Tyr Glu Asn Leu				
260		265	270	
gac ctg ccg aaa ctg gac gat ctt tct acc ggt gcg cgt tcc gaa aat				864
Asp Leu Pro Lys Leu Asp Asp Leu Ser Thr Gly Ala Arg Ser Glu Asn				
275		280	285	
att caa cac acc ctg tat aaa ggc atg atg cta cca ctg gct gtg ctg				912
Ile Gln His Thr Leu Tyr Lys Gly Met Met Leu Pro Leu Ala Val Leu				
290		295	300	
gcg ggc tta acc gtg ctg gtt cgt cgc aac acc aaa aac gac cat cac				960
Ala Gly Leu Thr Val Leu Val Arg Arg Asn Thr Lys Asn Asp His His				
305		310	315	320
gac gga gga gac gat cat gag tca tga				987
Asp Gly Gly Asp Asp His Glu Ser *				
325				
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Met Leu Gln Cys Gly Ala Lys Asn Val Asn Pro Leu Glu Arg Phe Val				
1	5	10	15	
tcg tcg ttg ccc gtt gct gcc gtc tta cct gaa tta ctt acc gct ctc				96
Ser Ser Leu Pro Val Ala Ala Val Leu Pro Glu Leu Leu Thr Ala Leu				
20		25	30	
gat tgt gcg ccg cag gta tta tta agt gcg ccg acc ggg gcc ggg aaa				144
Asp Cys Ala Pro Gln Val Leu Leu Ser Ala Pro Thr Gly Ala Gly Lys				
35		40	45	
tca acc tgg ctg ccg ctg caa ctg ctg gcg cat ccc ggc att aac ggg				192
Ser Thr Trp Leu Pro Leu Gln Leu Leu Ala His Pro Gly Ile Asn Gly				
50		55	60	
aaa att atc ctg ctg gag ccg cgt cgt ctg gcg gcg cgt aac gtc gcg				240
Lys Ile Ile Leu Leu Glu Pro Arg Arg Leu Ala Ala Arg Asn Val Ala				
65		70	75	80
caa cgg ctg gcg gag ctg ctt aac gaa aag cca ggc gat acc gtt ggc				288
Gln Arg Leu Ala Glu Leu Leu Asn Glu Lys Pro Gly Asp Thr Val Gly				
85		90	95	

tac cgg atg cgt gcg caa aac tgc gtc ggg ccg aat acc cgc ctg gaa Tyr Arg Met Arg Ala Gln Asn Cys Val Gly Pro Asn Thr Arg Leu Glu 100 105 110	336
gtg gtt acc gaa ggc gtg ctg acg cgc atg atc cag cgt gac ccg gaa Val Val Thr Glu Gly Val Leu Thr Arg Met Ile Gln Arg Asp Pro Glu 115 120 125	384
ctg agc ggt gtt gga ctg gtg atc ctt gat gaa ttt cat gag cgc agc Leu Ser Gly Val Gly Leu Val Ile Leu Asp Glu Phe His Glu Arg Ser 130 135 140	432
ttg cag gcg gat ttg gcg ttg gcg ctg tta ctc gat gtg caa caa ggt Leu Gln Ala Asp Leu Ala Leu Ala Leu Leu Asp Val Gln Gln Gly 145 150 155 160	480
ctg cgt gat gac ctt aaa ctg ctg att atg tgc gct acc ctg gac aac Leu Arg Asp Asp Leu Lys Leu Leu Ile Met Ser Ala Thr Leu Asp Asn 165 170 175	528
gac cgc ttg cag caa atg ctg cca gaa gcg cct gtc gtc atc tca gaa Asp Arg Leu Gln Gln Met Leu Pro Glu Ala Pro Val Val Ile Ser Glu 180 185 190	576
ggg cgc tgc ttt ccg gtt gaa cgc cgt tat tta ccg ctg ccc gcg cat Gly Arg Ser Phe Pro Val Glu Arg Arg Tyr Leu Pro Leu Pro Ala His 195 200 205	624
cag cgt ttt gac gat gcc gtt gcg gta gcc acc gct gaa atg ctg cgt Gln Arg Phe Asp Asp Ala Val Ala Val Ala Thr Ala Glu Met Leu Arg 210 215 220	672
cag gaa agc gga tca tta ctg tta ttt tta cct ggc gtc gga gaa att Gln Glu Ser Gly Ser Leu Leu Leu Phe Leu Pro Gly Val Gly Glu Ile 225 230 235 240	720
cag cgt gtg cag gaa caa ctg gct tgc cgc atc ggc agt gat gta ttg Gln Arg Val Gln Glu Gln Leu Ala Ser Arg Ile Gly Ser Asp Val Leu 245 250 255	768
ctc tgc ccg ctg tat ggc gcg ttg tgc ctg aac gat cag cga aaa gcg Leu Cys Pro Leu Tyr Gly Ala Leu Ser Leu Asn Asp Gln Arg Lys Ala 260 265 270	816
atc ctc ccg gca ccg caa ggg atg cgc aaa gtg gtg ctg gcg acc aat Ile Leu Pro Ala Pro Gln Gly Met Arg Lys Val Val Leu Ala Thr Asn 275 280 285	864
att gct gaa acc agt tta acc att gaa ggt att cgt ctg gtg gtg gat Ile Ala Glu Thr Ser Leu Thr Ile Glu Gly Ile Arg Leu Val Val Asp 290 295 300	912
tgt gcc cag gag cgt gtg gcg cgt ttt gat ccg cgc acg ggg ctt acg Cys Ala Gln Glu Arg Val Ala Arg Phe Asp Pro Arg Thr Gly Leu Thr 305 310 315 320	960
cga ctg att act caa cgc gtt agc cag gca tcc atg acg cag cgt gcc Arg Leu Ile Thr Gln Arg Val Ser Gln Ala Ser Met Thr Gln Arg Ala 325 330 335	1008

ggg cgc gcc ggg cgt ctg gag ccg ggt atc agc ctg cat tta atc gcc Gly Arg Ala Gly Arg Leu Glu Pro Gly Ile Ser Leu His Leu Ile Ala 340 345 350	1056
aaa gaa caa gca gaa cgc gcc gcg gcg caa agt gaa ccg gag atc tta Lys Glu Gln Ala Glu Arg Ala Ala Gln Ser Glu Pro Glu Ile Leu 355 360 365	1104
caa agc gat ctt tcc ggt ttg ctg atg gaa tta ctg caa tgg gga tgc Gln Ser Asp Leu Ser Gly Leu Leu Met Glu Leu Leu Gln Trp Gly Cys 370 375 380	1152
agc gat ccg gcg cag atg agc tgg ctg gat caa ccg cca gta gtg aat Ser Asp Pro Ala Gln Met Ser Trp Leu Asp Gln Pro Pro Val Val Asn 385 390 395 400	1200
cta ctg gcc gcg aaa cgt ctg tta caa atg ctg ggg gca ctg gag ggt Leu Leu Ala Ala Lys Arg Leu Leu Gln Met Leu Gly Ala Leu Glu Gly 405 410 415	1248
gaa ccg ctt agt gcg caa ggg caa aaa atg gca gcg ctg ggt aac gat Glu Arg Leu Ser Ala Gln Gly Gln Lys Met Ala Ala Leu Gly Asn Asp 420 425 430	1296
ccg cgt tta gcg gca atg ctg gtt agc gcg aag aac gac gac gaa gct Pro Arg Leu Ala Ala Met Leu Val Ser Ala Lys Asn Asp Asp Glu Ala 435 440 445	1344
gct acc gcg gca aaa att gcc gcc att ctc gaa gag ccg cca cgg atg Ala Thr Ala Ala Lys Ile Ala Ala Ile Leu Glu Glu Pro Pro Arg Met 450 455 460	1392
ggc aat agt gac ctg ggc gtg gcg ttt tcg cgc aat caa cca gcc tgg Gly Asn Ser Asp Leu Gly Val Ala Phe Ser Arg Asn Gln Pro Ala Trp 465 470 475 480	1440
cag caa cgt agt cag caa ctg tta aaa cgc tta aac gta cgt ggc ggt Gln Gln Arg Ser Gln Gln Leu Leu Lys Arg Leu Asn Val Arg Gly Gly 485 490 495	1488
gag gca gac agt tcg ctt atc gcg ccg cta ctt gcc ggg gcg ttt gcc Glu Ala Asp Ser Ser Leu Ile Ala Pro Leu Leu Ala Gly Ala Phe Ala 500 505 510	1536
gat cgc att gct cgt cgc cgt ggg caa gat gga cgc tat caa ctg gca Asp Arg Ile Ala Arg Arg Arg Gly Gln Asp Gly Arg Tyr Gln Leu Ala 515 520 525	1584
aac ggc atg gga gcg atg ctc gat gcc aac gac gcg cta agc cgc cac Asn Gly Met Gly Ala Met Leu Asp Ala Asn Asp Ala Leu Ser Arg His 530 535 540	1632
gaa tgg ttg atc gca ccg tta tta ttg cag ggc agc gcc tcg ccg gat Glu Trp Leu Ile Ala Pro Leu Leu Leu Gln Gly Ser Ala Ser Pro Asp 545 550 555 560	1680
gcg cgg att tta ctg gcg ctg ctg gtc gat att gat gag tta gta caa Ala Arg Ile Leu Leu Ala Leu Leu Val Asp Ile Asp Glu Leu Val Gln 565 570 575	1728

cgc tgc ccg cag ctg gta cag cag tct gac act gtg gag tgg gat gac Arg Cys Pro Gln Leu Val Gln Gln Ser Asp Thr Val Glu Trp Asp Asp 580 585 590	1776
gcg caa ggt acg ctg aaa gcc tgg cgt cgg cta caa atc ggt cag ttg Ala Gln Gly Thr Leu Lys Ala Trp Arg Arg Leu Gln Ile Gly Gln Leu 595 600 605	1824
acg gtg aaa gtg cag ccg ctg gcg aaa ccg tca gaa gac gag ttg cat Thr Val Lys Val Gln Pro Leu Ala Lys Pro Ser Glu Asp Glu Leu His 610 615 620	1872
cag gcg atg ctt aat ggc atc cgt gat aaa ggt tta agc gtg ctc aac Gln Ala Met Leu Asn Gly Ile Arg Asp Lys Gly Leu Ser Val Leu Asn 625 630 635 640	1920
tgg acg gcg gaa gcg gaa cag cta cgc ttg cgt ttg tta tgc gcc gca Trp Thr Ala Glu Ala Glu Gln Leu Arg Leu Arg Leu Leu Cys Ala Ala 645 650 655	1968
aag tgg ttg ccg gaa tat gac tgg cca gcg gtt gat gat gaa agt tta Lys Trp Leu Pro Glu Tyr Asp Trp Pro Ala Val Asp Asp Glu Ser Leu 660 665 670	2016
ttg gca gcg ctg gaa acg tgg ctg ctg cca cat atg act ggc gta cat Leu Ala Ala Leu Glu Thr Trp Leu Leu Pro His Met Thr Gly Val His 675 680 685	2064
tca cta cgc ggc ctg aaa tca ctc gac att tat cag gca cta cgc gga Ser Leu Arg Gly Leu Lys Ser Leu Asp Ile Tyr Gln Ala Leu Arg Gly 690 695 700	2112
tta ctt gat tgg gga atg cag caa cgt ctg gat agt gaa ttg cct gcg Leu Leu Asp Trp Gly Met Gln Gln Arg Leu Asp Ser Glu Leu Pro Ala 705 710 715 720	2160
cat tac act gtg ccg acg gga agc cgg atc gcc att cgt tat cat gaa His Tyr Thr Val Pro Thr Gly Ser Arg Ile Ala Ile Arg Tyr His Glu 725 730 735	2208
gat aac ccg ccc gcg ctg gcg gtg aga atg caa gag atg ttt ggc gag Asp Asn Pro Pro Ala Leu Ala Val Arg Met Gln Glu Met Phe Gly Glu 740 745 750	2256
gcc acc aat ccg acg atc gcc cag ggg cgc gtg ccg ctg gtg ctg gag Ala Thr Asn Pro Thr Ile Ala Gln Gly Arg Val Pro Leu Val Leu Glu 755 760 765	2304
ttg ctt tca cct gcc caa agg cca tta caa atc aca cga gat ttg agc Leu Leu Ser Pro Ala Gln Arg Pro Leu Gln Ile Thr Arg Asp Leu Ser 770 775 780	2352
gac ttc tgg aaa gga gcg tac cgt gag gtg caa aaa gag atg aaa ggg Asp Phe Trp Lys Gly Ala Tyr Arg Glu Val Gln Lys Glu Met Lys Gly 785 790 795 800	2400
cgt tat ccc aaa cat gtc tgg ccg gac gac ccg gca aat act gca ccg Arg Tyr Pro Lys His Val Trp Pro Asp Asp Pro Ala Asn Thr Ala Pro 805 810 815	2448

acg cga cgg acg aaa aag tat tcg taa
 Thr Arg Arg Thr Lys Lys Tyr Ser *
 820

2475

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 gtc agt ggc aca tct ttg atc tcc tct ctg tat ggt gat tcg ctt tcc 96
 Val Ser Gly Thr Ser Leu Ile Ser Ser Leu Tyr Gly Asp Ser Leu Ser
 20 25 30
 cat cgt ggt ggt gaa atc tgg ttg ggt agt ctg gct gct ttg ctg gaa 144
 His Arg Gly Gly Glu Ile Trp Leu Gly Ser Leu Ala Ala Leu Leu Glu
 35 40 45
 ggg ctg gga ttt ggt gag cgt ttc gtg cgc acc gct ttg ttt cgt ctt 192
 Gly Leu Gly Phe Gly Glu Arg Phe Val Arg Thr Ala Leu Phe Arg Leu
 50 55 60
 aat aaa gaa ggc tgg ctg gat gtt tcc cgc atc ggg cga cgc agt ttc 240
 Asn Lys Glu Gly Trp Leu Asp Val Ser Arg Ile Gly Arg Arg Ser Phe
 65 70 75 80
 tat agc ctc agt gat aaa ggc ttg cgc ctg acg cga cgg gca gaa agt 288
 Tyr Ser Leu Ser Asp Lys Gly Leu Arg Leu Thr Arg Arg Ala Glu Ser
 85 90 95
 aaa att tat cgc gca gag caa cct gca tgg gat ggt aaa tgg ctc ctg 336
 Lys Ile Tyr Arg Ala Glu Gln Pro Ala Trp Asp Gly Lys Trp Leu Leu
 100 105 110
 ttg ctc tcg gaa ggt tta gat aaa tca acg ctg gct gat gtc aaa aag 384
 Leu Leu Ser Glu Gly Leu Asp Lys Ser Thr Leu Ala Asp Val Lys Lys
 115 120 125
 cag ttg atc tgg caa ggt ttt ggc gca ctg gca ccc agc ctg atg gca 432
 Gln Leu Ile Trp Gln Gly Phe Gly Ala Leu Ala Pro Ser Leu Met Ala
 130 135 140
 tcg ccg tcg caa aaa ctg gcc gat gta cag aca ctt ttg cat gaa gcg 480
 Ser Pro Ser Gln Lys Leu Ala Asp Val Gln Thr Leu Leu His Glu Ala
 145 150 155 160
 ggt gtg gcg gat aac gtg att tgt ttt gaa gcg caa ata cca ctg gcg 528
 Gly Val Ala Asp Asn Val Ile Cys Phe Glu Ala Gln Ile Pro Leu Ala
 165 170 175

ctt tct cgc gca gca ctg cgt gcc aga gta gaa gag tgc tgg cat tta 576
 Leu Ser Arg Ala Ala Leu Arg Ala Arg Val Glu Glu Cys Trp His Leu
 180 185 190

act gaa caa aat gcc atg tac gaa acc ttt att cag tca ttc cgc ccg 624
 Thr Glu Gln Asn Ala Met Tyr Glu Thr Phe Ile Gln Ser Phe Arg Pro
 195 200 205

ctg gtg ccg ctt tta aaa gag gcg gca gac gag tta acc ccg gag cgg 672
 Leu Val Pro Leu Leu Lys Glu Ala Ala Asp Glu Leu Thr Pro Glu Arg
 210 215 220

gca ttt cat att cag ctt tta ctg atc cat ttt tat cgc cgt gtc gtc 720
 Ala Phe His Ile Gln Leu Leu Leu Ile His Phe Tyr Arg Arg Val Val
 225 230 235 240

ctt aaa gac cca ttg ttg ccg gag gag ttg ctt ccg gca cac tgg gca 768
 Leu Lys Asp Pro Leu Leu Pro Glu Glu Leu Leu Pro Ala His Trp Ala
 245 250 255

ggg cat acg gcg cgt cag ctg tgt atc aac att tat cag cgc gta gcg 816
 Gly His Thr Ala Arg Gln Leu Cys Ile Asn Ile Tyr Gln Arg Val Ala
 260 265 270

cct gct gct tta gcg ttc gtt agt gaa aaa ggt gaa acc tcg gtc ggt 864
 Pro Ala Ala Leu Ala Phe Val Ser Glu Lys Gly Glu Thr Ser Val Gly
 275 280 285

gaa ctg cct gcg ccg gga agc ctg tat ttt caa cgt ttt ggc ggc ttg 912
 Glu Leu Pro Ala Pro Gly Ser Leu Tyr Phe Gln Arg Phe Gly Gly Leu
 290 295 300

aat att gaa cag gag gcg tta tgc caa ttt atc aga tag 951
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 305 310 315

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 1 5 10 15

agt ttt gtc cat ccg aca gcg gta ttg atc ggc gat gtt att ctc ggc 96
 Ser Phe Val His Pro Thr Ala Val Leu Ile Gly Asp Val Ile Leu Gly
 20 25 30

aag ggc gtt tac gtt ggg cca aat gcc agc ctg cgt ggc gat ttt ggt 144
 Lys Gly Val Tyr Val Gly Pro Asn Ala Ser Leu Arg Gly Asp Phe Gly
 35 40 45

cgt atc gtg gtg aaa gat ggc gcg aac att cag gat aat tgc gtt atg 192

Arg	Ile	Val	Val	Lys	Asp	Gly	Ala	Asn	Ile	Gln	Asp	Asn	Cys	Val	Met	
50						55					60					
cac	ggt	ttt	ccc	gag	cag	gat	act	gtt	gta	gga	gaa	gat	gga	cat	att	240
His	Gly	Phe	Pro	Glu	Gln	Asp	Thr	Val	Val	Gly	Glu	Asp	Gly	His	Ile	
65					70					75					80	
ggt	cat	agc	gct	atc	ctt	cac	ggc	tgc	att	atc	cgc	cgc	aat	gca	tta	288
Gly	His	Ser	Ala	Ile	Leu	His	Gly	Cys	Ile	Ile	Arg	Arg	Asn	Ala	Leu	
				85					90					95		
gtg	gga	atg	aac	gcg	gta	gtg	atg	gac	ggg	gcg	gtg	att	ggc	gag	aac	336
Val	Gly	Met	Asn	Ala	Val	Val	Met	Asp	Gly	Ala	Val	Ile	Gly	Glu	Asn	
			100					105					110			
agc	att	gtt	ggt	gca	tcc	gca	ttt	gtg	aaa	gcc	aaa	gca	gaa	atg	cca	384
Ser	Ile	Val	Gly	Ala	Ser	Ala	Phe	Val	Lys	Ala	Lys	Ala	Glu	Met	Pro	
		115					120					125				
gct	aat	tac	ctg	att	gtc	ggc	agc	ccg	gcg	aaa	gcg	att	cgt	gaa	ctc	432
Ala	Asn	Tyr	Leu	Ile	Val	Gly	Ser	Pro	Ala	Lys	Ala	Ile	Arg	Glu	Leu	
	130					135					140					
agt	gag	cag	gag	ttg	gca	tgg	aaa	aag	cag	ggg	acg	cat	gag	tac	cag	480
Ser	Glu	Gln	Glu	Leu	Ala	Trp	Lys	Lys	Gln	Gly	Thr	His	Glu	Tyr	Gln	
145					150					155					160	
gtg	ctg	gtg	aca	cgc	tgt	aag	cag	acg	tta	cat	caa	gtc	gag	cca	ttg	528
Val	Leu	Val	Thr	Arg	Cys	Lys	Gln	Thr	Leu	His	Gln	Val	Glu	Pro	Leu	
				165					170					175		
cgg	gaa	att	gaa	cct	ggc	agg	aaa	cgc	ctg	gta	ttt	gat	gag	aat	ctg	576
Arg	Glu	Ile	Glu	Pro	Gly	Arg	Lys	Arg	Leu	Val	Phe	Asp	Glu	Asn	Leu	
			180					185					190			
cga	ccg	aaa	cag	taa												591
Arg	Pro	Lys	Gln	*												
			195													
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Met	Lys	His	Leu	Thr	Glu	Met	Val	Arg	Gln	His	Lys	Ala	Gly	Lys	Thr	
1				5				10					15			
aat	gga	att	tat	gcc	gtt	tgt	tcc	gca	cat	ccg	ctg	gtg	ctg	gaa	gct	96
Asn	Gly	Ile	Tyr	Ala	Val	Cys	Ser	Ala	His	Pro	Leu	Val	Leu	Glu	Ala	
			20					25					30			
gca	atc	cgc	tac	gcc	agt	gca	aac	caa	acg	ccg	tta	ctg	att	gaa	gca	144
Ala	Ile	Arg	Tyr	Ala	Ser	Ala	Asn	Gln	Thr	Pro	Leu	Leu	Ile	Glu	Ala	

35	40	45	
acc tcc aat cag gta gac	cag ttc ggc ggt tat	acc gga atg acg ccc	192
Thr Ser Asn Gln Val Asp	Gln Phe Gly Gly Tyr	Thr Gly Met Thr Pro	
50	55	60	
gcc gat ttt cgc ggc ttt gtt tgt cag ctc gcc gac tcg ttg aat ttc			240
Ala Asp Phe Arg Gly Phe Val Cys Gln Leu Ala Asp Ser Leu Asn Phe			
65	70	75	80
ccg cag gat gcg ttg att ctg ggt ggt gac cat ctg ggg cca aac cgc			288
Pro Gln Asp Ala Leu Ile Leu Gly Gly Asp His Leu Gly Pro Asn Arg			
85	90	95	
tgg caa aac ctg ccg gcc gct cag gca atg gcc aat gcc gat gat ttg			336
Trp Gln Asn Leu Pro Ala Ala Gln Ala Met Ala Asn Ala Asp Asp Leu			
100	105	110	
att aaa agc tac gtt gcg gca gga ttc aaa aaa atc cac ctt gat tgc			384
Ile Lys Ser Tyr Val Ala Ala Gly Phe Lys Lys Ile His Leu Asp Cys			
115	120	125	
agc atg tcc tgt cag gac gat ccg att ccc tta act gat gac atc gtg			432
Ser Met Ser Cys Gln Asp Asp Pro Ile Pro Leu Thr Asp Asp Ile Val			
130	135	140	
gct gaa cgc gcc gcc cgt ctg gcg aaa gtg gcg gaa gaa acc tgt ctt			480
Ala Glu Arg Ala Ala Arg Leu Ala Lys Val Ala Glu Glu Thr Cys Leu			
145	150	155	160
gaa cac ttt ggc gaa gcc gat ctg gag tat gtc att ggt acc gaa gtg			528
Glu His Phe Gly Glu Ala Asp Leu Glu Tyr Val Ile Gly Thr Glu Val			
165	170	175	
ccg gta cct ggc ggc gcg cat gaa acc tta agc gag ctg gcg gtc acc			576
Pro Val Pro Gly Gly Ala His Glu Thr Leu Ser Glu Leu Ala Val Thr			
180	185	190	
acg ccg gat gcc gcc cgc gcc acg ctg gaa gcc cat cgt cac gcc ttt			624
Thr Pro Asp Ala Ala Arg Ala Thr Leu Glu Ala His Arg His Ala Phe			
195	200	205	
gaa aag caa ggt ttg aat gcc atc tgg cca cgc atc att gcc ctg gtg			672
Glu Lys Gln Gly Leu Asn Ala Ile Trp Pro Arg Ile Ile Ala Leu Val			
210	215	220	
gtt caa ccc ggc gtc gaa ttc gat cac acc aac gtt att gat tat cag			720
Val Gln Pro Gly Val Glu Phe Asp His Thr Asn Val Ile Asp Tyr Gln			
225	230	235	240
ccc gcc aaa gcg agc gcc tta agc cag atg gtc gaa aac tac gaa acg			768
Pro Ala Lys Ala Ser Ala Leu Ser Gln Met Val Glu Asn Tyr Glu Thr			
245	250	255	
ctg att ttc gaa gcg cac tct acc gat tat caa acg ccg caa tcg ctg			816
Leu Ile Phe Glu Ala His Ser Thr Asp Tyr Gln Thr Pro Gln Ser Leu			
260	265	270	
cgc cag ctg gtg att gac cac ttt gcc att ctg aaa gtt ggc cca gcg			864
Arg Gln Leu Val Ile Asp His Phe Ala Ile Leu Lys Val Gly Pro Ala			

275	280	285	
ctg acc ttc gcc ctg cgt gaa gct ctg ttc tct ctg gcg gcg att gaa Leu Thr Phe Ala Leu Arg Glu Ala Leu Phe Ser Leu Ala Ala Ile Glu 290 295 300			912
gaa gaa ctg gtg cca gcg aaa gcc tgt tct ggt ctg cgt cag gtg ctg Glu Glu Leu Val Pro Ala Lys Ala Cys Ser Gly Leu Arg Gln Val Leu 305 310 315 320			960
gaa gac gtg atg ctc gac cgc ccg gaa tac tgg caa agc cac tac cac Glu Asp Val Met Leu Asp Arg Pro Glu Tyr Trp Gln Ser His Tyr His 325 330 335			1008
ggt gac ggc aac gcg cgt cgt ctg gcg cgt ggt tat agc tac tcg gat Gly Asp Gly Asn Ala Arg Arg Leu Ala Arg Gly Tyr Ser Tyr Ser Asp 340 345 350			1056
cgc gtg cgc tat tac tgg ccg gac agc cag att gat gac gct ttc gct Arg Val Arg Tyr Tyr Trp Pro Asp Ser Gln Ile Asp Asp Ala Phe Ala 355 360 365			1104
cat ctg gta cgt aat ctg gcg gat tca cca att ccg ctg ccg ctg atc His Leu Val Arg Asn Leu Ala Asp Ser Pro Ile Pro Leu Pro Leu Ile 370 375 380			1152
agc cag tat ctg ccg ctg cag tac gtg aaa gtt cgc tcc ggc gag ctg Ser Gln Tyr Leu Pro Leu Gln Tyr Val Lys Val Arg Ser Gly Glu Leu 385 390 395 400			1200
cag cca acg cca cgg gaa ctc att atc aac cat att cag gac atc ctg Gln Pro Thr Pro Arg Glu Leu Ile Ile Asn His Ile Gln Asp Ile Leu 405 410 415			1248
gcg cag tac cac aca gcc tgt gaa ggc caa taa Ala Gln Tyr His Thr Ala Cys Glu Gly Gln *			1281
420 425			
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ggt tta agc cgg att gat gaa cgc ttg att cac ggt cag gtc ggc gtt Val Leu Ser Arg Ile Asp Glu Arg Leu Ile His Gly Gln Val Gly Val 20 25 30			96
caa tgg gtc gga ttt gcg ggg gca aat ctg gtg ctg gta gcc aac gat Gln Trp Val Gly Phe Ala Gly Ala Asn Leu Val Leu Val Ala Asn Asp 35 40 45			144

gag gtt gcc gaa gat ccg gta caa caa aac ctg atg gaa atg gta ctg 192
 Glu Val Ala Glu Asp Pro Val Gln Gln Asn Leu Met Glu Met Val Leu
 50 55 60

gca gaa ggg atc gcc gta cgt ttc tgg acg ctg caa aaa gtt atc gac 240
 Ala Glu Gly Ile Ala Val Arg Phe Trp Thr Leu Gln Lys Val Ile Asp
 65 70 75 80

aac att cat cgc gcc gcc gat cga cag aaa atc ctg ctg gtt tgt aaa 288
 Asn Ile His Arg Ala Ala Asp Arg Gln Lys Ile Leu Leu Val Cys Lys
 85 90 95

aca ccc gcc gat ttc ctg acg ctg gtg aaa ggt ggc gtt ccg gtg aat 336
 Thr Pro Ala Asp Phe Leu Thr Leu Val Lys Gly Gly Val Pro Val Asn
 100 105 110

cgc att aac gtt ggc aat atg cac tac gcc aat ggc aaa caa caa atc 384
 Arg Ile Asn Val Gly Asn Met His Tyr Ala Asn Gly Lys Gln Gln Ile
 115 120 125

gcc aaa acg gtt tct gtg gat gcg ggc gat atc gca gca ttt aac gac 432
 Ala Lys Thr Val Ser Val Asp Ala Gly Asp Ile Ala Ala Phe Asn Asp
 130 135 140

ctg aaa acc gct ggg gtg gaa tgc ttc gtt cag ggc gtc ccg aca gag 480
 Leu Lys Thr Ala Gly Val Glu Cys Phe Val Gln Gly Val Pro Thr Glu
 145 150 155 160

cct gct gtg gac ctc ttt aaa tta ctt tga 510
 Pro Ala Val Asp Leu Phe Lys Leu Leu *
 165

<210> 211
 <211> 402
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(402)

<400> 211

atg gaa atc agc ctg ttg cag gca ttt gcg ttg ggc att atc gcc ttt 48
 Met Glu Ile Ser Leu Leu Gln Ala Phe Ala Leu Gly Ile Ile Ala Phe
 1 5 10 15

atc gct ggc ctg gat atg ttt aac ggc cta acc cat atg cac cgc ccg 96
 Ile Ala Gly Leu Asp Met Phe Asn Gly Leu Thr His Met His Arg Pro
 20 25 30

gtg gtc ctc ggc ccg ttg gtc ggg ctg gta ctt ggc gat ctg cat acc 144
 Val Val Leu Gly Pro Leu Val Gly Leu Val Leu Gly Asp Leu His Thr
 35 40 45

gga att tta acc ggc ggt acg ctg gaa ctg gtg tgg atg ggg ctg gcc 192
 Gly Ile Leu Thr Gly Gly Thr Leu Glu Leu Val Trp Met Gly Leu Ala
 50 55 60

ccg ctg gcg ggc gca cag ccg cct aac gtg att atc ggt act atc gtc 240
 Pro Leu Ala Gly Ala Gln Pro Pro Asn Val Ile Ile Gly Thr Ile Val
 65 70 75 80

ggc acg gcg ttt gcc att act act ggc gtg aaa ccc gat gtc gca gta 288
 Gly Thr Ala Phe Ala Ile Thr Thr Gly Val Lys Pro Asp Val Ala Val
 85 90 95

ggt gtc gcc gta cct ttc gct gtc gca gta cag atg ggg att acc ttc 336
 Gly Val Ala Val Pro Phe Ala Val Ala Val Gln Met Gly Ile Thr Phe
 100 105 110

ctg ttc tcg gtg atg tcc ggc gtg atg tct cgc tgc gac ctg gca aca 384
 Leu Phe Ser Val Met Ser Gly Val Met Ser Arg Cys Asp Leu Ala Thr
 115 120 125

aac ccg cgc cgc att tga 402
 Asn Pro Arg Arg Ile *
 130

<210> 212
 <211> 504
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(504)

<400> 212

gtg cat tgc tat aac ggg atg aca ggt tta cat cac cgc gaa ccg gga 48
 Met His Cys Tyr Asn Gly Met Thr Gly Leu His His Arg Glu Pro Gly
 1 5 10 15

atg gtt ggc gcg gga tta acg gac aag cgc gcc tgg ctg gaa ctg ata 96
 Met Val Gly Ala Gly Leu Thr Asp Lys Arg Ala Trp Leu Glu Leu Ile
 20 25 30

gcc gat ggt cat cat gtg cat ccg gcg gca atg tcg ctg tgt tgt tgc 144
 Ala Asp Gly His His Val His Pro Ala Ala Met Ser Leu Cys Cys Cys
 35 40 45

tgt gcg aaa gag aga atc gta ctg atc acc gac gcg atg cag gca gct 192
 Cys Ala Lys Glu Arg Ile Val Leu Ile Thr Asp Ala Met Gln Ala Ala
 50 55 60

ggg atg ccg gat ggt cgc tat acg tta tgt ggt gaa gaa gtg cag atg 240
 Gly Met Pro Asp Gly Arg Tyr Thr Leu Cys Gly Glu Glu Val Gln Met
 65 70 75 80

cac ggt ggc gtt gtc cgt acc gcg tct ggt ggg ctg gcg ggc agt acg 288
 His Gly Gly Val Val Arg Thr Ala Ser Gly Gly Leu Ala Gly Ser Thr
 85 90 95

ctg tct gtt gat gcg gca gtg cgc aat atg gtc gag ttg acg ggc gta 336
 Leu Ser Val Asp Ala Ala Val Arg Asn Met Val Glu Leu Thr Gly Val
 100 105 110

acg cct gcg gaa gcc atc cat atg gcg tcg ctg cat ccg gcg cga atg 384

Thr	Pro	Ala	Glu	Ala	Ile	His	Met	Ala	Ser	Leu	His	Pro	Ala	Arg	Met	
		115					120					125				
ctg	ggt	ggt	gat	ggt	ggt	ctg	gga	tcg	ctt	aaa	ccg	ggc	aaa	cgc	gcc	432
Leu	Gly	Val	Asp	Gly	Val	Leu	Gly	Ser	Leu	Lys	Pro	Gly	Lys	Arg	Ala	
		130					135					140				
aga	gtc	ggt	gcg	ctg	gat	agc	ggg	cta	cat	gtg	caa	caa	atc	tgg	att	480
Arg	Val	Val	Ala	Leu	Asp	Ser	Gly	Leu	His	Val	Gln	Gln	Ile	Trp	Ile	
		145			150					155					160	
cag	ggt	caa	tta	gct	tcg	ttt	tga									504
Gln	Gly	Gln	Leu	Ala	Ser	Phe	*									
				165												
<210> 213																
<211> 1155																
<212> DNA																
<213> Escherichia coli																
<220>																
<221> CDS																
<222> (1)...(1155)																
<400> 213																
atg	cca	gaa	aat	tac	acc	cct	gct	gcc	gcc	gca	acc	ggt	aca	tgg	act	48
Met	Pro	Glu	Asn	Tyr	Thr	Pro	Ala	Ala	Ala	Ala	Thr	Gly	Thr	Trp	Thr	
	1			5					10					15		
gaa	gaa	gag	atc	cgc	cat	cag	cct	cgc	gca	tgg	atc	cgt	tca	ctc	acc	96
Glu	Glu	Glu	Ile	Arg	His	Gln	Pro	Arg	Ala	Trp	Ile	Arg	Ser	Leu	Thr	
			20					25					30			
aac	atc	gac	gcg	cta	cgt	tcc	gcg	ctc	aat	aac	ttc	ctt	gaa	ccg	tta	144
Asn	Ile	Asp	Ala	Leu	Arg	Ser	Ala	Leu	Asn	Asn	Phe	Leu	Glu	Pro	Leu	
		35					40					45				
ctg	cgc	aaa	gag	aat	ctg	cgg	atc	atc	ctg	acc	gga	gcc	gga	acg	tcg	192
Leu	Arg	Lys	Glu	Asn	Leu	Arg	Ile	Ile	Leu	Thr	Gly	Ala	Gly	Thr	Ser	
	50					55					60					
gca	ttt	atc	ggt	gac	atc	atc	gcg	ccg	tgg	ctc	gcc	agc	cat	acc	ggt	240
Ala	Phe	Ile	Gly	Asp	Ile	Ile	Ala	Pro	Trp	Leu	Ala	Ser	His	Thr	Gly	
	65				70				75						80	
aaa	aac	ttc	agc	gcc	gta	ccg	acc	acc	gat	ctg	gtc	acc	aat	ccg	atg	288
Lys	Asn	Phe	Ser	Ala	Val	Pro	Thr	Thr	Asp	Leu	Val	Thr	Asn	Pro	Met	
				85					90					95		
gac	tac	ctg	aac	cca	gct	cat	ccg	ctg	ctg	ttg	atc	tcc	ttc	ggt	cga	336
Asp	Tyr	Leu	Asn	Pro	Ala	His	Pro	Leu	Leu	Leu	Ile	Ser	Phe	Gly	Arg	
			100					105					110			
tcc	ggc	aac	agc	ccg	gaa	agc	gtc	gca	gcc	gtg	gaa	ctg	gca	aat	caa	384
Ser	Gly	Asn	Ser	Pro	Glu	Ser	Val	Ala	Ala	Val	Glu	Leu	Ala	Asn	Gln	
		115					120					125				
ttt	gta	ccg	gaa	tgc	tat	cac	ctg	ccg	atc	acc	tgc	aac	gaa	gcg	ggc	432
Phe	Val	Pro	Glu	Cys	Tyr	His	Leu	Pro	Ile	Thr	Cys	Asn	Glu	Ala	Gly	

130	135	140	
gct ctt tac caa aac gcg atc aac agc gat aac gcg ttt gcc ctg ctg Ala Leu Tyr Gln Asn Ala Ile Asn Ser Asp Asn Ala Phe Ala Leu Leu 145 150 155 160			480
atg ccc gca gaa acg cac gat cgc ggc ttt gcg atg acc agc agc att Met Pro Ala Glu Thr His Asp Arg Gly Phe Ala Met Thr Ser Ser Ile 165 170 175			528
acc acc atg atg gcc agc tgc ctc gcg gtt ttc gca cct gag acg atc Thr Thr Met Met Ala Ser Cys Leu Ala Val Phe Ala Pro Glu Thr Ile 180 185 190			576
aac agc caa acc ttc cgc gac gtg gcg gat cgt tgc cag gcg atc ctg Asn Ser Gln Thr Phe Arg Asp Val Ala Asp Arg Cys Gln Ala Ile Leu 195 200 205			624
acc tca ctg ggc gat ttc agc gaa ggt gtg ttt ggt tac gca ccg tgg Thr Ser Leu Gly Asp Phe Ser Glu Gly Val Phe Gly Tyr Ala Pro Trp 210 215 220			672
aaa cgg atc gtt tat ctc ggt agc ggt ggc tta cag ggc gca gca cgc Lys Arg Ile Val Tyr Leu Gly Ser Gly Gly Leu Gln Gly Ala Ala Arg 225 230 235 240			720
gag tcg gcg ctg aaa gtg ctg gaa ctg acg gcg ggt aaa ctg gcg gcc Glu Ser Ala Leu Lys Val Leu Glu Leu Thr Ala Gly Lys Leu Ala Ala 245 250 255			768
ttt tat gat tct cca acc gga ttc cgt cat gga cca aaa tcg ctg gtc Phe Tyr Asp Ser Pro Thr Gly Phe Arg His Gly Pro Lys Ser Leu Val 260 265 270			816
gat gac gaa acg ctg gtg gtg gta ttt gtc tcc agc cac cct tac acc Asp Asp Glu Thr Leu Val Val Val Phe Val Ser Ser His Pro Tyr Thr 275 280 285			864
cgt cag tat gat ctt gat ctg ctg gct gaa ctt cgc cgt gac aac cag Arg Gln Tyr Asp Leu Asp Leu Leu Ala Glu Leu Arg Arg Asp Asn Gln 290 295 300			912
gca atg cgt gta atc gcc atc gcc gcg gaa agc agc gac atc gtc gct Ala Met Arg Val Ile Ala Ile Ala Ala Glu Ser Ser Asp Ile Val Ala 305 310 315 320			960
gcc ggt cca cat atc atc ctg cca ccg tca cgt cac ttt atc gac gtt Ala Gly Pro His Ile Ile Leu Pro Pro Ser Arg His Phe Ile Asp Val 325 330 335			1008
gag cag gca ttt tgc ttc ctg atg tac gcc cag acg ttt gca ctg atg Glu Gln Ala Phe Cys Phe Leu Met Tyr Ala Gln Thr Phe Ala Leu Met 340 345 350			1056
cag tcg ctg cac atg ggc aat acg ccg gat acc cca tca gcc agt ggc Gln Ser Leu His Met Gly Asn Thr Pro Asp Thr Pro Ser Ala Ser Gly 355 360 365			1104
acc gtt aac cgc gtg gtg caa ggc gta atc att cat ccg tgg cag gca Thr Val Asn Arg Val Val Gln Gly Val Ile Ile His Pro Trp Gln Ala			1152

370 375 380

taa 1155
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<210> 214
<211> 861
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(861)

<400> 214

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Met Ser Ile Ile Ser Thr Lys Tyr Leu Leu Gln Asp Ala Gln Ala Asn	
1 5 10 15	
ggc tac gcg gtg cct gct ttt aac att cat aac gcc gag acg atc caa	96
Gly Tyr Ala Val Pro Ala Phe Asn Ile His Asn Ala Glu Thr Ile Gln	
20 25 30	
gcg atc ctc gaa gtg tgc agt gaa atg cga tcg ccg gtg atc ctc gcc	144
Ala Ile Leu Glu Val Cys Ser Glu Met Arg Ser Pro Val Ile Leu Ala	
35 40 45	
gga acg ccg ggg acc ttt aaa cac atc gcg ctg gaa gag atc tac gcc	192
Gly Thr Pro Gly Thr Phe Lys His Ile Ala Leu Glu Glu Ile Tyr Ala	
50 55 60	
ctg tgt agc gcc tat tcc aca acc tac aac atg cca ctg gcg ctg cat	240
Leu Cys Ser Ala Tyr Ser Thr Thr Tyr Asn Met Pro Leu Ala Leu His	
65 70 75 80	
ctc gac cac cac gaa tcg ctg gat gat att cgc cgt aaa gtc cac gca	288
Leu Asp His His Glu Ser Leu Asp Asp Ile Arg Arg Lys Val His Ala	
85 90 95	
ggt gtg cgc agt gcg atg atc gac ggc agc cac ttc ccg ttt gcc gag	336
Gly Val Arg Ser Ala Met Ile Asp Gly Ser His Phe Pro Phe Ala Glu	
100 105 110	
aac gtg aag ctg gtg aaa tcg gtt gtt gac ttc tgc cac tca caa gat	384
Asn Val Lys Leu Val Lys Ser Val Val Asp Phe Cys His Ser Gln Asp	
115 120 125	
tgc agc gtg gaa gca gaa ctg ggc cgc ctg ggc ggt gtt gaa gat gac	432
Cys Ser Val Glu Ala Glu Leu Gly Arg Leu Gly Gly Val Glu Asp Asp	
130 135 140	
atg agc gtt gac gcc gaa agt gca ttc ctg acc gat cca caa gaa gct	480
Met Ser Val Asp Ala Glu Ser Ala Phe Leu Thr Asp Pro Gln Glu Ala	
145 150 155 160	
aaa cgc ttt gtc gaa ctg act ggc gtc gac agc ctg gcg gta gcg att	528
Lys Arg Phe Val Glu Leu Thr Gly Val Asp Ser Leu Ala Val Ala Ile	
165 170 175	

ggt acg gcg cac ggc tta tac agc aaa acg ccg aag att gat ttc cag 576
 Gly Thr Ala His Gly Leu Tyr Ser Lys Thr Pro Lys Ile Asp Phe Gln
 180 185 190
 cgg ctg gcg gaa att cgt gaa gtg gtg gat gtt cct ctg gtg ctg cat 624
 Arg Leu Ala Glu Ile Arg Glu Val Val Asp Val Pro Leu Val Leu His
 195 200 205
 ggt gcc agc gat gtt ccg gat gaa ttt gtc cgt cgc act att gaa ctt 672
 Gly Ala Ser Asp Val Pro Asp Glu Phe Val Arg Arg Thr Ile Glu Leu
 210 215 220
 ggc gtc aca aaa gtg aac gtt gcc aca gaa tta aaa ata gcc ttc gct 720
 Gly Val Thr Lys Val Asn Val Ala Thr Glu Leu Lys Ile Ala Phe Ala
 225 230 235 240
 ggc gcg gtt aaa gcc tgg ttt gcg gaa aat ccg cag ggt aat gat cct 768
 Gly Ala Val Lys Ala Trp Phe Ala Glu Asn Pro Gln Gly Asn Asp Pro
 245 250 255
 cgt tat tat atg cgc gtc gga atg gat gcg atg aaa gaa gtt gtc aga 816
 Arg Tyr Tyr Met Arg Val Gly Met Asp Ala Met Lys Glu Val Val Arg
 260 265 270
 aat aaa att aat gtc tgt ggt tca gcg aat cga att tca gca taa 861
 Asn Lys Ile Asn Val Cys Gly Ser Ala Asn Arg Ile Ser Ala *
 275 280 285

<210> 215

<211> 357

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(357)

<400> 215

gtg gcc cgt ata gca ggc att aac att cct gat cat aag cat gcc gta 48
 Met Ala Arg Ile Ala Gly Ile Asn Ile Pro Asp His Lys His Ala Val
 1 5 10 15
 atc gca tta act tcg att tat ggc gtc ggc aag acc cgt tct aaa gcc 96
 Ile Ala Leu Thr Ser Ile Tyr Gly Val Gly Lys Thr Arg Ser Lys Ala
 20 25 30
 atc ctg gct gca gcg ggt atc gct gaa gat gtt aag atc agt gag ctg 144
 Ile Leu Ala Ala Ala Gly Ile Ala Glu Asp Val Lys Ile Ser Glu Leu
 35 40 45
 tct gaa gga caa atc gac acg ctg cgt gac gaa gtt gcc aaa ttt gtc 192
 Ser Glu Gly Gln Ile Asp Thr Leu Arg Asp Glu Val Ala Lys Phe Val
 50 55 60
 gtt gaa ggt gat ctg cgc cgt gaa atc agc atg agc atc aag cgc ctg 240
 Val Glu Gly Asp Leu Arg Arg Glu Ile Ser Met Ser Ile Lys Arg Leu
 65 70 75 80

```

atg gat ctt ggt tgc tat cgc ggt ttg cgt cat cgt cgt ggt ctc ccg      288
Met Asp Leu Gly Cys Tyr Arg Gly Leu Arg His Arg Arg Gly Leu Pro
      85                      90                      95

gtt cgc ggt cag cgt acc aag acc aac gca cgt acc cgt aag ggt ccg      336
Val Arg Gly Gln Arg Thr Lys Thr Asn Ala Arg Thr Arg Lys Gly Pro
      100                      105                      110

cgc aaa ccg atc aag aaa taa      357
Arg Lys Pro Ile Lys Lys *
      115

<210> 216
<211> 390
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(390)

<400> 216
atg gca aag gca cca att cgt gca cgt aaa cgt gta aga aaa caa gtc      48
Met Ala Lys Ala Pro Ile Arg Ala Arg Lys Arg Val Arg Lys Gln Val
      1                      5                      10                      15

tct gac ggc gtg gct cat atc cat gct tct ttc aac aac acc atc gtg      96
Ser Asp Gly Val Ala His Ile His Ala Ser Phe Asn Asn Thr Ile Val
      20                      25                      30

act atc act gat cgt cag ggt aac gcg ttg ggt tgg gca aca gcc ggt      144
Thr Ile Thr Asp Arg Gln Gly Asn Ala Leu Gly Trp Ala Thr Ala Gly
      35                      40                      45

ggt tcc ggt ttc cgt ggt tct cgc aaa tcc act ccg ttt gca gct cag      192
Gly Ser Gly Phe Arg Gly Ser Arg Lys Ser Thr Pro Phe Ala Ala Gln
      50                      55                      60

gtt gca gca gag cgt tgc gct gac gcc gtg aaa gaa tac ggc atc aag      240
Val Ala Ala Glu Arg Cys Ala Asp Ala Val Lys Glu Tyr Gly Ile Lys
      65                      70                      75                      80

aat ctg gaa gtt atg gtt aaa ggt ccg ggt cca ggc cgc gaa tct act      288
Asn Leu Glu Val Met Val Lys Gly Pro Gly Pro Gly Arg Glu Ser Thr
      85                      90                      95

att cgt gct ctg aac gcc gca ggt ttc cgc atc act aac att act gat      336
Ile Arg Ala Leu Asn Ala Ala Gly Phe Arg Ile Thr Asn Ile Thr Asp
      100                      105                      110

gtg act ccg atc cct cat aac ggt tgt cgt ccg ccg aaa aaa cgt cgc      384
Val Thr Pro Ile Pro His Asn Gly Cys Arg Pro Pro Lys Lys Arg Arg
      115                      120                      125

gta taa      390
Val *

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<210> 217
 <211> 621
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(621)

<400> 217
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 Met Ala Arg Tyr Leu Gly Pro Lys Leu Lys Leu Ser Arg Arg Glu Gly
 1 5 10 15
 acc gac tta ttc ctt aag tct ggc gtt cgc gcg atc gat acc aag tgt 96
 Thr Asp Leu Phe Leu Lys Ser Gly Val Arg Ala Ile Asp Thr Lys Cys
 20 25 30
 aaa att gaa caa gct cct ggc cag cac ggt gcg cgt aaa ccg cgt ctg 144
 Lys Ile Glu Gln Ala Pro Gly Gln His Gly Ala Arg Lys Pro Arg Leu
 35 40 45
 tct gac tat ggt gtg cag ttg cgt gaa aag caa aaa gtt cgc cgt atc 192
 Ser Asp Tyr Gly Val Gln Leu Arg Glu Lys Gln Lys Val Arg Arg Ile
 50 55 60
 tat ggt gtg ctg gag cgt cag ttc cgt aac tac tac aaa gaa gca gca 240
 Tyr Gly Val Leu Glu Arg Gln Phe Arg Asn Tyr Tyr Lys Glu Ala Ala
 65 70 75 80
 cgt ctg aaa ggc aac acc ggt gaa aac ctg ttg gct ctg ctg gaa ggt 288
 Arg Leu Lys Gly Asn Thr Gly Glu Asn Leu Leu Ala Leu Leu Glu Gly
 85 90 95
 cgt ctg gac aac gtt gta tac cgt atg ggc ttc ggt gcc act cgt gca 336
 Arg Leu Asp Asn Val Val Tyr Arg Met Gly Phe Gly Ala Thr Arg Ala
 100 105 110
 gaa gca cgt cag ctg gtt agc cat aaa gca att atg gta aac ggt cgt 384
 Glu Ala Arg Gln Leu Val Ser His Lys Ala Ile Met Val Asn Gly Arg
 115 120 125
 gtt gtt aac atc gct tct tat cag gtt agt ccg aat gac gtt gta agc 432
 Val Val Asn Ile Ala Ser Tyr Gln Val Ser Pro Asn Asp Val Val Ser
 130 135 140
 att cgt gag aaa gcg aag aag cag tct cgc gtg aaa gcc gct ctg gag 480
 Ile Arg Glu Lys Ala Lys Lys Gln Ser Arg Val Lys Ala Ala Leu Glu
 145 150 155 160
 ctg gct gag cag cgt gaa aag cca acc tgg ctg gaa gtt gat gct ggc 528
 Leu Ala Glu Gln Arg Glu Lys Pro Thr Trp Leu Glu Val Asp Ala Gly
 165 170 175
 aag atg gaa ggt acg ttt aag cgt aag ccg gag cgt tct gat ctg tct 576
 Lys Met Glu Gly Thr Phe Lys Arg Lys Pro Glu Arg Ser Asp Leu Ser
 180 185 190
 gcg gac att aac gaa cac ctg atc gtc gag ctt tac tcc aag taa 621
 Ala Asp Ile Asn Glu His Leu Ile Val Glu Leu Tyr Ser Lys *

195	200	205	
<210> 218			
<211> 990			
<212> DNA			
<213> Escherichia coli			
<220>			
<221> CDS			
<222> (1)...(990)			
<400> 218			
atg cag ggt tct gtg aca gag ttt cta aaa ccg cgc ctg gtt gat atc			48
Met Gln Gly Ser Val Thr Glu Phe Leu Lys Pro Arg Leu Val Asp Ile			
1 5 10 15			
gag caa gtg agt tcg acg cac gcc aag gtg acc ctt gag cct tta gag			
Glu Gln Val Ser Ser Thr His Ala Lys Val Thr Leu Glu Pro Leu Glu			96
20 25 30			
cgt ggc ttt ggc cat act ctg ggt aac gca ctg cgc cgt att ctg ctc			
Arg Gly Phe Gly His Thr Leu Gly Asn Ala Leu Arg Arg Ile Leu Leu			144
35 40 45			
tca tcg atg ccg ggt tgc gcg gtg acc gag gtt gag att gat ggt gta			
Ser Ser Met Pro Gly Cys Ala Val Thr Glu Val Glu Ile Asp Gly Val			192
50 55 60			
cta cat gag tac agc acc aaa gaa ggc gtt cag gaa gat atc ctg gaa			
Leu His Glu Tyr Ser Thr Lys Glu Gly Val Gln Glu Asp Ile Leu Glu			240
65 70 75 80			
atc ctg ctc aac ctg aaa ggg ctg gcg gtg aga gtt cag ggc aaa gat			
Ile Leu Leu Asn Leu Lys Gly Leu Ala Val Arg Val Gln Gly Lys Asp			288
85 90 95			
gaa gtt att ctt acc ttg aat aaa tct ggc att ggc cct gtg act gca			
Glu Val Ile Leu Thr Leu Asn Lys Ser Gly Ile Gly Pro Val Thr Ala			336
100 105 110			
gcc gat atc acc cac gac ggt gat gtc gaa atc gtc aag ccg cag cac			
Ala Asp Ile Thr His Asp Gly Asp Val Glu Ile Val Lys Pro Gln His			384
115 120 125			
gtg atc tgc cac ctg acc gat gag aac gcg tct att agc atg cgt atc			
Val Ile Cys His Leu Thr Asp Glu Asn Ala Ser Ile Ser Met Arg Ile			432
130 135 140			
aaa gtt cag cgc ggt cgt ggt tat gtg ccg gct tct acc cga att cat			
Lys Val Gln Arg Gly Arg Gly Tyr Val Pro Ala Ser Thr Arg Ile His			480
145 150 155 160			
tcg gaa gaa gat gag cgc cca atc ggc cgt ctg ctg gtc gac gca tgc			
Ser Glu Glu Asp Glu Arg Pro Ile Gly Arg Leu Leu Val Asp Ala Cys			528
165 170 175			
tac agc cct gtg gag cgt att gcc tac aat gtt gaa gca gcg cgt gta			
Tyr Ser Pro Val Glu Arg Ile Ala Tyr Asn Val Glu Ala Ala Arg Val			576
180 185 190			

gaa cag cgt acc gac ctg gac aag ctg gtc atc gaa atg gaa acc aac Glu Gln Arg Thr Asp Leu Asp Lys Leu Val Ile Glu Met Glu Thr Asn 195 200 205	624
ggc aca atc gat cct gaa gag gcg att cgt cgt gcg gca acc att ctg Gly Thr Ile Asp Pro Glu Glu Ala Ile Arg Arg Ala Ala Thr Ile Leu 210 215 220	672
gct gaa caa ctg gaa gct ttc gtt gac tta cgt gat gta cgt cag cct Ala Glu Gln Leu Glu Ala Phe Val Asp Leu Arg Asp Val Arg Gln Pro 225 230 235 240	720
gaa gtg aaa gaa gag aaa cca gag ttc gat ccg atc ctg ctg cgc cct Glu Val Lys Glu Glu Lys Pro Glu Phe Asp Pro Ile Leu Leu Arg Pro 245 250 255	768
gtt gac gat ctg gaa ttg act gtc cgc tct gct aac tgc ctt aaa gca Val Asp Asp Leu Glu Leu Thr Val Arg Ser Ala Asn Cys Leu Lys Ala 260 265 270	816
gaa gct atc cac tat atc ggt gat ctg gta cag cgt acc gag gtt gag Glu Ala Ile His Tyr Ile Gly Asp Leu Val Gln Arg Thr Glu Val Glu 275 280 285	864
ctc ctt aaa acg cct aac ctt ggt aaa aaa tct ctt act gag att aaa Leu Leu Lys Thr Pro Asn Leu Gly Lys Lys Ser Leu Thr Glu Ile Lys 290 295 300	912
gac gtg ctg gct tcc cgt gga ctg tct ctg ggc atg cgc ctg gaa aac Asp Val Leu Ala Ser Arg Gly Leu Ser Leu Gly Met Arg Leu Glu Asn 305 310 315 320	960
tgg cca ccg gca agc atc gct gac gag taa Trp Pro Pro Ala Ser Ile Ala Asp Glu *	990
325	
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<211> 384	
<212> DNA	
<213> Escherichia coli	
<220>	
<221> CDS	
<222> (1)...(384)	
<400> 219	
atg cgc cat cgt aag agt ggt cgt caa ctg aac cgc aac agc agc cat Met Arg His Arg Lys Ser Gly Arg Gln Leu Asn Arg Asn Ser Ser His 1 5 10 15	48
cgc cag gct atg ttc cgc aat atg gca ggt tca ctg gtt cgt cat gaa Arg Gln Ala Met Phe Arg Asn Met Ala Gly Ser Leu Val Arg His Glu 20 25 30	96
atc atc aag acg act ctg cct aaa gcg aaa gag ctg cgc cgc gta gtt Ile Ile Lys Thr Thr Leu Pro Lys Ala Lys Glu Leu Arg Arg Val Val 35 40 45	144

gag ccg ctg att act ctt gcc aag act gat agc gtt gct aat cgt cgt	192
Glu Pro Leu Ile Thr Leu Ala Lys Thr Asp Ser Val Ala Asn Arg Arg	
50 55 60	
ctg gca ttc gcc cgt act cgt gat aac gag atc gtg gca aaa ctg ttt	240
Leu Ala Phe Ala Arg Thr Arg Asp Asn Glu Ile Val Ala Lys Leu Phe	
65 70 75 80	
aac gaa ctg ggc ccg cgt ttc gcg agc cgt gcc ggt ggt tac act cgt	288
Asn Glu Leu Gly Pro Arg Phe Ala Ser Arg Ala Gly Gly Tyr Thr Arg	
85 90 95	
att ctg aag tgt ggc ttc cgt gca ggc gac aac gcg ccg atg gct tac	336
Ile Leu Lys Cys Gly Phe Arg Ala Gly Asp Asn Ala Pro Met Ala Tyr	
100 105 110	
atc gag ctg gtt gat cgt tca gag aaa gca gaa gct gct gca gag taa	384
Ile Glu Leu Val Asp Arg Ser Glu Lys Ala Glu Ala Ala Ala Glu *	
115 120 125	
<210> 220	
<211> 732	
<212> DNA	
<213> Escherichia coli	
<220>	
<221> CDS	
<222> (1)...(732)	
<400> 220	
atg aag atg ttg cgc gat ccg ctg ttc tgg ctc att gct ctg ttt gtg	48
Met Lys Met Leu Arg Asp Pro Leu Phe Trp Leu Ile Ala Leu Phe Val	
1 5 10 15	
gcg ctg att ttc tgg ctg cct tac agc cag ccg ctg ttt gct gcc ttg	96
Ala Leu Ile Phe Trp Leu Pro Tyr Ser Gln Pro Leu Phe Ala Ala Leu	
20 25 30	
ttc cca caa ctg cca cga ccc gtt tat cag caa gaa agt ttt gca gct	144
Phe Pro Gln Leu Pro Arg Pro Val Tyr Gln Gln Glu Ser Phe Ala Ala	
35 40 45	
ctg gca ctg gct cat ttc tgg ctg gtg gga att tcg agt ttg ttt gcg	192
Leu Ala Leu Ala His Phe Trp Leu Val Gly Ile Ser Ser Leu Phe Ala	
50 55 60	
gtg atc att ggc act ggt gcc gga att gct gtc act cgc ccg tgg ggc	240
Val Ile Ile Gly Thr Gly Ala Gly Ile Ala Val Thr Arg Pro Trp Gly	
65 70 75 80	
gcg gaa ttt cgc cca ctg gtg gaa act att gcc gcc gtt gga cag act	288
Ala Glu Phe Arg Pro Leu Val Glu Thr Ile Ala Ala Val Gly Gln Thr	
85 90 95	
ttt ccg ccc gtc gca gtg ctg gcg atc gcc gtt ccg gtg atc ggc ttt	336
Phe Pro Pro Val Ala Val Leu Ala Ile Ala Val Pro Val Ile Gly Phe	
100 105 110	
ggt ctg caa cca gcg att atc gcc ttg atc ctt tac ggt gtg ctg ccc	384

Gly Leu Gln Pro Ala Ile Ile Ala Leu Ile Leu Tyr Gly Val Leu Pro
 115 120 125

gtc ctg cag gcg aca ctt gcc ggg ctg gga gcg att gat gcc agc gtg 432
 Val Leu Gln Ala Thr Leu Ala Gly Leu Gly Ala Ile Asp Ala Ser Val
 130 135 140

aca gaa gtt gcg aaa ggt atg gga atg agt cgt ggt cag cga gtg cgt 480
 Thr Glu Val Ala Lys Gly Met Gly Met Ser Arg Gly Gln Arg Val Arg
 145 150 155 160

aag gtc gag cta ccg ctg gcg gct ccg gtg att ctg gcg ggc gtg cga 528
 Lys Val Glu Leu Pro Leu Ala Ala Pro Val Ile Leu Ala Gly Val Arg
 165 170 175

act tcg gtg att atc aac att ggt acg gcg acg atc gcc tca acg gta 576
 Thr Ser Val Ile Ile Asn Ile Gly Thr Ala Thr Ile Ala Ser Thr Val
 180 185 190

ggg gcc agc acg ctg ggt acg ccc atc atc atc ggg ctt agc gga ttt 624
 Gly Ala Ser Thr Leu Gly Thr Pro Ile Ile Ile Gly Leu Ser Gly Phe
 195 200 205

aat acc gcg tat gtg atc cag ggg gcg tta ctg gtg gca ctg gcg gcg 672
 Asn Thr Ala Tyr Val Ile Gln Gly Ala Leu Leu Val Ala Leu Ala Ala
 210 215 220

atc atc gca gac cgc ctg ttt gaa agg ctg gtg cag gcg ctt agc cag 720
 Ile Ile Ala Asp Arg Leu Phe Glu Arg Leu Val Gln Ala Leu Ser Gln
 225 230 235 240

cac gca aaa taa 732
 His Ala Lys *

<210> 221
 <211> 927
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(927)

<400> 221

atg att gaa ttt agc cat gtc agc aaa ctg ttc ggc gca caa aaa gcc 48
 Met Ile Glu Phe Ser His Val Ser Lys Leu Phe Gly Ala Gln Lys Ala
 1 5 10 15

gtt aac gat ctc aat ctc aat ttt cag gaa ggg agt ttt tcg gtg ctg 96
 Val Asn Asp Leu Asn Leu Asn Phe Gln Glu Gly Ser Phe Ser Val Leu
 20 25 30

att ggc aca tct ggc tcc ggc aaa tcc acc acc ctg aaa atg att aac 144
 Ile Gly Thr Ser Gly Ser Gly Lys Ser Thr Thr Leu Lys Met Ile Asn
 35 40 45

cgc ctg gtg gag cat gac agc gga gag atc cgc ttt gcc gga gaa gaa 192
 Arg Leu Val Glu His Asp Ser Gly Glu Ile Arg Phe Ala Gly Glu Glu

50	55	60	
att cgc tcg ctg cca gta ctg gag ttg cgc cgc cgg atg ggc tat gcc Ile Arg Ser Leu Pro Val Leu Glu Leu Arg Arg Arg Met Gly Tyr Ala 65 70 75 80			240
att caa tct att ggc ctg ttc ccc cac tgg agc gtg gcg caa aac atc Ile Gln Ser Ile Gly Leu Phe Pro His Trp Ser Val Ala Gln Asn Ile 85 90 95			288
gct acc gtg ccg caa tta caa aaa tgg tcg cgg gcg cgg att gac gat Ala Thr Val Pro Gln Leu Gln Lys Trp Ser Arg Ala Arg Ile Asp Asp 100 105 110			336
cgt atc gac gaa tta atg gcg cta ctg ggg ctg gag tca aat ttg cgt Arg Ile Asp Glu Leu Met Ala Leu Gly Leu Glu Ser Asn Leu Arg 115 120 125			384
gag cgt tat ccg cat cag ctt tcc ggt ggt cag cag caa cgt gtg gga Glu Arg Tyr Pro His Gln Leu Ser Gly Gly Gln Gln Gln Arg Val Gly 130 135 140			432
gtg gcg cgt gca ctg gct gcc gat ccg caa gtc tta cta atg gat gaa Val Ala Arg Ala Leu Ala Ala Asp Pro Gln Val Leu Leu Met Asp Glu 145 150 155 160			480
cct ttt ggc gca ctg gac ccg gta acg cgc ggc gcg ttg caa caa gag Pro Phe Gly Ala Leu Asp Pro Val Thr Arg Gly Ala Leu Gln Gln Glu 165 170 175			528
atg acg cgc att cac cgt ttg ctg ggg cgt acc att gtg ctg gtc act Met Thr Arg Ile His Arg Leu Leu Gly Arg Thr Ile Val Leu Val Thr 180 185 190			576
cat gat att gat gag gcg cta ccg ctg gca gaa cat ctg gta ttg atg His Asp Ile Asp Glu Ala Leu Arg Leu Ala Glu His Leu Val Leu Met 195 200 205			624
gat cac ggt gaa gta gtg cag cag ggc aat ccg ctg acg atg ctg act Asp His Gly Glu Val Val Gln Gln Gly Asn Pro Leu Thr Met Leu Thr 210 215 220			672
cgt ccg gcg aat gat ttt gtc cgc cag ttt ttt gga cgt agt gaa ctg Arg Pro Ala Asn Asp Phe Val Arg Gln Phe Phe Gly Arg Ser Glu Leu 225 230 235 240			720
ggg gtg cgc ctg ctt tcg tta cgt agt gtg gcg gat tac gtg cgt cgc Gly Val Arg Leu Leu Ser Leu Arg Ser Val Ala Asp Tyr Val Arg Arg 245 250 255			768
gaa gaa cga gca gat ggt gag gca ctg gca gaa gag atg acg cta cgc Glu Glu Arg Ala Asp Gly Glu Ala Leu Ala Glu Glu Met Thr Leu Arg 260 265 270			816
gat gcg ctc tct ctg ttt gtt gcg cgg gga tgc gag gtg ctg ccg gtg Asp Ala Leu Ser Leu Phe Val Ala Arg Gly Cys Glu Val Leu Pro Val 275 280 285			864
gtg aac atg cag ggc cag cct tgc ggc acg ctg cat ttt cag gat ctg Val Asn Met Gln Gly Gln Pro Cys Gly Thr Leu His Phe Gln Asp Leu 290 295 300			912

290 295 300

ctg gtg gag gcg taa 927
 Leu Val Glu Ala *
 305

<210> 222
 <211> 1158
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1158)

<400> 222

gtg act tat ttc cgt att aat cct gtt ctg gcg ctg ctg ctg ttg ctg 48
 Met Thr Tyr Phe Arg Ile Asn Pro Val Leu Ala Leu Leu Leu Leu Leu
 1 5 10 15

acg gca atc gca gcg gcg ctg ccg ttt atc agt tac gcg cct aat cgt 96
 Thr Ala Ile Ala Ala Ala Leu Pro Phe Ile Ser Tyr Ala Pro Asn Arg
 20 25 30

tta gtt tcg ggt gag ggg cgt cat ctc tgg cag ctg tgg ccg caa acg 144
 Leu Val Ser Gly Glu Gly Arg His Leu Trp Gln Leu Trp Pro Gln Thr
 35 40 45

atc tgg atg ctg gtg ggc gtt ggt tgc gcc tgg ctg acg gcc tgt ttt 192
 Ile Trp Met Leu Val Gly Val Gly Cys Ala Trp Leu Thr Ala Cys Phe
 50 55 60

att ccc ggt aaa aaa ggc agc att tgt gca ctc att ctg gcg caa ttc 240
 Ile Pro Gly Lys Lys Gly Ser Ile Cys Ala Leu Ile Leu Ala Gln Phe
 65 70 75 80

gtc ttc gta ttg ctg gtg tgg gga gct gga aag gcg gcg acc caa ctg 288
 Val Phe Val Leu Leu Val Trp Gly Ala Gly Lys Ala Ala Thr Gln Leu
 85 90 95

gcg caa aat ggc agt gcg ctg gcg cgt acc agc ctc ggc agt ggt ttc 336
 Ala Gln Asn Gly Ser Ala Leu Ala Arg Thr Ser Leu Gly Ser Gly Phe
 100 105 110

tgg ctg gct gcg gcg ctg gca ttg ctg gcc tgt agc gat gcc atc cgc 384
 Trp Leu Ala Ala Ala Leu Ala Leu Leu Ala Cys Ser Asp Ala Ile Arg
 115 120 125

cga atc tcc acg cat ccg ctg tgg cgc tgg ttg ttg cat atg cag att 432
 Arg Ile Ser Thr His Pro Leu Trp Arg Trp Leu Leu His Met Gln Ile
 130 135 140

gcc att att ccg ctg tgg ttg ctg tac tcc ggc acg ctt aac gat ctc 480
 Ala Ile Ile Pro Leu Trp Leu Leu Tyr Ser Gly Thr Leu Asn Asp Leu
 145 150 155 160

tca cta atg aaa gaa tac gcc aac cgt cag gat gtg ttt gac gac gcg 528
 Ser Leu Met Lys Glu Tyr Ala Asn Arg Gln Asp Val Phe Asp Asp Ala
 165 170 175

ctg gca caa cat ctg acg ttg ctg ttt ggt gcg gtg ctg cct gcg tta Leu Ala Gln His Leu Thr Leu Leu Phe Gly Ala Val Leu Pro Ala Leu 180 185 190	576
gtg att ggt gtg ccg ttg ggc atc tgg tgc tac ttt tcc act gct cgg Val Ile Gly Val Pro Leu Gly Ile Trp Cys Tyr Phe Ser Thr Ala Arg 195 200 205	624
cag ggg gca att ttt tct ctg ctc aat gtg att cag acc gtg cct tcg Gln Gly Ala Ile Phe Ser Leu Leu Asn Val Ile Gln Thr Val Pro Ser 210 215 220	672
gtg gcg ctc ttt ggc ctg ttg att gcg ccg ctt gcc gcg ctg gtt acg Val Ala Leu Phe Gly Leu Leu Ile Ala Pro Leu Ala Ala Leu Val Thr 225 230 235 240	720
gcc ttt ccg tgg ctg ggg acg ctc ggc ata gca gga acc gga atg aca Ala Phe Pro Trp Leu Gly Thr Leu Gly Ile Ala Gly Thr Gly Met Thr 245 250 255	768
ccc gca ctg att gcg ctg gtg ctc tat gcc ttg ctg ccg ctg gtg cgc Pro Ala Leu Ile Ala Leu Val Leu Tyr Ala Leu Leu Pro Leu Val Arg 260 265 270	816
ggc gtg gta gtc ggt ttg aac cag atc ccg cgc gat gtg ctg gaa agc Gly Val Val Val Gly Leu Asn Gln Ile Pro Arg Asp Val Leu Glu Ser 275 280 285	864
gcc aga gcg atg ggg atg agc ggg gcg cag cgt ttc ctg cat gtt cag Ala Arg Ala Met Gly Met Ser Gly Ala Gln Arg Phe Leu His Val Gln 290 295 300	912
tta ccg ctg gcg tta ccg gta ttt ctg cgc agc ctg cgg gtg gtg atg Leu Pro Leu Ala Leu Pro Val Phe Leu Arg Ser Leu Arg Val Val Met 305 310 315 320	960
gtg caa act gta ggt atg gcg gtg att gcg gcg tta atc ggc gca ggc Val Gln Thr Val Gly Met Ala Val Ile Ala Ala Leu Ile Gly Ala Gly 325 330 335	1008
ggc ttt ggt gcg ctg gtt ttc cag ggg ctg cta agc agc gcc att gat Gly Phe Gly Ala Leu Val Phe Gln Gly Leu Leu Ser Ser Ala Ile Asp 340 345 350	1056
tta gtg ttg ctg ggg gtg atc ccg gta att gtt ctg gcg gtg ctt acc Leu Val Leu Leu Gly Val Ile Pro Val Ile Val Leu Ala Val Leu Thr 355 360 365	1104
gac gcg ctg ttc gat ttg ctt atc gca ctg ctg aag gtg aaa cgt aat Asp Ala Leu Phe Asp Leu Leu Ile Ala Leu Leu Lys Val Lys Arg Asn 370 375 380	1152
gat tga Asp * 385	1158

<210> 223

<211> 918

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(918)

<400> 223

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Met Pro Leu Leu Lys Leu Trp Ala Gly Ser Leu Val Met Leu Ala Ala	
1 5 10 15	
gtg agc ctg ccg cta cag gcg gct tcc ccc gtt aaa gtc ggt tca aaa	96
Val Ser Leu Pro Leu Gln Ala Ala Ser Pro Val Lys Val Gly Ser Lys	
20 25 30	
atc gat acc gaa ggt gcg cta ctc ggc aat atc att ttg cag gtg ctg	144
Ile Asp Thr Glu Gly Ala Leu Leu Gly Asn Ile Ile Leu Gln Val Leu	
35 40 45	
gaa agc cac ggc gta ccg acg gtg aat aaa gtg caa ctc gga acg act	192
Glu Ser His Gly Val Pro Thr Val Asn Lys Val Gln Leu Gly Thr Thr	
50 55 60	
cct gtg gtg cgc ggg gcg att act tcc ggt gaa ctg gat atc tat ccg	240
Pro Val Val Arg Gly Ala Ile Thr Ser Gly Glu Leu Asp Ile Tyr Pro	
65 70 75 80	
gaa tat acc ggc aat ggc gct ttc ttc ttt aaa gat gaa aac gat gca	288
Glu Tyr Thr Gly Asn Gly Ala Phe Phe Phe Lys Asp Glu Asn Asp Ala	
85 90 95	
gcg tgg aaa aac gcg cag caa ggt tac gag aaa gtc aaa aag ctc gat	336
Ala Trp Lys Asn Ala Gln Gln Gly Tyr Glu Lys Val Lys Lys Leu Asp	
100 105 110	
tcg gag cac aac aag tta atc tgg ctg acg ccc gcg cct gca aat aac	384
Ser Glu His Asn Lys Leu Ile Trp Leu Thr Pro Ala Pro Ala Asn Asn	
115 120 125	
acc tgg act atc gcc gtg cgt cag gat gtg gca gag aaa aat aaa ctc	432
Thr Trp Thr Ile Ala Val Arg Gln Asp Val Ala Glu Lys Asn Lys Leu	
130 135 140	
act tcg ctt gcc gac ctg agt cgt tat ctg caa gag ggc ggc acc ttc	480
Thr Ser Leu Ala Asp Leu Ser Arg Tyr Leu Gln Glu Gly Gly Thr Phe	
145 150 155 160	
aaa ctg gca gcc tcg gca gag ttt atc gaa cgc gcc gat gcg tta ccc	528
Lys Leu Ala Ala Ser Ala Glu Phe Ile Glu Arg Ala Asp Ala Leu Pro	
165 170 175	
gcg ttt gaa aaa gcc tat ggc ttt aag ctc ggt cag gat cag ttg ctg	576
Ala Phe Glu Lys Ala Tyr Gly Phe Lys Leu Gly Gln Asp Gln Leu Leu	
180 185 190	
tca ctg gct ggt ggc gac acg gcg gtg acg atc aaa gcc gct gcc cag	624
Ser Leu Ala Gly Gly Asp Thr Ala Val Thr Ile Lys Ala Ala Ala Gln	
195 200 205	

caa acc tct ggc gtt aat gct gca atg gct tac ggc act gac ggc ccg	672
Gln Thr Ser Gly Val Asn Ala Ala Met Ala Tyr Gly Thr Asp Gly Pro	
210 215 220	
gta gcg gcg ctg ggg ctg caa acc tta agc gat ccg caa ggt gtg caa	720
Val Ala Ala Leu Gly Leu Gln Thr Leu Ser Asp Pro Gln Gly Val Gln	
225 230 235 240	
cct atc tac gcg cct gca cca gtg gtg cgt gag tcc gtg ttg agg gag	768
Pro Ile Tyr Ala Pro Ala Pro Val Val Arg Glu Ser Val Leu Arg Glu	
245 250 255	
tat ccg caa atg gca cag tgg cta cag cca gtc ttc gcc agc ctc gat	816
Tyr Pro Gln Met Ala Gln Trp Leu Gln Pro Val Phe Ala Ser Leu Asp	
260 265 270	
gca aaa aca ttg cag caa ctg aat gcc agc att gct gtg gaa gga ctg	864
Ala Lys Thr Leu Gln Gln Leu Asn Ala Ser Ile Ala Val Glu Gly Leu	
275 280 285	
gat gcc aaa aaa qtg gct gcc gac tac ctg aaa caa aaa ggg tgg acg	912
Asp Ala Lys Lys Val Ala Ala Asp Tyr Leu Lys Gln Lys Gly Trp Thr	
290 295 300	
aag taa	918
Lys *	
305	

<210> 224
 <211> 624
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(624)

<400> 224	
atg ctc gtc tat tgg ctg gat ata gtc ggc aca gcg gta ttt gcc atc	48
Met Leu Val Tyr Trp Leu Asp Ile Val Gly Thr Ala Val Phe Ala Ile	
1 5 10 15	
tcc ggc gtt ttg tta gcc gga aaa ttg cgt atg gac cct ttt ggt gtt	96
Ser Gly Val Leu Leu Ala Gly Lys Leu Arg Met Asp Pro Phe Gly Val	
20 25 30	
ctg gta ctg ggc gtg gta acc gca gta ggc ggc ggg aca att cgc gac	144
Leu Val Leu Gly Val Val Thr Ala Val Gly Gly Gly Thr Ile Arg Asp	
35 40 45	
atg gcg ctg gat cac ggc ccg gta ttt tgg gtg aaa gat ccc acc gat	192
Met Ala Leu Asp His Gly Pro Val Phe Trp Val Lys Asp Pro Thr Asp	
50 55 60	
ctg gtc gtt gca atg gtc acc agc atg ctg acc atc gtg ctg gtg cgc	240
Leu Val Val Ala Met Val Thr Ser Met Leu Thr Ile Val Leu Val Arg	
65 70 75 80	
cag cca aga cgc tta cca aaa tgg atg ttg ccg gtg ctg gac gcc gtt	288

Gln	Pro	Arg	Arg	Leu	Pro	Lys	Trp	Met	Leu	Pro	Val	Leu	Asp	Ala	Val		
				85					90					95			
ggt	ctg	gcg	gtg	ttt	gtc	ggc	att	ggc	gtg	aat	aaa	gcc	ttt	aat	gcg		336
Gly	Leu	Ala	Val	Phe	Val	Gly	Ile	Gly	Val	Asn	Lys	Ala	Phe	Asn	Ala		
			100					105					110				
gaa	gcc	ggt	ccg	tta	atc	gcg	gtt	tgt	atg	ggc	gtc	att	act	ggc	gtt		384
Glu	Ala	Gly	Pro	Leu	Ile	Ala	Val	Cys	Met	Gly	Val	Ile	Thr	Gly	Val		
		115					120					125					
ggc	ggc	ggg	atc	att	cgt	gat	gtt	ctg	gcc	cgc	gaa	atc	ccc	atg	att		432
Gly	Gly	Gly	Ile	Ile	Arg	Asp	Val	Leu	Ala	Arg	Glu	Ile	Pro	Met	Ile		
		130				135					140						
tta	cgt	aca	gaa	atc	tac	gca	act	gcc	tgt	att	atc	ggc	ggt	att	gtc		480
Leu	Arg	Thr	Glu	Ile	Tyr	Ala	Thr	Ala	Cys	Ile	Ile	Gly	Gly	Ile	Val		
	145				150				155						160		
cac	gct	acg	gct	tat	tac	aca	ttt	tcc	gta	cca	ctg	gaa	aca	gcc	agt		528
His	Ala	Thr	Ala	Tyr	Tyr	Thr	Phe	Ser	Val	Pro	Leu	Glu	Thr	Ala	Ser		
			165					170						175			
atg	atg	ggc	atg	gtc	gtg	acg	cta	ttg	att	cgg	ctg	gcg	gct	att	cgt		576
Met	Met	Gly	Met	Val	Val	Thr	Leu	Leu	Ile	Arg	Leu	Ala	Ala	Ile	Arg		
		180						185					190				
tgg	cat	ctt	aag	cta	ccg	acg	ttt	gcg	ctg	gat	gag	aat	ggg	cgt	tga		624
Trp	His	Leu	Lys	Leu	Pro	Thr	Phe	Ala	Leu	Asp	Glu	Asn	Gly	Arg	*		
		195					200					205					

<210> 225
 <211> 801
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(801)

<400> 225																	
atg	gct	aag	tca	ctg	ttc	agg	gcg	ctg	gtc	gcc	ctg	tct	ttt	ctt	gcg		48
Met	Ala	Lys	Ser	Leu	Phe	Arg	Ala	Leu	Val	Ala	Leu	Ser	Phe	Leu	Ala		
	1				5				10					15			
cca	ctg	tgg	ctc	aac	gcc	gcg	ccg	cgc	gtc	atc	acg	ctt	tct	ccc	gcc		96
Pro	Leu	Trp	Leu	Asn	Ala	Ala	Pro	Arg	Val	Ile	Thr	Leu	Ser	Pro	Ala		
		20					25					30					
aac	act	gaa	ctt	gcc	ttt	gcc	gcc	ggg	atc	acg	ccg	gtt	ggg	gtc	agc		144
Asn	Thr	Glu	Leu	Ala	Phe	Ala	Ala	Gly	Ile	Thr	Pro	Val	Gly	Val	Ser		
		35					40					45					
agc	tat	tcc	gac	tat	cct	cca	caa	gcg	caa	aag	att	gag	cag	gtt	tcc		192
Ser	Tyr	Ser	Asp	Tyr	Pro	Pro	Gln	Ala	Gln	Lys	Ile	Glu	Gln	Val	Ser		
	50					55					60						
acc	tgg	cag	ggg	atg	aat	ctg	gaa	cgc	att	gtc	gcg	ctg	aaa	ccc	gat		240
Thr	Trp	Gln	Gly	Met	Asn	Leu	Glu	Arg	Ile	Val	Ala	Leu	Lys	Pro	Asp		

65	70	75	80	
ctg gtg att gcc tgg cgt gga ggt aat gcc gag cgg cag gtt gac cag				288
Leu Val Ile Ala Trp Arg Gly Gly Asn Ala Glu Arg Gln Val Asp Gln	85	90	95	
ctg gct tcg ctg gga ata aaa gtg atg tgg gtc gat gcg aca agc att				336
Leu Ala Ser Leu Gly Ile Lys Val Met Trp Val Asp Ala Thr Ser Ile	100	105	110	
gaa caa att gcc aat gcg tta cgt caa ctg gcc ccc tgg agt ccg caa				384
Glu Gln Ile Ala Asn Ala Leu Arg Gln Leu Ala Pro Trp Ser Pro Gln	115	120	125	
cca gac aag gcc gaa caa gcc gcg caa tcc ctg ctg gat cag tac gcg				432
Pro Asp Lys Ala Glu Gln Ala Ala Gln Ser Leu Leu Asp Gln Tyr Ala	130	135	140	
caa ttg aaa gcg caa tat gct gat aaa cct aaa aaa cgt gtt ttt ctg				480
Gln Leu Lys Ala Gln Tyr Ala Asp Lys Pro Lys Lys Arg Val Phe Leu	145	150	155	160
caa ttc ggc att aat ccg cca ttt acc agt gga aaa gag tcg att cag				528
Gln Phe Gly Ile Asn Pro Pro Phe Thr Ser Gly Lys Glu Ser Ile Gln	165	170	175	
aac cag gta ctc gaa gtt tgt ggc gga gaa aac atc ttt aaa gac agc				576
Asn Gln Val Leu Glu Val Cys Gly Gly Glu Asn Ile Phe Lys Asp Ser	180	185	190	
cgg gtt ccc tgg ccg caa gtt agc cgc gaa cag gtg tta gca cgc tcg				624
Arg Val Pro Trp Pro Gln Val Ser Arg Glu Gln Val Leu Ala Arg Ser	195	200	205	
cca cag gcg att gtc att aca ggc gga ccg gac caa att cct aaa atc				672
Pro Gln Ala Ile Val Ile Thr Gly Gly Pro Asp Gln Ile Pro Lys Ile	210	215	220	
aaa caa tac tgg ggt gaa cag ctc aaa att ccc gtt att cct ctc acg				720
Lys Gln Tyr Trp Gly Glu Gln Leu Lys Ile Pro Val Ile Pro Leu Thr	225	230	235	240
agt gac tgg ttt gaa cgt gca agc cca cgt att atc ctc gct gca caa				768
Ser Asp Trp Phe Glu Arg Ala Ser Pro Arg Ile Ile Leu Ala Ala Gln	245	250	255	
cag ctc tgt aat gcg ctt tca cag gta gat tag				801
Gln Leu Cys Asn Ala Leu Ser Gln Val Asp *	260	265		

<210> 226

<211> 699

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(699)

<400> 226
 atg aaa atc ggc atc att ggt gca atg gaa gaa gaa gtt acg ctg ctg 48
 Met Lys Ile Gly Ile Ile Gly Ala Met Glu Glu Glu Val Thr Leu Leu
 1 5 10 15

cgt gac aaa atc gaa aac cgt caa act atc agt ctc ggc ggt tgc gaa 96
 Arg Asp Lys Ile Glu Asn Arg Gln Thr Ile Ser Leu Gly Gly Cys Glu
 20 25 30

atc tat acc ggc caa ctg aat gga acc gag gtt gcg ctt ctg aaa tcg 144
 Ile Tyr Thr Gly Gln Leu Asn Gly Thr Glu Val Ala Leu Leu Lys Ser
 35 40 45

ggc atc ggt aaa gtc gct gcg gcg ctg ggt gcc act ttg ctg ttg gaa 192
 Gly Ile Gly Lys Val Ala Ala Leu Gly Ala Thr Leu Leu Leu Glu
 50 55 60

cac tgc aag cca gat gtg att att aac acc ggt tct gcc ggt ggc ctg 240
 His Cys Lys Pro Asp Val Ile Ile Asn Thr Gly Ser Ala Gly Gly Leu
 65 70 75 80

gca cca acg ttg aaa gtg ggc gat atc gtt gtc tcg gac gaa gca cgt 288
 Ala Pro Thr Leu Lys Val Gly Asp Ile Val Val Ser Asp Glu Ala Arg
 85 90 95

tat cac gac gcg gat gtc acg gca ttt ggt tat gaa tac ggt cag tta 336
 Tyr His Asp Ala Asp Val Thr Ala Phe Gly Tyr Glu Tyr Gly Gln Leu
 100 105 110

cca ggc tgt ccg gca ggc ttt aaa gct gac gat aaa ctg atc gct gcc 384
 Pro Gly Cys Pro Ala Gly Phe Lys Ala Asp Asp Lys Leu Ile Ala Ala
 115 120 125

gct gag gcc tgc att gcc gaa ctg aat ctt aac gct gta cgt ggc ctg 432
 Ala Glu Ala Cys Ile Ala Glu Leu Asn Leu Asn Ala Val Arg Gly Leu
 130 135 140

att gtt agc ggc gac gct ttc atc aac ggt tct gtt ggt ctg gcg aaa 480
 Ile Val Ser Gly Asp Ala Phe Ile Asn Gly Ser Val Gly Leu Ala Lys
 145 150 155 160

atc cgc cac aac ttc cca cag gcc att gct gta gag atg gaa gcg acg 528
 Ile Arg His Asn Phe Pro Gln Ala Ile Ala Val Glu Met Glu Ala Thr
 165 170 175

gca atc gcc cat gtc tgc cac aat ttc aac gtc ccg ttt gtt gtc gta 576
 Ala Ile Ala His Val Cys His Asn Phe Asn Val Pro Phe Val Val Val
 180 185 190

cgc gcc atc tcc gac gtg gcc gat caa cag tct cat ctt agc ttc gat 624
 Arg Ala Ile Ser Asp Val Ala Asp Gln Gln Ser His Leu Ser Phe Asp
 195 200 205

gag ttc ctg gct gtt gcc gct aaa cag tcc agc ctg atg gtt gag tca 672
 Glu Phe Leu Ala Val Ala Lys Gln Ser Ser Leu Met Val Glu Ser
 210 215 220

ctg gtg cag aaa ctt gca cat ggc taa 699
 Leu Val Gln Lys Leu Ala His Gly *
 225 230

<210> 227
 <211> 789
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(789)

<400> 227
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 Met Ile Asp Lys Ser Ala Phe Val His Pro Thr Ala Ile Val Glu Glu
 1 5 10 15
 ggc gcg tca att ggc gcg aac gca cac att ggt cct ttt tgt atc gtt 96
 Gly Ala Ser Ile Gly Ala Asn Ala His Ile Gly Pro Phe Cys Ile Val
 20 25 30
 gga ccc cat gtc gaa att ggt gag ggt acc gta ctg aaa tct cac gtt 144
 Gly Pro His Val Glu Ile Gly Glu Gly Thr Val Leu Lys Ser His Val
 35 40 45
 gtc gtg aat ggt cat act aaa att ggc cgc gat aat gag att tat cag 192
 Val Val Asn Gly His Thr Lys Ile Gly Arg Asp Asn Glu Ile Tyr Gln
 50 55 60
 ttc gcc tcc atc ggc gaa gtt aac cag gat ctg aaa tat gct ggc gaa 240
 Phe Ala Ser Ile Gly Glu Val Asn Gln Asp Leu Lys Tyr Ala Gly Glu
 65 70 75 80
 ccg acc cgt gtg gaa atc ggc gat cgt aac cgc att cgc gaa agc gtc 288
 Pro Thr Arg Val Glu Ile Gly Asp Arg Asn Arg Ile Arg Glu Ser Val
 85 90 95
 acc att cat cgt ggc aca gtc cag ggc ggt gga ttg acg aag gtg ggc 336
 Thr Ile His Arg Gly Thr Val Gln Gly Gly Gly Leu Thr Lys Val Gly
 100 105 110
 agc gac aac tta ctg atg atc aac gcg cac att gcg cac gat tgt acg 384
 Ser Asp Asn Leu Leu Met Ile Asn Ala His Ile Ala His Asp Cys Thr
 115 120 125
 gta ggt aac cgc tgt att ctc gcc aac aac gca acg ctg gcg ggt cac 432
 Val Gly Asn Arg Cys Ile Leu Ala Asn Asn Ala Thr Leu Ala Gly His
 130 135 140
 gta tcg gtt gac gac ttc gcg atc atc ggc ggc atg acc gca gtc cat 480
 Val Ser Val Asp Asp Phe Ala Ile Ile Gly Gly Met Thr Ala Val His
 145 150 155 160
 cag ttc tgc atc att ggt gcg cac gtg atg gtt ggc ggc tgc tcc ggt 528
 Gln Phe Cys Ile Ile Gly Ala His Val Met Val Gly Gly Cys Ser Gly
 165 170 175
 gtg gcg cag gac gtc cct cct tat gtc att gcg cag ggt aac cac gca 576
 Val Ala Gln Asp Val Pro Pro Tyr Val Ile Ala Gln Gly Asn His Ala
 180 185 190

acg ccg ttc ggt gtc aat atc gaa ggg ctg aag cgc cgc gga ttc agc 624
 Thr Pro Phe Gly Val Asn Ile Glu Gly Leu Lys Arg Arg Gly Phe Ser
 195 200 205

cgt gag gcg att acc gct atc cgc aat gcg tat aag ctg att tat cgt 672
 Arg Glu Ala Ile Thr Ala Ile Arg Asn Ala Tyr Lys Leu Ile Tyr Arg
 210 215 220

agc ggt aaa acg ctc gat gaa gtg aaa ccg gaa att gct gaa ctg gcg 720
 Ser Gly Lys Thr Leu Asp Glu Val Lys Pro Glu Ile Ala Glu Leu Ala
 225 230 235 240

gaa aca tat ccg gaa gtg aaa gcc ttt acc gat ttc ttt gca cgc tca 768
 Glu Thr Tyr Pro Glu Val Lys Ala Phe Thr Asp Phe Phe Ala Arg Ser
 245 250 255

acg cgc ggt ctg att cgt taa 789
 Thr Arg Gly Leu Ile Arg *
 260

<210> 228
 <211> 1149
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1149)

<400> 228
 atg act gaa cag cgt cca tta acg att gcc ctg gtc gcc gga gaa acc 48
 Met Thr Glu Gln Arg Pro Leu Thr Ile Ala Leu Val Ala Gly Glu Thr
 1 5 10 15

tcc ggc gat atc ctg ggg gcc ggt tta atc cgc gct ctg aaa gaa cat 96
 Ser Gly Asp Ile Leu Gly Ala Gly Leu Ile Arg Ala Leu Lys Glu His
 20 25 30

gtg ccc aac gcc cgc ttt gtt ggt gtt gcc ggg cca cga atg cag gct 144
 Val Pro Asn Ala Arg Phe Val Gly Val Ala Gly Pro Arg Met Gln Ala
 35 40 45

gaa ggc tgc gaa gcc tgg tac gaa atg gaa gaa ctg gcg gtg atg ggc 192
 Glu Gly Cys Glu Ala Trp Tyr Glu Met Glu Glu Leu Ala Val Met Gly
 50 55 60

att gtt gaa gtg ctc ggt cgt ctg cgt cgc tta ctg cat att cgt gcc 240
 Ile Val Glu Val Leu Gly Arg Leu Arg Arg Leu Leu His Ile Arg Ala
 65 70 75 80

gat ctg aca aag cgt ttt ggc gaa ctg aag cca gat gtt ttt gtt ggt 288
 Asp Leu Thr Lys Arg Phe Gly Glu Leu Lys Pro Asp Val Phe Val Gly
 85 90 95

att gat gcg cct gac ttc aat att act ctt gaa ggt aac ctc aaa aag 336
 Ile Asp Ala Pro Asp Phe Asn Ile Thr Leu Glu Gly Asn Leu Lys Lys
 100 105 110

cag ggt atc aaa acc att cat tac gtc agt ccg tca gtc tgg gcg tgg 384

Gln	Gly	Ile	Lys	Thr	Ile	His	Tyr	Val	Ser	Pro	Ser	Val	Trp	Ala	Trp		
		115					120					125					
cga	cag	aaa	cgt	gtt	ttc	aaa	ata	ggc	aga	gcc	acc	gat	ctg	gtg	ctc	432	
Arg	Gln	Lys	Arg	Val	Phe	Lys	Ile	Gly	Arg	Ala	Thr	Asp	Leu	Val	Leu		
	130					135					140						
gca	ttt	ctg	cct	ttc	gaa	aaa	gcg	ttt	tat	gac	aaa	tac	aac	gta	ccg	480	
Ala	Phe	Leu	Pro	Phe		Lys	Ala	Phe	Tyr	Asp	Lys	Tyr	Asn	Val	Pro		
145					150					155					160		
tgc	cgc	ttt	atc	ggg	cat	acc	atg	gct	gat	gcc	atg	cca	tta	gat	cca	528	
Cys	Arg	Phe	Ile	Gly	His	Thr	Met	Ala	Asp	Ala	Met	Pro	Leu	Asp	Pro		
				165					170					175			
gat	aaa	aat	gcc	gcc	cgt	gat	gtg	ctg	ggg	atc	cct	cac	gat	gcc	cac	576	
Asp	Lys	Asn	Ala	Ala	Arg	Asp	Val	Leu	Gly	Ile	Pro	His	Asp	Ala	His		
			180					185					190				
tgc	ctg	gcg	ttg	cta	ccg	ggg	agc	cgt	ggt	gca	gaa	gtt	gaa	atg	ctt	624	
Cys	Leu	Ala	Leu	Leu	Pro	Gly	Ser	Arg	Gly	Ala	Glu	Val	Glu	Met	Leu		
		195					200					205					
agt	gcc	gat	ttc	ctg	aaa	acg	gcc	cag	ctt	ttg	cgc	cag	aca	tat	ccg	672	
Ser	Ala	Asp	Phe	Leu	Lys	Thr	Ala	Gln	Leu	Leu	Arg	Gln	Thr	Tyr	Pro		
	210					215					220						
gat	ctc	gaa	atc	gtg	gtg	cca	ctg	gtg	aat	gcc	aaa	cgc	cgc	gag	cag	720	
Asp	Leu	Glu	Ile	Val	Pro	Leu	Val	Asn	Ala	Lys	Arg	Arg	Glu	Gln			
225					230				235					240			
ttt	gaa	cgc	atc	aaa	gct	gaa	gtc	gcg	cca	gac	ctt	tca	gtt	cat	ttg	768	
Phe	Glu	Arg	Ile	Lys	Ala	Glu	Val	Ala	Pro	Asp	Leu	Ser	Val	His	Leu		
				245					250					255			
ctg	gat	ggg	atg	ggc	cgt	gag	gcg	atg	gtc	gcc	agc	gat	gcg	gcg	cta	816	
Leu	Asp	Gly	Met	Gly	Arg	Glu	Ala	Met	Val	Ala	Ser	Asp	Ala	Ala	Leu		
			260					265					270				
ctg	gcg	tcg	ggt	acg	gca	gcc	ctg	gag	tgt	atg	ctg	gcg	aaa	tgc	ccg	864	
Leu	Ala	Ser	Gly	Thr	Ala	Ala	Leu	Glu	Cys	Met	Leu	Ala	Lys	Cys	Pro		
		275					280					285					
atg	gtg	gtg	gga	tat	cgc	atg	aag	cct	ttt	acc	ttc	tgg	ttg	gcg	aag	912	
Met	Val	Val	Gly	Tyr	Arg	Met	Lys	Pro	Phe	Thr	Phe	Trp	Leu	Ala	Lys		
	290					295					300						
cgg	ctg	gtg	aaa	act	gat	tat	gtc	tcg	ctg	cca	aat	ctg	ctg	gcg	ggc	960	
Arg	Leu	Val	Lys	Thr	Asp	Tyr	Val	Ser	Leu	Pro	Asn	Leu	Leu	Ala	Gly		
305					310					315					320		
aga	gag	tta	gtc	aaa	gaa	tta	ttg	cag	gaa	gag	tgt	gag	ccg	caa	aaa	1008	
Arg	Glu	Leu	Val	Lys	Glu	Leu	Leu	Gln	Glu	Glu	Cys	Glu	Pro	Gln	Lys		
				325					330					335			
ctg	gct	gcg	gcg	ctg	tta	ccg	ctg	ttg	gcg	aac	ggg	aaa	acc	agc	cac	1056	
Leu	Ala	Ala	Ala	Leu	Leu	Pro	Leu	Leu	Ala	Asn	Gly	Lys	Thr	Ser	His		
			340					345					350				
gcg	atg	cac	gat	acc	ttc	cgt	gaa	ctg	cat	cag	cag	atc	cgc	tgc	aat	1104	

Ala Met His Asp Thr Phe Arg Glu Leu His Gln Gln Ile Arg Cys Asn	
355 360 365	
gcc gat gag cag gcg gca caa gcc gtt ctg gag tta gca caa tga	1149
Ala Asp Glu Gln Ala Ala Gln Ala Val Leu Glu Leu Ala Gln *	
370 375 380	
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<211> 597	
<212> DNA	
<213> Escherichia coli	
<220>	
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<222> (1)...(597)	
<400> 229	
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Met Ile Glu Phe Val Tyr Pro His Thr Gln Leu Val Ala Gly Val Asp	
1 5 10 15	
gaa gtc gga cgc ggg ccg tta gtt ggc gcg gtc gtc acc gct gcg gtg	96
Glu Val Gly Arg Gly Pro Leu Val Gly Ala Val Val Thr Ala Ala Val	
20 25 30	
atc ctt gac ccg gcg cgc ccg att gcc ggg ctg aat gat tcc aaa aag	144
Ile Leu Asp Pro Ala Arg Pro Ile Ala Gly Leu Asn Asp Ser Lys Lys	
35 40 45	
ctg agc gaa aaa cgc cgt ctg gcg ctc tat gaa gag atc aaa gag aaa	192
Leu Ser Glu Lys Arg Arg Leu Ala Leu Tyr Glu Glu Ile Lys Glu Lys	
50 55 60	
gcg ttg agc tgg agt ctg ggc cgc gcg gaa ccc cac gaa atc gac gag	240
Ala Leu Ser Trp Ser Leu Gly Arg Ala Glu Pro His Glu Ile Asp Glu	
65 70 75 80	
ctg aac att ctt cat gcg acc atg ctg gcg atg cag cgt gcc gtc gct	288
Leu Asn Ile Leu His Ala Thr Met Leu Ala Met Gln Arg Ala Val Ala	
85 90 95	
ggg ctg cat att gcg ccg gaa tat gtg ttg att gat ggt aac cgc tgc	336
Gly Leu His Ile Ala Pro Glu Tyr Val Leu Ile Asp Gly Asn Arg Cys	
100 105 110	
ccg aaa tta ccg atg cct gcg atg gct gtg gtg aaa ggc gat agc cgc	384
Pro Lys Leu Pro Met Pro Ala Met Ala Val Val Lys Gly Asp Ser Arg	
115 120 125	
gta ccg gaa atc agt gcc gcg tct atc ctg gcg aaa gtg acg cgt gac	432
Val Pro Glu Ile Ser Ala Ala Ser Ile Leu Ala Lys Val Thr Arg Asp	
130 135 140	
gcc gaa atg gcg gcg ctg gat att gtt ttc ccg caa tat ggt ttt gcc	480
Ala Glu Met Ala Ala Leu Asp Ile Val Phe Pro Gln Tyr Gly Phe Ala	
145 150 155 160	
caa cac aaa ggg tac cca acc gct ttt cat ctg gaa aaa ctg gct gaa	528
Gln His Lys Gly Tyr Pro Thr Ala Phe His Leu Glu Lys Leu Ala Glu	

165	170	175	
cac ggc gcg acc gaa cac cat cgg cgc agc ttt ggg cct gtc aaa cgc			576
His Gly Ala Thr Glu His His Arg Arg Ser Phe Gly Pro Val Lys Arg			
180	185	190	
gca ctg gga ctt gcg tcc tga			597
Ala Leu Gly Leu Ala Ser *			
195			
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atg tct gaa cca cgt ttc gta cac ctg cgg gtg cac agc gac tac tcg			48
Met Ser Glu Pro Arg Phe Val His Leu Arg Val His Ser Asp Tyr Ser			
1	5	10	15
atg atc gat ggc ctg gcc aaa acc gca ccg ttg gta aaa aag gcg gcg			96
Met Ile Asp Gly Leu Ala Lys Thr Ala Pro Leu Val Lys Lys Ala Ala			
20	25	30	
gcg ttg ggt atg cca gca ctg gcg atc acc gat ttc acc aac ctt tgt			144
Ala Leu Gly Met Pro Ala Leu Ala Ile Thr Asp Phe Thr Asn Leu Cys			
35	40	45	
ggt ctg gtg aag ttc tac gga gcg gga cat ggc gca ggg att aag cct			192
Gly Leu Val Lys Phe Tyr Gly Ala Gly His Gly Ala Gly Ile Lys Pro			
50	55	60	
atc gtc ggg gca gat ttt aac gtc cag tgc gac ctg ctg ggt gat gag			240
Ile Val Gly Ala Asp Phe Asn Val Gln Cys Asp Leu Leu Gly Asp Glu			
65	70	75	80
tta acc cac ctg acg gta ctg gcg gcg aac aat acc ggc tat cag aat			288
Leu Thr His Leu Thr Val Leu Ala Ala Asn Asn Thr Gly Tyr Gln Asn			
85	90	95	
ctg acg ttg ctg atc tca aaa gcg tat cag cgc ggg tac ggt gcc gcc			336
Leu Thr Leu Leu Ile Ser Lys Ala Tyr Gln Arg Gly Tyr Gly Ala Ala			
100	105	110	
ggg ccg atc atc gat cgc gac tgg ctt atc gaa tta aac gaa ggg ttg			384
Gly Pro Ile Ile Asp Arg Asp Trp Leu Ile Glu Leu Asn Glu Gly Leu			
115	120	125	
atc ctt ctt tcc ggc gga cgc atg ggc gac gtc gga cgc agt ctt ttg			432
Ile Leu Leu Ser Gly Gly Arg Met Gly Asp Val Gly Arg Ser Leu Leu			
130	135	140	
cgt ggt aac agc gcg ctg gta gat gag tgt gtc gcg ttt tat gaa gaa			480
Arg Gly Asn Ser Ala Leu Val Asp Glu Cys Val Ala Phe Tyr Glu Glu			
145	150	155	160

cac ttc ccg gat cgc tat ttt ctc gag ctg atc cgc acc ggc agg ccg His Phe Pro Asp Arg Tyr Phe Leu Glu Leu Ile Arg Thr Gly Arg Pro 165 170 175	528
gat gaa gaa agc tat ctg cac gcg gcg gtg gaa ctg gcg gaa gcg cgc Asp Glu Glu Ser Tyr Leu His Ala Ala Val Glu Leu Ala Glu Ala Arg 180 185 190	576
ggt ttg ccc gtc gtg gcg acc aac gac gtg cgc ttt atc gac agc agc Gly Leu Pro Val Val Ala Thr Asn Asp Val Arg Phe Ile Asp Ser Ser 195 200 205	624
gac ttt gac gca cac gaa atc cgc gtc gcg atc cac gac ggc ttt acc Asp Phe Asp Ala His Glu Ile Arg Val Ala Ile His Asp Gly Phe Thr 210 215 220	672
ctc gac gat cct aaa cgc ccg cgt aac tat tcg ccg cag caa tat atg Leu Asp Asp Pro Lys Arg Pro Arg Asn Tyr Ser Pro Gln Gln Tyr Met 225 230 235 240	720
cgt agc gaa gag gag atg tgt gag ctg ttt gcc gac atc ccc gaa gcc Arg Ser Glu Glu Glu Met Cys Glu Leu Phe Ala Asp Ile Pro Glu Ala 245 250 255	768
ctt gcc aac acc gtt gag atc gcc aaa cgc tgt aac gta acc gtg cgt Leu Ala Asn Thr Val Glu Ile Ala Lys Arg Cys Asn Val Thr Val Arg 260 265 270	816
ctt ggt gaa tac ttc ctg ccg cag ttc ccg acc ggg gac atg agc acc Leu Gly Glu Tyr Phe Leu Pro Gln Phe Pro Thr Gly Asp Met Ser Thr 275 280 285	864
gaa gat tat ctg gtc aag cgt gca aaa gag ggc ctg gaa gag cgt ctg Glu Asp Tyr Leu Val Lys Arg Ala Lys Glu Gly Leu Glu Glu Arg Leu 290 295 300	912
gcc ttt tta ttc cct gat gag gaa gaa cgt ctt aag cgc cgc ccg gaa Ala Phe Leu Phe Pro Asp Glu Glu Glu Arg Leu Lys Arg Arg Pro Glu 305 310 315 320	960
tat gac gaa cgt ctg gag act gaa ctt cag gtt atc aac cag atg ggc Tyr Asp Glu Arg Leu Glu Thr Glu Leu Gln Val Ile Asn Gln Met Gly 325 330 335	1008
ttc ccg ggc tac ttc ctc atc gtt atg gaa ttt atc cag tgg tcg aaa Phe Pro Gly Tyr Phe Leu Ile Val Met Glu Phe Ile Gln Trp Ser Lys 340 345 350	1056
gat aac ggc gta ccg gta ggg cca ggc cgt ggc tcc ggt gcg ggt tca Asp Asn Gly Val Pro Val Gly Pro Gly Arg Gly Ser Gly Ala Gly Ser 355 360 365	1104
ctg gtg gcc tac gcg ctg aaa atc acc gac ctc gat ccg ctg gaa ttt Leu Val Ala Tyr Ala Leu Lys Ile Thr Asp Leu Asp Pro Leu Glu Phe 370 375 380	1152
gac ctg ctg ttc gaa cgt ttc ctt aac ccg gaa cgt gtc tcc atg cct Asp Leu Leu Phe Glu Arg Phe Leu Asn Pro Glu Arg Val Ser Met Pro 385 390 395 400	1200

gac ttc gac gtt gac ttc tgt atg gag aaa cgc gat cag gtt atc gag Asp Phe Asp Val Asp Phe Cys Met Glu Lys Arg Asp Gln Val Ile Glu 405 410 415	1248
cac gta gcg gac atg tac ggt cgt gat gcg gta tcg cag atc atc acc His Val Ala Asp Met Tyr Gly Arg Asp Ala Val Ser Gln Ile Ile Thr 420 425 430	1296
ttc ggt aca atg gcg gcg aaa gcg gtg atc cgc gac gta ggc cgc gtg Phe Gly Thr Met Ala Ala Lys Ala Val Ile Arg Asp Val Gly Arg Val 435 440 445	1344
ctg ggg cat ccg tac ggc ttt gtc gat cgt atc tcg aaa ctg atc ccg Leu Gly His Pro Tyr Gly Phe Val Asp Arg Ile Ser Lys Leu Ile Pro 450 455 460	1392
ccc gat ccg ggg atg acg ctg gcg aaa gcg ttt gaa gcc gag ccg cag Pro Asp Pro Gly Met Thr Leu Ala Lys Ala Phe Glu Ala Glu Pro Gln 465 470 475 480	1440
ctg ccg gaa atc tac gaa gcg gat gaa gaa gtt aag gcg ctg atc gac Leu Pro Glu Ile Tyr Glu Ala Asp Glu Glu Val Lys Ala Leu Ile Asp 485 490 495	1488
atg gcg cgc aaa ctg gaa ggg gtc acc cgt aac gcc ggt aag cac gcc Met Ala Arg Lys Leu Glu Gly Val Thr Arg Asn Ala Gly Lys His Ala 500 505 510	1536
ggt ggg gtg gtt atc gcg ccg acc aaa att acc gat ttt gcg ccg ctt Gly Gly Val Val Ile Ala Pro Thr Lys Ile Thr Asp Phe Ala Pro Leu 515 520 525	1584
tac tgc gat gaa gag ggc aaa cat ccg gtc acc cag ttt gat aaa agc Tyr Cys Asp Glu Glu Gly Lys His Pro Val Thr Gln Phe Asp Lys Ser 530 535 540	1632
gac gtt gaa tac gcc gga ctg gtg aag ttc gac ttc ctt ggt ttg cgt Asp Val Glu Tyr Ala Gly Leu Val Lys Phe Asp Phe Leu Gly Leu Arg 545 550 555 560	1680
acg ctc acc atc atc aac tgg gcg ctg gag atg atc aac aag cgg cgg Thr Leu Thr Ile Ile Asn Trp Ala Leu Glu Met Ile Asn Lys Arg Arg 565 570 575	1728
gcg aag aat ggc gag ccg ccg ctg gat atc gct gcg atc ccg ctg gat Ala Lys Asn Gly Glu Pro Pro Leu Asp Ile Ala Ala Ile Pro Leu Asp 580 585 590	1776
gat aag aaa agc ttc gac atg ctg caa cgc tcg gaa acc acg gcg gta Asp Lys Lys Ser Phe Asp Met Leu Gln Arg Ser Glu Thr Thr Ala Val 595 600 605	1824
ttc cag ctt gaa tcg cgc ggc atg aag gac ctg atc aag cgt cta caa Phe Gln Leu Glu Ser Arg Gly Met Lys Asp Leu Ile Lys Arg Leu Gln 610 615 620	1872
cct gac tgc ttc gaa gat atg atc gcc cta gtg gca ctg ttc cgc ccc Pro Asp Cys Phe Glu Asp Met Ile Ala Leu Val Ala Leu Phe Arg Pro 625 630 635 640	1920

ggt ccg ttg caa tca ggg atg gtg gat aac ttt atc gac cgt aaa cat	1968
Gly Pro Leu Gln Ser Gly Met Val Asp Asn Phe Ile Asp Arg Lys His	
645 650 655	
ggt cgt gaa gag atc tcc tat ccg gac gta cag tgg cag cat gaa agc	2016
Gly Arg Glu Glu Ile Ser Tyr Pro Asp Val Gln Trp Gln His Glu Ser	
660 665 670	
ctg aaa ccg gta ctg gag cca acc tac ggc att atc ctg tat cag gaa	2064
Leu Lys Pro Val Leu Glu Pro Thr Tyr Gly Ile Ile Leu Tyr Gln Glu	
675 680 685	
cag gtc atg cag att gcg cag gtg ctt tct ggt tat acc ctc ggt ggc	2112
Gln Val Met Gln Ile Ala Gln Val Leu Ser Gly Tyr Thr Leu Gly Gly	
690 695 700	
gcg gat atg ctg cgt cgt gcg atg ggt aag aaa aag ccg gaa gag atg	2160
Ala Asp Met Leu Arg Arg Ala Met Gly Lys Lys Lys Pro Glu Glu Met	
705 710 715 720	
gct aag caa cgt tct gta ttt gct gaa ggt gca gaa aag aac gga atc	2208
Ala Lys Gln Arg Ser Val Phe Ala Glu Gly Ala Glu Lys Asn Gly Ile	
725 730 735	
aac gct gaa ctg gcg atg aaa atc ttc gac ctg gtg gag aaa ttc gct	2256
Asn Ala Glu Leu Ala Met Lys Ile Phe Asp Leu Val Glu Lys Phe Ala	
740 745 750	
ggt tac gga ttt aac aaa tcg cac tct gcg gcc tat gct ttg gtg tca	2304
Gly Tyr Gly Phe Asn Lys Ser His Ser Ala Ala Tyr Ala Leu Val Ser	
755 760 765	
tat caa acg tta tgg ctg aaa gcg cac tat cct gcg gag ttt atg gcg	2352
Tyr Gln Thr Leu Trp Leu Lys Ala His Tyr Pro Ala Glu Phe Met Ala	
770 775 780	
gcg gta atg acc gcc gat atg gac aac acc gag aag gtg gtg ggt ctg	2400
Ala Val Met Thr Ala Asp Met Asp Asn Thr Glu Lys Val Val Gly Leu	
785 790 795 800	
gtg gat gag tgc tgg cgg atg ggg ctg aaa atc ctg cca cca gat ata	2448
Val Asp Glu Cys Trp Arg Met Gly Leu Lys Ile Leu Pro Pro Asp Ile	
805 810 815	
aac tcc ggt ctt tac cat ttc cac gtc aac gac gac ggc gaa atc gtg	2496
Asn Ser Gly Leu Tyr His Phe His Val Asn Asp Asp Gly Glu Ile Val	
820 825 830	
tat ggt att ggc gcg atc aaa ggg gtc ggt gaa ggt ccg att gag gcc	2544
Tyr Gly Ile Gly Ala Ile Lys Gly Val Gly Glu Gly Pro Ile Glu Ala	
835 840 845	
atc atc gaa gcc cgt aat aaa ggc ggc tac ttc cgc gaa ctg ttt gat	2592
Ile Ile Glu Ala Arg Asn Lys Gly Gly Tyr Phe Arg Glu Leu Phe Asp	
850 855 860	
ctc tgc gcc cgt acc gac acc aaa aag ttg aac cgt cgc gtg ctg gaa	2640
Leu Cys Ala Arg Thr Asp Thr Lys Lys Leu Asn Arg Arg Val Leu Glu	
865 870 875 880	

aaa ctg atc atg tcc ggg gcg ttt gac cgt ctt ggg cca cat cgc gca Lys Leu Ile Met Ser Gly Ala Phe Asp Arg Leu Gly Pro His Arg Ala 885 890 895	2688
gcg ctg atg aac tcg ctg ggc gat gcg tta aaa gcg gca gat caa cac Ala Leu Met Asn Ser Leu Gly Asp Ala Leu Lys Ala Ala Asp Gln His 900 905 910	2736
gcg aaa gcg gaa gct atc ggt cag gcc gat atg ttc ggc gtg ctg gcc Ala Lys Ala Glu Ala Ile Gly Gln Ala Asp Met Phe Gly Val Leu Ala 915 920 925	2784
gaa gag ccg gaa caa att gaa caa tcc tac gcc agc tgc caa ccg tgg Glu Glu Pro Glu Gln Ile Glu Gln Ser Tyr Ala Ser Cys Gln Pro Trp 930 935 940	2832
ccg gag cag gtg gta tta gat ggg gaa cgt gaa acg tta ggc ctg tac Pro Glu Gln Val Val Leu Asp Gly Glu Arg Glu Thr Leu Gly Leu Tyr 945 950 955 960	2880
ctg acc gga cac cct atc aac cag tat tta aaa gag att gag cgt tat Leu Thr Gly His Pro Ile Asn Gln Tyr Leu Lys Glu Ile Glu Arg Tyr 965 970 975	2928
gtc gga ggc gta agg ctg aaa gac atg cac ccg aca gaa cgt ggt aaa Val Gly Gly Val Arg Leu Lys Asp Met His Pro Thr Glu Arg Gly Lys 980 985 990	2976
gtc atc acg gct gcg ggg ctc gtt gtt gcc gcg cgg gtt atg gtc acc Val Ile Thr Ala Ala Gly Leu Val Val Ala Ala Arg Val Met Val Thr 995 1000 1005	3024
aag cgc ggc aat cgt atc ggt atc tgc acg ctg gat gac cgt tcc ggg Lys Arg Gly Asn Arg Ile Gly Ile Cys Thr Leu Asp Asp Arg Ser Gly 1010 1015 1020	3072
cgg ctg gaa gtg atg ttg ttt act gac gcc ctg gat aaa tac cag caa Arg Leu Glu Val Met Leu Phe Thr Asp Ala Leu Asp Lys Tyr Gln Gln 1025 1030 1035 1040	3120
ttg ctg gaa aaa gac cgc ata ctt atc gtc agc gga cag gtc agc ttt Leu Leu Glu Lys Asp Arg Ile Leu Ile Val Ser Gly Gln Val Ser Phe 1045 1050 1055	3168
gat gac ttc agc ggt ggg ctt aaa atg acc gct cgc gaa gtg atg gat Asp Asp Phe Ser Gly Gly Leu Lys Met Thr Ala Arg Glu Val Met Asp 1060 1065 1070	3216
att gac gaa gcc cgg gaa aaa tat gct cgc ggg ctt gct atc tcg ctg Ile Asp Glu Ala Arg Glu Lys Tyr Ala Arg Gly Leu Ala Ile Ser Leu 1075 1080 1085	3264
acg gac agg caa att gat gac cag ctt tta aac cga ctc cgt cag tct Thr Asp Arg Gln Ile Asp Gln Leu Leu Asn Arg Leu Arg Gln Ser 1090 1095 1100	3312
ctg gaa ccc cac cgc tct ggg aca att cca gta cat ctc tac tat cag Leu Glu Pro His Arg Ser Gly Thr Ile Pro Val His Leu Tyr Tyr Gln 1105 1110 1115 1120	3360

agg gcg gat gca cgc gcg cgg ttg cgt ttt ggc gcg acg tgg cgt gtc 3408
 Arg Ala Asp Ala Arg Ala Arg Leu Arg Phe Gly Ala Thr Trp Arg Val
 1125 1130 1135

tct ccg agc gat cgt tta tta aac gat ctc cgt ggc ctc att ggt tcg 3456
 Ser Pro Ser Asp Arg Leu Leu Asn Asp Leu Arg Gly Leu Ile Gly Ser
 1140 1145 1150

gag cag gtg gaa ctg gag ttt gac taa 3483
 Glu Gln Val Glu Leu Glu Phe Asp *
 1155 1160

<210> 231
 <211> 720
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(720)

<400> 231

gtg aat gtc aat ttc ttt gtc acc tgt att ggt gac gcc ctg aaa tca 48
 Met Asn Val Asn Phe Phe Val Thr Cys Ile Gly Asp Ala Leu Lys Ser
 1 5 10 15

aga atg gca cga gac tcc gtg ctg cta ctg gaa aaa ctc ggc tgt cgc 96
 Arg Met Ala Arg Asp Ser Val Leu Leu Leu Glu Lys Leu Gly Cys Arg
 20 25 30

gta aat ttc ccg gag aaa cag gga tgc tgc ggt cag cct gcg atc aat 144
 Val Asn Phe Pro Glu Lys Gln Gly Cys Cys Gly Gln Pro Ala Ile Asn
 35 40 45

agc ggt tat atc aaa gaa gcg att cca ggg atg aaa aat ctg atc gcc 192
 Ser Gly Tyr Ile Lys Glu Ala Ile Pro Gly Met Lys Asn Leu Ile Ala
 50 55 60

gca ctg gag gat aac gac gat ccc att att tca ccg gct ggc tct tgc 240
 Ala Leu Glu Asp Asn Asp Asp Pro Ile Ile Ser Pro Ala Gly Ser Cys
 65 70 75 80

acc tat gcc gta aaa agt tac ccg acg tat ctg gcg gat gaa cct gaa 288
 Thr Tyr Ala Val Lys Ser Tyr Pro Thr Tyr Leu Ala Asp Glu Pro Glu
 85 90 95

tgg gca tca cgt gcc gca aag gtt gcc gcg cgt atg cag gat ctc acc 336
 Trp Ala Ser Arg Ala Ala Lys Val Ala Ala Arg Met Gln Asp Leu Thr
 100 105 110

tct ttt att gtt aat aaa tta ggg gta gtc gat gta ggt gcc agt ttg 384
 Ser Phe Ile Val Asn Lys Leu Gly Val Val Asp Val Gly Ala Ser Leu
 115 120 125

caa ggg aga gcg gtg tat cac cca tct tgt agc ctg gcc cgt aag ctg 432
 Gln Gly Arg Ala Val Tyr His Pro Ser Cys Ser Leu Ala Arg Lys Leu
 130 135 140

gga gtg aag gac gag cca ctt acg ctg ctg aaa aat gtg cgt gga ctg 480
 Gly Val Lys Asp Glu Pro Leu Thr Leu Leu Lys Asn Val Arg Gly Leu
 145 150 155 160

gag ctg ttg acc ttt gct gaa cag gat acc tgc tgc gga ttt ggc ggc 528
 Glu Leu Leu Thr Phe Ala Glu Gln Asp Thr Cys Cys Gly Phe Gly Gly
 165 170 175

acg ttc tcg gtc aaa atg gcc gaa ata tcc ggc gag atg gtg aaa gaa 576
 Thr Phe Ser Val Lys Met Ala Glu Ile Ser Gly Glu Met Val Lys Glu
 180 185 190

aag gtt gcg cac ctg atg gaa gtc cgc cct gag tat tta att ggt gct 624
 Lys Val Ala His Leu Met Glu Val Arg Pro Glu Tyr Leu Ile Gly Ala
 195 200 205

gac gtg agt tgc ctg cta aac atc agt ggg cga tta caa cgg gaa ggg 672
 Asp Val Ser Cys Leu Leu Asn Ile Ser Gly Arg Leu Gln Arg Glu Gly
 210 215 220

cag aaa gtc aaa gtg atg cat att gct gaa gtg ttg atg agc cgc tga 720
 Gln Lys Val Lys Val Met His Ile Ala Glu Val Leu Met Ser Arg *
 225 230 235

<210> 232
 <211> 1428
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1428)

<400> 232

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 Met Ser Ile Lys Thr Ser Asn Thr Asp Phe Lys Thr Arg Ile Arg Gln
 1 5 10 15

caa att gaa gat ccg atc atg cgc aaa gcg gtg gca aac gcg cag cag 96
 Gln Ile Glu Asp Pro Ile Met Arg Lys Ala Val Ala Asn Ala Gln Gln
 20 25 30

cgt att ggg gca aat cgg caa aaa atg gtc gat gaa ttg ggg cac tgg 144
 Arg Ile Gly Ala Asn Arg Gln Lys Met Val Asp Glu Leu Gly His Trp
 35 40 45

gag gag tgg cgc gat cgg gcc gcc cag ata cgt gat cat gtt ctg agt 192
 Glu Glu Trp Arg Asp Arg Ala Ala Gln Ile Arg Asp His Val Leu Ser
 50 55 60

aat ctc gac gct tat ctg tac cag ctc tca gaa aaa gtg acg caa aac 240
 Asn Leu Asp Ala Tyr Leu Tyr Gln Leu Ser Glu Lys Val Thr Gln Asn
 65 70 75 80

ggc ggt cac gtc tat ttt gca aga acc aaa gaa gac gct acc cgc tac 288
 Gly Gly His Val Tyr Phe Ala Arg Thr Lys Glu Asp Ala Thr Arg Tyr
 85 90 95

att tta cag gtt gcc caa cgc aaa aat gcc cgg aag gtg gtg aaa tct 336

Ile Leu Gln Val Ala Gln Arg Lys Asn Ala Arg Lys Val Val Lys Ser	
100 105 110	
aaa tcg atg gtg acc gaa gag att ggt gtc aat cat gtg ttg cag gat	384
Lys Ser Met Val Thr Glu Glu Ile Gly Val Asn His Val Leu Gln Asp	
115 120 125	
gct ggc att cag gtg att gaa acc gat ctg ggt gaa tat att ctc cag	432
Ala Gly Ile Gln Val Ile Glu Thr Asp Leu Gly Glu Tyr Ile Leu Gln	
130 135 140	
ctg gat caa gat ccg cca tct cat gtt gtg gtc ccg gca att cat aaa	480
Leu Asp Gln Asp Pro Pro Ser His Val Val Val Pro Ala Ile His Lys	
145 150 155 160	
gat cgc cat cag atc cgt cga gtg cta cac gaa cgt ctg ggc tat gag	528
Asp Arg His Gln Ile Arg Arg Val Leu His Glu Arg Leu Gly Tyr Glu	
165 170 175	
ggg ccg gaa acg cct gaa gcg atg acc tta ttc atc cgg caa aaa atc	576
Gly Pro Glu Thr Pro Glu Ala Met Thr Leu Phe Ile Arg Gln Lys Ile	
180 185 190	
cgc gaa gat ttc ctc agt gct gaa ata ggt att acc ggc tgt aat ttc	624
Arg Glu Asp Phe Leu Ser Ala Glu Ile Gly Ile Thr Gly Cys Asn Phe	
195 200 205	
gcg gtg gca gag acc ggt tcg gta tgc ctg gtg acc aat gaa ggt aat	672
Ala Val Ala Glu Thr Gly Ser Val Cys Leu Val Thr Asn Glu Gly Asn	
210 215 220	
gcg cga atg tgt acc acg ctg cct aaa acg cat att gca gtg atg gga	720
Ala Arg Met Cys Thr Thr Leu Pro Lys Thr His Ile Ala Val Met Gly	
225 230 235 240	
atg gag cgt att gcc ccc acg ttt gcc gag gta gat gta ttg atc acc	768
Met Glu Arg Ile Ala Pro Thr Phe Ala Glu Val Asp Val Leu Ile Thr	
245 250 255	
atg ctg gcg cgc agt gcc gtt ggt gca cgt ttg acg gga tac aac acc	816
Met Leu Ala Arg Ser Ala Val Gly Ala Arg Leu Thr Gly Tyr Asn Thr	
260 265 270	
tgg ctg aca gga ccg cgc gaa gct ggg cac gtt gat ggt cct gaa gag	864
Trp Leu Thr Gly Pro Arg Glu Ala Gly His Val Asp Gly Pro Glu Glu	
275 280 285	
ttt cat ctg gtt att gtc gat aac ggg cgt tct gag gtg ctg gcc tct	912
Phe His Leu Val Ile Val Asp Asn Gly Arg Ser Glu Val Leu Ala Ser	
290 295 300	
gaa ttt ccg gat gtg ctg cgc tgt att cgc tgc ggg gct tgt atg aat	960
Glu Phe Arg Asp Val Leu Arg Cys Ile Arg Cys Gly Ala Cys Met Asn	
305 310 315 320	
act tgt ccg gca tat cgc cat att ggc ggt cat gga tat ggc tct att	1008
Thr Cys Pro Ala Tyr Arg His Ile Gly Gly His Gly Tyr Gly Ser Ile	
325 330 335	
tat cca ggg cca att ggt gcg gtg att tct ccg cta ctt ggc ggc tat	1056

Tyr	Pro	Gly	Pro	Ile	Gly	Ala	Val	Ile	Ser	Pro	Leu	Leu	Gly	Gly	Tyr		
			340					345					350				
aaa	gat	ttt	aaa	gat	tta	ccc	tac	gcc	tgc	tct	tta	tgc	aca	gct	tgt	1104	
Lys	Asp	Phe	Lys	Asp	Leu	Pro	Tyr	Ala	Cys	Ser	Leu	Cys	Thr	Ala	Cys		
		355					360					365					
gac	aac	gtg	tgt	ccg	gtg	cgt	att	ccg	ctg	tca	aaa	ctg	att	ttg	cgt	1152	
Asp	Asn	Val	Cys	Pro	Val	Arg	Ile	Pro	Leu	Ser	Lys	Leu	Ile	Leu	Arg		
	370					375					380						
cat	cgt	cgg	gtg	atg	gct	gaa	aaa	ggg	atc	acc	gca	aaa	gca	gag	caa	1200	
His	Arg	Arg	Val	Met	Ala	Glu	Lys	Gly	Ile	Thr	Ala	Lys	Ala	Glu	Gln		
385					390					395					400		
cgg	gcg	ata	aaa	atg	ttc	gct	tat	gcc	aat	agt	cat	cca	gga	ttg	tgg	1248	
Arg	Ala	Ile	Lys	Met	Phe	Ala	Tyr	Ala	Asn	Ser	His	Pro	Gly	Leu	Trp		
			405						410					415			
aaa	gtc	ggg	atg	atg	gcc	ggt	gct	cat	gcg	gca	agc	tgg	ttt	atc	aat	1296	
Lys	Val	Gly	Met	Met	Ala	Gly	Ala	His	Ala	Ala	Ser	Trp	Phe	Ile	Asn		
		420						425					430				
ggc	ggc	aaa	aca	cca	ctc	aaa	ttt	ggc	gcg	att	agc	gac	tgg	atg	gaa	1344	
Gly	Gly	Lys	Thr	Pro	Leu	Lys	Phe	Gly	Ala	Ile	Ser	Asp	Trp	Met	Glu		
		435					440					445					
gca	cgc	gat	ctt	cct	gaa	gct	gac	gga	gag	agt	ttc	cgt	agt	tgg	ttt	1392	
Ala	Arg	Asp	Leu	Pro	Glu	Ala	Asp	Gly	Glu	Ser	Phe	Arg	Ser	Trp	Phe		
	450					455					460						
aag	aaa	cat	cag	gcg	cag	gag	aaa	aag	aat	gga	taa					1428	
Lys	Lys	His	Gln	Ala	Gln	Glu	Lys	Lys	Asn	Gly	*						
465					470					475							
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<211> 849																	
<212> DNA																	
<213> Escherichia coli																	
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Met	Leu	Met	Arg	Gln	Ala	Gly	Leu	Ser	Met	Ala	Ala	Lys	His	His	Ser		
1				5					10					15			
aat	ttg	gcg	cga	tta	gcg	act	gga	tgg	aag	cac	gcg	atc	ttc	ctg	aag	96	
Asn	Leu	Ala	Arg	Leu	Ala	Thr	Gly	Trp	Lys	His	Ala	Ile	Phe	Leu	Lys		
			20					25					30				
ctg	acg	gag	aga	gtt	tcc	gta	gtt	ggt	tta	aga	aac	atc	agg	cgc	agg	144	
Leu	Thr	Glu	Arg	Val	Ser	Val	Val	Gly	Leu	Arg	Asn	Ile	Arg	Arg	Arg		
		35					40					45					
aga	aaa	aga	atg	gat	aat	cga	ggc	gaa	ttt	ttg	aat	aac	gtt	gct	cag	192	
Arg	Lys	Arg	Met	Asp	Asn	Arg	Gly	Glu	Phe	Leu	Asn	Asn	Val	Ala	Gln		

50	55	60	
gca ctg ggt cgc ccg ctg cga ctt gaa ccg caa gca gaa gat gcg ccg Ala Leu Gly Arg Pro Leu Arg Leu Glu Pro Gln Ala Glu Asp Ala Pro 65 70 75 80			240
ctt aac aac tat gct aac gag cgg ctt acc caa ctt aac caa cag cag Leu Asn Asn Tyr Ala Asn Glu Arg Leu Thr Gln Leu Asn Gln Gln Gln 85 90 95			288
cgc tgt gac gcg ttt att cag ttt gcc agc gat gtt atg ttg acg cgc Arg Cys Asp Ala Phe Ile Gln Phe Ala Ser Asp Val Met Leu Thr Arg 100 105 110			336
tgt gag ctg acc agc gag gcg aag gcg gca gaa gct gca ata cgt ctg Cys Glu Leu Thr Ser Glu Ala Lys Ala Ala Glu Ala Ala Ile Arg Leu 115 120 125			384
tgt aaa gag ctg gga gat cag tcg gtc gtg att agc ggt gac acg agg Cys Lys Glu Leu Gly Asp Gln Ser Val Val Ile Ser Gly Asp Thr Arg 130 135 140			432
ctg gag gaa ttg ggg att agc gaa cgt ttg cag cag gaa tgc aat gcc Leu Glu Glu Leu Gly Ile Ser Glu Arg Leu Gln Gln Glu Cys Asn Ala 145 150 155 160			480
gtt gtt tgg gat ccg gcg aaa ggt gcc gag aat atc tcg cag gca gag Val Val Trp Asp Pro Ala Lys Gly Ala Glu Asn Ile Ser Gln Ala Glu 165 170 175			528
cag gct aaa gtg ggt gtt gtg tat gct gaa tat ggt tta acc gaa tcg Gln Ala Lys Val Gly Val Val Tyr Ala Glu Tyr Gly Leu Thr Glu Ser 180 185 190			576
gga ggc gtg gtt ctt ttt tcc gcc gcc gag cgc ggg cgt tca ttg agc Gly Gly Val Val Leu Phe Ser Ala Ala Glu Arg Gly Arg Ser Leu Ser 195 200 205			624
ctg ctc ccg gaa tat tct ctt ttt atc ctg cgt aaa agc act atc ctg Leu Leu Pro Glu Tyr Ser Leu Phe Ile Leu Arg Lys Ser Thr Ile Leu 210 215 220			672
ccg cgt gta gcg caa ctc gca gaa aaa ttg cat cag aaa gcg cag gcc Pro Arg Val Ala Gln Leu Ala Glu Lys Leu His Gln Lys Ala Gln Ala 225 230 235 240			720
ggt gaa cga atg cct tcc tgc att aac atc att agc ggc ccc agt tca Gly Glu Arg Met Pro Ser Cys Ile Asn Ile Ile Ser Gly Pro Ser Ser 245 250 255			768
acg gcg gat att gag ctt atc aaa gtc gtc gga gtt cat ggc ccg gtg Thr Ala Asp Ile Glu Leu Ile Lys Val Val Gly Val His Gly Pro Val 260 265 270			816
aaa gcg gtg tat ctg att att gag gat tgt tga Lys Ala Val Tyr Leu Ile Ile Glu Asp Cys *			849
275 280			

<210> 234

<211> 1173

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1173)

<400> 234

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Met Ser Glu Ile Ala Met His Val Thr Ala Lys Pro Ser Ser Phe Gln	
1 5 10 15	
tgt aat ctc aaa tgt gat tac tgt ttt tac ctt gaa aaa gag tcg cag	96
Cys Asn Leu Lys Cys Asp Tyr Cys Phe Tyr Leu Glu Lys Glu Ser Gln	
20 25 30	
ttt act cat gaa aaa tgg atg gat gac agc act ctg aaa gag ttc atc	144
Phe Thr His Glu Lys Trp Met Asp Asp Ser Thr Leu Lys Glu Phe Ile	
35 40 45	
aaa caa tat atc gca gcg tct ggc aat cag gtc tat ttt acc tgg caa	192
Lys Gln Tyr Ile Ala Ala Ser Gly Asn Gln Val Tyr Phe Thr Trp Gln	
50 55 60	
ggc ggt gaa ccc act ctg gct ggc ctg gat ttt ttc cgt aaa gtt att	240
Gly Gly Glu Pro Thr Leu Ala Gly Leu Asp Phe Phe Arg Lys Val Ile	
65 70 75 80	
cac tat caa caa cgc tat gca ggc caa aaa cgt att ttt aat gca tta	288
His Tyr Gln Gln Arg Tyr Ala Gly Gln Lys Arg Ile Phe Asn Ala Leu	
85 90 95	
caa acg aat ggc att tta ttg aat aat gaa tgg tgt gcc ttt ctc aaa	336
Gln Thr Asn Gly Ile Leu Leu Asn Asn Glu Trp Cys Ala Phe Leu Lys	
100 105 110	
gaa cat gaa ttt ctg gtt ggt atc tcg atc gat ggc ccc cag gag tta	384
Glu His Glu Phe Leu Val Gly Ile Ser Ile Asp Gly Pro Gln Glu Leu	
115 120 125	
cat gac cgt tac aga cgc agt aat tca ggt aac ggt act ttt gca aaa	432
His Asp Arg Tyr Arg Arg Ser Asn Ser Gly Asn Gly Thr Phe Ala Lys	
130 135 140	
gtg ata gca gcc atc gag cgt ctg aaa tca tat caa gta gag ttt aat	480
Val Ile Ala Ala Ile Glu Arg Leu Lys Ser Tyr Gln Val Glu Phe Asn	
145 150 155 160	
acg tta acc gtc att aat aac gtt aat gtc cat tac cct ctt gag gtt	528
Thr Leu Thr Val Ile Asn Asn Val Asn Val His Tyr Pro Leu Glu Val	
165 170 175	
tat cat ttt tta aaa tct atc ggc agt aaa cat atg caa ttt atc gaa	576
Tyr His Phe Leu Lys Ser Ile Gly Ser Lys His Met Gln Phe Ile Glu	
180 185 190	
ttg cta gaa acc ggg acg ccg aat att gat ttc agt ggt cat agt gag	624
Leu Leu Glu Thr Gly Thr Pro Asn Ile Asp Phe Ser Gly His Ser Glu	
195 200 205	

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aac aca ttc cgt atc att gat ttt tct gtg cct ccc acg gct tat ggc      672
Asn Thr Phe Arg Ile Ile Asp Phe Ser Val Pro Pro Thr Ala Tyr Gly
    210                      215                      220

aag ttt atg tca acc att ttt atg caa tgg gtt aaa aac gat gtg ggt      720
Lys Phe Met Ser Thr Ile Phe Met Gln Trp Val Lys Asn Asp Val Gly
    225                      230                      235                      240

gaa att ttc atc cgt cag ttt gaa agc ttt gtc agc cgt ttt ttg ggg      768
Glu Ile Phe Ile Arg Gln Phe Glu Ser Phe Val Ser Arg Phe Leu Gly
                245                      250                      255

aat ggg cat acc agt tgt att ttc cag gag tcc tgc aag gat aat ctg      816
Asn Gly His Thr Ser Cys Ile Phe Gln Glu Ser Cys Lys Asp Asn Leu
                260                      265                      270

gtt gtt gaa agt aat gga gac att tac gaa tgc gac cat ttt gtc tat      864
Val Val Glu Ser Asn Gly Asp Ile Tyr Glu Cys Asp His Phe Val Tyr
                275                      280                      285

cca cag tac aaa att gga aac att aat aaa tct gaa ctc aaa acg atg      912
Pro Gln Tyr Lys Ile Gly Asn Ile Asn Lys Ser Glu Leu Lys Thr Met
    290                      295                      300

aac agt gta caa ctg aca gcg caa aaa aaa cgg att cca gcg aaa tgt      960
Asn Ser Val Gln Leu Thr Ala Gln Lys Lys Arg Ile Pro Ala Lys Cys
    305                      310                      315                      320

cag caa tgt gca tat aaa cct atc tgc aat ggc ggt tgt cct aag cat      1008
Gln Gln Cys Ala Tyr Lys Pro Ile Cys Asn Gly Gly Cys Pro Lys His
                325                      330                      335

cgt att act aaa gta aac aat gag act gtt tct tat ttt tgc gaa ggt      1056
Arg Ile Thr Lys Val Asn Asn Glu Thr Val Ser Tyr Phe Cys Glu Gly
                340                      345                      350

tat aaa atc ctt ttt tca acc atg gta cct tat atg aac gcc atg gta      1104
Tyr Lys Ile Leu Phe Ser Thr Met Val Pro Tyr Met Asn Ala Met Val
                355                      360                      365

gag tta gct aag aac aga gta ccg ctt tac cac att atg gat gtt gca      1152
Glu Leu Ala Lys Asn Arg Val Pro Leu Tyr His Ile Met Asp Val Ala
    370                      375                      380

aaa caa atg gag aat aat taa      1173
Lys Gln Met Glu Asn Asn *
    385                      390

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<210> 235
<211> 1716
<212> DNA
<213> Escherichia coli

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<220>
<221> CDS
<222> (1)...(1716)

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<400> 235

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1 5 10 15	
aag aaa agt gtc gta agt acc tcg ata tct ttg ata ctg gca tct ggt	96
Lys Lys Ser Val Val Ser Thr Ser Ile Ser Leu Ile Leu Ala Ser Gly	
20 25 30	
atg gct gca ttt gct gct cat gcg gca gat gat gta aag ctg aaa gca	144
Met Ala Ala Phe Ala Ala His Ala Ala Asp Asp Val Lys Leu Lys Ala	
35 40 45	
acc aaa aca aac gtt gct ttc tca gac ttt acg ccg aca gaa tac agt	192
Thr Lys Thr Asn Val Ala Phe Ser Asp Phe Thr Pro Thr Glu Tyr Ser	
50 55 60	
acc aaa gga aag cca aat att atc gta ctg acc atg gat gat ctt ggt	240
Thr Lys Gly Lys Pro Asn Ile Ile Val Leu Thr Met Asp Asp Leu Gly	
65 70 75 80	
tat gga caa ctt cct ttt gat aag gga tct ttt gac cca aaa aca atg	288
Tyr Gly Gln Leu Pro Phe Asp Lys Gly Ser Phe Asp Pro Lys Thr Met	
85 90 95	
gaa aat cgt gaa gtt gtc gat acc tac aaa ata ggg ata gat aaa gcc	336
Glu Asn Arg Glu Val Val Asp Thr Tyr Lys Ile Gly Ile Asp Lys Ala	
100 105 110	
att gaa gct gca caa aaa tca acg ccg acg ctc ctt tca tta atg gat	384
Ile Glu Ala Ala Gln Lys Ser Thr Pro Thr Leu Leu Ser Leu Met Asp	
115 120 125	
gaa ggc gta cgt ttt act aac ggc tat gtg gca cac ggt gtt tcc ggc	432
Glu Gly Val Arg Phe Thr Asn Gly Tyr Val Ala His Gly Val Ser Gly	
130 135 140	
ccc tcc cgc gcc gca ata atg acc ggt cga gct ccc gcc cgc ttt ggt	480
Pro Ser Arg Ala Ala Ile Met Thr Gly Arg Ala Pro Ala Arg Phe Gly	
145 150 155 160	
gtc tat tcc aat acc gat gct cag gat ggt att ccg cta aca gaa act	528
Val Tyr Ser Asn Thr Asp Ala Gln Asp Gly Ile Pro Leu Thr Glu Thr	
165 170 175	
ttc ttg cct gaa tta ttc cag aat cat ggt tat tac act gca gca gta	576
Phe Leu Pro Glu Leu Phe Gln Asn His Gly Tyr Tyr Thr Ala Ala Val	
180 185 190	
ggt aaa tgg cac ttg tca aaa atc agt aat gtg ccg gta ccg gaa gat	624
Gly Lys Trp His Leu Ser Lys Ile Ser Asn Val Pro Val Pro Glu Asp	
195 200 205	
aaa caa acg cgt gac tat cat gac aac ttc acc aca ttt tct gcg gaa	672
Lys Gln Thr Arg Asp Tyr His Asp Asn Phe Thr Thr Phe Ser Ala Glu	
210 215 220	
gaa tgg caa cct caa aac cgt ggc ttt gat tac ttt atg gga ttc cac	720
Glu Trp Gln Pro Gln Asn Arg Gly Phe Asp Tyr Phe Met Gly Phe His	
225 230 235 240	

gct gca gga acg gca tat tac aac tcc cct tca ctg ttc aaa aat cgt Ala Ala Gly Thr Ala Tyr Tyr Asn Ser Pro Ser Leu Phe Lys Asn Arg 245 250 255	768
gaa cgt gtc ccc gca aaa ggt tat atc agc gat cag tta acc gat gag Glu Arg Val Pro Ala Lys Gly Tyr Ile Ser Asp Gln Leu Thr Asp Glu 260 265 270	816
gca att ggc gtt gtt gat cgt gcc aaa aca ctt gac cag cct ttt atg Ala Ile Gly Val Val Asp Arg Ala Lys Thr Leu Asp Gln Pro Phe Met 275 280 285	864
ctt tac ctg gct tat aat gct ccg cac ctg cca aat gat aat cct gca Leu Tyr Leu Ala Tyr Asn Ala Pro His Leu Pro Asn Asp Asn Pro Ala 290 295 300	912
ccg gat caa tat cag aag caa ttt aat acc ggt agt caa aca gca gat Pro Asp Gln Tyr Gln Lys Gln Phe Asn Thr Gly Ser Gln Thr Ala Asp 305 310 315 320	960
aac tac tac gct tcc gtt tat tct gtt gat cag ggt gta aaa cgc att Asn Tyr Tyr Ala Ser Val Tyr Ser Val Asn Gln Gly Val Lys Arg Ile 325 330 335	1008
ctc gaa caa ctg aag aaa aac gga cag tat gac aat aca att att ctc Leu Glu Gln Leu Lys Lys Asn Gly Gln Tyr Asp Asn Thr Ile Ile Leu 340 345 350	1056
ttt acc tcc gat aat ggt gcg gtt atc gat ggt cct ctg ccg ctg aac Phe Thr Ser Asp Asn Gly Ala Val Ile Asp Gly Pro Leu Pro Leu Asn 355 360 365	1104
ggg gcg caa aaa ggc tat aag agt cag acc tat cct ggc ggt act cac Gly Ala Gln Lys Gly Tyr Lys Ser Gln Thr Tyr Pro Gly Gly Thr His 370 375 380	1152
acc cca atg ttt atg tgg tgg aaa gga aaa ctt caa ccc ggt aat tat Thr Pro Met Phe Met Trp Trp Lys Gly Lys Leu Gln Pro Gly Asn Tyr 385 390 395 400	1200
gac aag ctg att tcc gca atg gat ttc tac ccg aca gct ctt gat gca Asp Lys Leu Ile Ser Ala Met Asp Phe Tyr Pro Thr Ala Leu Asp Ala 405 410 415	1248
gcc gat atc agc att cca aaa gac ctt aag ctg gat ggc gtt tcc ttg Ala Asp Ile Ser Ile Pro Lys Asp Leu Lys Leu Asp Gly Val Ser Leu 420 425 430	1296
ctg ccc tgg ttg caa gat aag aaa caa ggc gag cca cat aaa aat ctg Leu Pro Trp Leu Gln Asp Lys Lys Gln Gly Glu Pro His Lys Asn Leu 435 440 445	1344
acc tgg ata acc tct tat tct cac tgg ttt gac gag gaa aat att cca Thr Trp Ile Thr Ser Tyr Ser His Trp Phe Asp Glu Glu Asn Ile Pro 450 455 460	1392
ttc tgg gat aat tac cac aaa ttt gtt cgc cat cag tca gac gat tac Phe Trp Asp Asn Tyr His Lys Phe Val Arg His Gln Ser Asp Asp Tyr 465 470 475 480	1440

ccg cat aac ccc aac act gag gac tta agc caa ttc tct tat acg gtg	1488
Pro His Asn Pro Asn Thr Glu Asp Leu Ser Gln Phe Ser Tyr Thr Val	
485 490 495	
aga aat aac gat tat tcg ctt gtc tat aca gta gaa aac aat cag tta	1536
Arg Asn Asn Asp Tyr Ser Leu Val Tyr Thr Val Glu Asn Asn Gln Leu	
500 505 510	
ggc ctc tac aaa ctg acg gat cta cag caa aaa gat aac ctt gcc gcc	1584
Gly Leu Tyr Lys Leu Thr Asp Leu Gln Gln Lys Asp Asn Leu Ala Ala	
515 520 525	
gcc aat ccg cag gtc gtt aaa gag atg caa ggc gtg gta aga gag ttt	1632
Ala Asn Pro Gln Val Val Lys Glu Met Gln Gly Val Val Arg Glu Phe	
530 535 540	
atc gac agc agc cag cca ccg ctt agc gag gta aat cag gag aag ttt	1680
Ile Asp Ser Ser Gln Pro Pro Leu Ser Glu Val Asn Gln Glu Lys Phe	
545 550 555 560	
aac aat atc aag aaa gca cta agc gaa gcg aaa taa	1716
Asn Asn Ile Lys Lys Ala Leu Ser Glu Ala Lys *	
565 570	
<210> 236	
<211> 825	
<212> DNA	
<213> Escherichia coli	
<220>	
<221> CDS	
<222> (1)...(825)	
<400> 236	
atg acc gaa ttt aca act ctt ctt cag caa gga aac gcc tgg ttc ttc	48
Met Thr Glu Phe Thr Thr Leu Leu Gln Gln Gly Asn Ala Trp Phe Phe	
1 5 10 15	
atc ccc agc gcc atc tta ctt ggt gcg ctt cat ggc ctg gaa cca ggg	96
Ile Pro Ser Ala Ile Leu Leu Gly Ala Leu His Gly Leu Glu Pro Gly	
20 25 30	
cac tca aaa acg atg atg gcg gcg ttt atc atc gcc atc aaa ggc acc	144
His Ser Lys Thr Met Met Ala Ala Phe Ile Ile Ala Ile Lys Gly Thr	
35 40 45	
att aaa caa gcg gtg atg ctc gga ctg gca gca act att tcg cat acc	192
Ile Lys Gln Ala Val Met Leu Gly Leu Ala Ala Thr Ile Ser His Thr	
50 55 60	
gca gtg gtc tgg tta att gcc ttt ggc ggg atg gtg atc agc aag cgc	240
Ala Val Val Trp Leu Ile Ala Phe Gly Gly Met Val Ile Ser Lys Arg	
65 70 75 80	
ttt act gct caa tca gca gaa ccg tgg ctc cag ctg att tcc gca gtg	288
Phe Thr Ala Gln Ser Ala Glu Pro Trp Leu Gln Leu Ile Ser Ala Val	
85 90 95	
atc att att agc acc gcg ttc tgg atg ttc tgg cgt acc tgg cgc ggc	336

Ile Ile Ile	Ser Thr Ala Phe Trp Met Phe Trp Arg Thr Trp Arg Gly	
100	105 110	
gaa cgc aac tgg ctg gag aat atg cac ggg cat gat tat gag cat cat		384
Glu Arg Asn Trp Leu Glu Asn Met His Gly His Asp Tyr Glu His His	115 120 125	
cat cac gat cac gaa cat cac cac gac cat gga cat cat cac cat cac		432
His His Asp His Glu His His His Asp His Gly His His His His His	130 135 140	
gaa cat ggc gag tat cag gat gcc cat gca cga gcc cat gcc aat gac		480
Glu His Gly Glu Tyr Gln Asp Ala His Ala Arg Ala His Ala Asn Asp	145 150 155 160	
att aaa cga cgc ttt gat ggt aga gag gtc acc aac tgg caa att ttg		528
Ile Lys Arg Arg Phe Asp Gly Arg Glu Val Thr Asn Trp Gln Ile Leu	165 170 175	
tta ttt ggc tta acc ggt ggc ctt atc ccc tgc ccg gca gca att acc		576
Leu Phe Gly Leu Thr Gly Gly Leu Ile Pro Cys Pro Ala Ala Ile Thr	180 185 190	
gtg ctg ttg ata tgc att cag ttg aaa gcc ctg aca ctg ggc gca aca		624
Val Leu Leu Ile Cys Ile Gln Leu Lys Ala Leu Thr Leu Gly Ala Thr	195 200 205	
ctg gtc gtc agt ttc agc att ggc ctg gcg tta acg ctt gtc acc gta		672
Leu Val Val Ser Phe Ser Ile Gly Leu Ala Leu Thr Leu Val Thr Val	210 215 220	
ggc gtt ggc gca gca atc agc gtt cag cag gtc gca aaa cgc tgg agc		720
Gly Val Gly Ala Ala Ile Ser Val Gln Gln Val Ala Lys Arg Trp Ser	225 230 235 240	
gga ttt aac act ctc gct aaa cgc gcc ccc tat ttt tcc agt ctg ttg		768
Gly Phe Asn Thr Leu Ala Lys Arg Ala Pro Tyr Phe Ser Ser Leu Leu	245 250 255	
att ggc tta gtc ggt gtg tat atg ggc gta cat ggc ttc atg ggc ata		816
Ile Gly Leu Val Gly Val Tyr Met Gly Val His Gly Phe Met Gly Ile	260 265 270	
atg cga taa		825
Met Arg *		

<210> 237

<211> 519

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(519)

<400> 237

atg att ctt aaa tca gct att tcc gct gac tct ctg ctc gct aag gat	48
Met Ile Leu Lys Ser Ala Ile Ser Ala Asp Ser Leu Leu Ala Lys Asp	

1	5	10	15	
gct ttt agg gca tcc ttt cat tta cac ttt tta cga aat cat ggg atc				96
Ala Phe Arg Ala Ser Phe His Leu His Phe Leu Arg Asn His Gly Ile	20	25	30	
act aac aaa ata tcg ctt gtc agt tat att gta tgg cag gaa aga tat				144
Thr Asn Lys Ile Ser Leu Val Ser Tyr Ile Val Trp Gln Glu Arg Tyr	35	40	45	
gcg act gat att aca gat ccc caa agt gga gag ttt atg acc att aaa				192
Ala Thr Asp Ile Thr Asp Pro Gln Ser Gly Glu Phe Met Thr Ile Lys	50	55	60	
aat aag atg ttg ctg ggt gcg ctt ttg ctg gtt acc agt gcc gcc tgg				240
Asn Lys Met Leu Leu Gly Ala Leu Leu Leu Val Thr Ser Ala Ala Trp	65	70	75	80
gcc gca cca gcc acc gcg ggt tcg acc aat acc tcg gga att tct aag				288
Ala Ala Pro Ala Thr Ala Gly Ser Thr Asn Thr Ser Gly Ile Ser Lys	85	90	95	
tat gag tta agt agt ttc att gct gac ttt aag cat ttc aaa cca ggg				336
Tyr Glu Leu Ser Ser Phe Ile Ala Asp Phe Lys His Phe Lys Pro Gly	100	105	110	
gac acc gta cca gaa atg tac cgt acc gat gag tac aac att aag cag				384
Asp Thr Val Pro Glu Met Tyr Arg Thr Asp Glu Tyr Asn Ile Lys Gln	115	120	125	
tgg cag ttg cgt aac ctg ccc gcg cct gat gcc ggg acg cac tgg acc				432
Trp Gln Leu Arg Asn Leu Pro Ala Pro Asp Ala Gly Thr His Trp Thr	130	135	140	
tat atg ggt ggc gcg tac gtg ttg atc agc gac acc gac ggt aaa atc				480
Tyr Met Gly Gly Ala Tyr Val Leu Ile Ser Asp Thr Asp Gly Lys Ile	145	150	155	160
att aaa gcc tac gac ggt gag att ttt tat cat cgc taa				519
Ile Lys Ala Tyr Asp Gly Glu Ile Phe Tyr His Arg *	165	170		

<210> 238

<211> 1704

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1704)

<400> 238

atg gct ttt gta tca gaa aga gaa att gta aga aag ata ttt agc aaa				48
Met Ala Phe Val Ser Glu Arg Glu Ile Val Arg Lys Ile Phe Ser Lys	1	5	10	15
aaa att gac ttt acg atc ttg gca ttt ttc tat att tcc tct att ttt				96
Lys Ile Asp Phe Thr Ile Leu Ala Phe Phe Tyr Ile Ser Ser Ile Phe	20	25	30	

ttt ctt ctt tgt agt ggc gtt ctc ttt caa tat ttt acc gct gcc ttc Phe Leu Leu Cys Ser Gly Val Leu Phe Gln Tyr Phe Thr Ala Ala Phe 35 40 45	144
aca aaa ggt aat tgt tat gaa tgc tca atg aaa ctt gat tac ata aaa Thr Lys Gly Asn Cys Tyr Glu Cys Ser Met Lys Leu Asp Tyr Ile Lys 50 55 60	192
caa ttt tat ttt tca ctg gaa acc gca tgg tac ctc ata tct gct gtt Gln Phe Tyr Phe Ser Leu Glu Thr Ala Trp Tyr Leu Ile Ser Ala Val 65 70 75 80	240
gca gta ttt att gca tct gtt ttt ata cag cat aga att aaa gct tat Ala Val Phe Ile Ala Ser Val Phe Ile Gln His Arg Ile Lys Ala Tyr 85 90 95	288
tta aca tta tta gct att aca tgg att gta cta aca ata aca gat gtg Leu Thr Leu Leu Ala Ile Thr Trp Ile Val Leu Thr Ile Thr Asp Val 100 105 110	336
gcg tta ata cac gcc tta gac aat ata gcc atg aat aat att ttg tta Ala Leu Ile His Ala Leu Asp Asn Ile Ala Met Asn Asn Ile Leu Leu 115 120 125	384
aat ata cta tat aat ctt ttt ggg gcg att tta ttg tca ctg ttt atg Asn Ile Leu Tyr Asn Leu Phe Gly Ala Ile Leu Leu Ser Leu Phe Met 130 135 140	432
tgt tta tca aat tcc ctc ctt ttc cac ctt aat aag ata aaa cat att Cys Leu Ser Asn Ser Leu Leu Phe His Leu Asn Lys Ile Lys His Ile 145 150 155 160	480
cca atg att tta tcc gca atg att cca tta gtt tcc gca ata ata ata Pro Met Ile Leu Ser Ala Met Ile Pro Leu Val Ser Ala Ile Ile Ile 165 170 175	528
gcc ata ctc ata acc gct gtt ata tat tta ttg ttt gcc cgg cag gcg Ala Ile Leu Ile Thr Ala Val Ile Tyr Leu Leu Phe Ala Arg Gln Ala 180 185 190	576
gta gag att gag atg gat ata tct gaa ggt tca gac atc gca tat gta Val Glu Ile Glu Met Asp Ile Ser Glu Gly Ser Asp Ile Ala Tyr Val 195 200 205	624
ggg gta aaa gat aat gag gaa tca ttt ggg ttt tta aat gat aaa aaa Gly Val Lys Asp Asn Glu Glu Ser Phe Gly Phe Leu Asn Asp Lys Lys 210 215 220	672
aca gac aca cca acg tat ctg gat gta atc aaa aat ggt agt ttg ata Thr Asp Thr Pro Thr Tyr Leu Asp Val Ile Lys Asn Gly Ser Leu Ile 225 230 235 240	720
tat aat gat aca cag ggt tta agt ggt gct gat att tat att gtc tcc Tyr Asn Asp Thr Gln Gly Leu Ser Gly Ala Asp Ile Tyr Ile Val Ser 245 250 255	768
ggg tgt tat gcc ctt cca gat tta ctt cgc aat gta ccg ctt gat gct Gly Cys Tyr Ala Leu Pro Asp Leu Leu Arg Asn Val Pro Leu Asp Ala 260 265 270	816

aaa aaa tct ttt ctg aat gta aaa aag cta gaa atc aca cag aaa ctt Lys Lys Ser Phe Leu Asn Val Lys Lys Leu Glu Ile Thr Gln Lys Leu 275 280 285	864
cca atg atg ggg ttc ata caa ggt gaa tcc gct gat gtg atg cct aaa Pro Met Met Gly Phe Ile Gln Gly Glu Ser Ala Asp Val Met Pro Lys 290 295 300	912
gca gca tcc agg tta agt ttg agc aag caa gat gat aaa ttt atg cta Ala Ala Ser Arg Leu Ser Leu Ser Lys Gln Asp Asp Lys Phe Met Leu 305 310 315 320	960
gcc tca agt gtt act gac tct caa ata aaa ttt aaa tca aac aat gca Ala Ser Ser Val Thr Asp Ser Gln Ile Lys Phe Lys Ser Asn Asn Ala 325 330 335	1008
caa ttg atg gtt gct ttc gca ttt atg cca ata aca acg aat ggt att Gln Leu Met Val Ala Phe Ala Phe Met Pro Ile Thr Thr Asn Gly Ile 340 345 350	1056
tta cat gat tat aca tac gat ata ata ata aat gat aaa aaa tat aaa Leu His Asp Tyr Thr Tyr Asp Ile Ile Ile Asn Asp Lys Lys Tyr Lys 355 360 365	1104
att gaa aat cat gtt gca cct cta tct agg ctt gat aaa aat aag aag Ile Glu Asn His Val Ala Pro Leu Ser Arg Leu Asp Lys Asn Lys Lys 370 375 380	1152
atg aag tgt gaa tac cag caa ata tcg gat tta aca aat acg tat aac Met Lys Cys Glu Tyr Gln Gln Ile Ser Asp Leu Thr Asn Thr Tyr Asn 385 390 395 400	1200
att aat gca aat tac tta acg ggt ttt tta ctt gtc cta aaa cca gat Ile Asn Ala Asn Tyr Leu Thr Gly Phe Leu Leu Val Leu Lys Pro Asp 405 410 415	1248
gat att att aat tac aac aat agc cct tcc gta cta ctc aag act gat Asp Ile Ile Asn Tyr Asn Asn Ser Pro Ser Val Leu Leu Lys Thr Asp 420 425 430	1296
ttt gcg ttc tat aaa aaa aca tac cag aag ctt gat aaa ata tat gat Phe Ala Phe Tyr Lys Lys Thr Tyr Gln Lys Leu Asp Lys Ile Tyr Asp 435 440 445	1344
gac ata agc aat gga aaa tta tct tca ctg aga gca aca ggt atc tcc Asp Ile Ser Asn Gly Lys Leu Ser Ser Leu Arg Ala Thr Gly Ile Ser 450 455 460	1392
cag ttt agt atc aac ggg aaa cat ttg tcg tta agg cca gaa tcg gag Gln Phe Ser Ile Asn Gly Lys His Leu Ser Leu Arg Pro Glu Ser Glu 465 470 475 480	1440
att att att tct gaa ggg agt ttg tat gga cta gtt aat aaa agc aaa Ile Ile Ile Ser Glu Gly Ser Leu Tyr Gly Leu Val Asn Lys Ser Lys 485 490 495	1488
aaa atc aaa ata tat ggc aca gca gat ctt gtt ttt gtt gat aac aag Lys Ile Lys Ile Tyr Gly Thr Ala Asp Leu Val Phe Val Asp Asn Lys 500 505 510	1536

ata atg aac ctt cgt aaa ata act tat ttg caa tct aag cta gaa att 1584
 Ile Met Asn Leu Arg Lys Ile Thr Tyr Leu Gln Ser Lys Leu Glu Ile
 515 520 525

ttt ggt tct tct att atg gat ata tta aag tat ata ttt ggt tta ggt 1632
 Phe Gly Ser Ser Ile Met Asp Ile Leu Lys Tyr Ile Phe Gly Leu Gly
 530 535 540

ctg cta gca att tct ata aaa ttc att cat tct tac ttt aag aat gat 1680
 Leu Leu Ala Ile Ser Ile Lys Phe Ile His Ser Tyr Phe Lys Asn Asp
 545 550 555 560

gtg aat gaa aat tta ttc ttg taa 1704
 Val Asn Glu Asn Leu Phe Leu *
 565

<210> 239

<211> 1092

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1092)

<400> 239

atg tct aac ttt atc aat att cat gtt ctg atc tct cac agc cct tca 48
 Met Ser Asn Phe Ile Asn Ile His Val Leu Ile Ser His Ser Pro Ser
 1 5 10 15

tgt ctg aac cgc gac gat atg aac atg cag aaa gac gct att ttc ggc 96
 Cys Leu Asn Arg Asp Asp Met Asn Met Gln Lys Asp Ala Ile Phe Gly
 20 25 30

ggc aaa aga cga gta aga att tca agt caa agc ctt aaa cgt gcg atg 144
 Gly Lys Arg Arg Val Arg Ile Ser Ser Gln Ser Leu Lys Arg Ala Met
 35 40 45

cgt aaa agt ggt tat tac gca caa aat att ggt gaa tcc agt ctc aga 192
 Arg Lys Ser Gly Tyr Tyr Ala Gln Asn Ile Gly Glu Ser Ser Leu Arg
 50 55 60

acc att cat ctt gca caa tta cgt gat gtt ctt cgg caa aaa ctt ggt 240
 Thr Ile His Leu Ala Gln Leu Arg Asp Val Leu Arg Gln Lys Leu Gly
 65 70 75 80

gaa cgt ttt gac caa aaa atc atc gat aag aca tta gcg ctg ctc tcc 288
 Glu Arg Phe Asp Gln Lys Ile Ile Asp Lys Thr Leu Ala Leu Leu Ser
 85 90 95

ggt aaa tca gtt gat gaa gcc gaa aag att tct gcc gat gcg gtt act 336
 Gly Lys Ser Val Asp Glu Ala Glu Lys Ile Ser Ala Asp Ala Val Thr
 100 105 110

ccc tgg gtt gtg gga gaa ata gcc tgg ttc tgt gag cag gtt gca aaa 384
 Pro Trp Val Val Gly Glu Ile Ala Trp Phe Cys Glu Gln Val Ala Lys
 115 120 125

gca gag gct gat aat ctg gat gat aaa aag ctg ctc aaa gtt ctt aag Ala Glu Ala Asp Asn Leu Asp Lys Lys Leu Leu Lys Val Leu Lys 130 135 140	432
gaa gat att gcc gcc ata cgt gtg aat tta cag cag ggt gtt gat att Glu Asp Ile Ala Ala Ile Arg Val Asn Leu Gln Gln Gly Val Asp Ile 145 150 155 160	480
gcg ctt agt gga aga atg gca acc agc ggc atg atg act gag ttg gga Ala Leu Ser Gly Arg Met Ala Thr Ser Gly Met Met Thr Glu Leu Gly 165 170 175	528
aaa gtt gat ggt gca atg tcc att gcg cat gcg atc act act cat cag Lys Val Asp Gly Ala Met Ser Ile Ala His Ala Ile Thr Thr His Gln 180 185 190	576
gtt gat tct gat att gac tgg ttc acc gct gta gat gat tta cag gaa Val Asp Ser Asp Ile Asp Trp Phe Thr Ala Val Asp Asp Leu Gln Glu 195 200 205	624
caa ggt tct gca cat ctg gga act cag gaa ttt tca tcg ggt gtt ttt Gln Gly Ser Ala His Leu Gly Thr Gln Glu Phe Ser Ser Gly Val Phe 210 215 220	672
tat cgt tat gcc aac att aac ctc gct caa ctt cag gaa aat tta ggt Tyr Arg Tyr Ala Asn Ile Asn Leu Ala Gln Leu Gln Glu Asn Leu Gly 225 230 235 240	720
ggg gcc tcc agg gag cag gct ctg gaa att gca acc cat gtt gtt cat Gly Ala Ser Arg Glu Gln Ala Leu Glu Ile Ala Thr His Val Val His 245 250 255	768
atg ctg gca aca gag gtc cct gga gca aaa cag cgt act tat gcc gct Met Leu Ala Thr Glu Val Pro Gly Ala Lys Gln Arg Thr Tyr Ala Ala 260 265 270	816
ttt aac cct gcg gat atg gta atg gtt aat ttc tcc gat atg cca ctt Phe Asn Pro Ala Asp Met Val Met Val Asn Phe Ser Asp Met Pro Leu 275 280 285	864
tct atg gca aat gct ttt gaa aaa gcg gtt aaa gcg aaa gat ggc ttt Ser Met Ala Asn Ala Phe Glu Lys Ala Val Lys Ala Lys Asp Gly Phe 290 295 300	912
ttg caa ccg tct ata cag gcg ttt aat caa tat tgg gat cgc gtt gcc Leu Gln Pro Ser Ile Gln Ala Phe Asn Gln Tyr Trp Asp Arg Val Ala 305 310 315 320	960
aat gga tat ggt ctg aac gga gct gct gcg caa ttc agc tta tct gat Asn Gly Tyr Gly Leu Asn Gly Ala Ala Ala Gln Phe Ser Leu Ser Asp 325 330 335	1008
gta gac cca att act gct caa gtt aaa caa atg cct act tta gaa cag Val Asp Pro Ile Thr Ala Gln Val Lys Gln Met Pro Thr Leu Glu Gln 340 345 350	1056
tta aaa tcc tgg gtt cgt aat aat ggc gag gcg tga Leu Lys Ser Trp Val Arg Asn Asn Gly Glu Ala *	1092
355 360	

<210> 240
 <211> 366
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(366)

<400> 240
 atg atg tcc acc acg tta ttt aaa gat ttc acc ttc gaa gcc gct cac 48
 Met Met Ser Thr Thr Leu Phe Lys Asp Phe Thr Phe Glu Ala Ala His
 1 5 10 15
 cgc tta cca cac gtc ccg gaa ggg cat aaa tgt ggt cgc ctg cac ggg 96
 Arg Leu Pro His Val Pro Glu Gly His Lys Cys Gly Arg Leu His Gly
 20 25 30
 cat tcc ttt atg gtg cga ctg gaa att acc ggg gaa gtc gat ccg cat 144
 His Ser Phe Met Val Arg Leu Glu Ile Thr Gly Glu Val Asp Pro His
 35 40 45
 acg ggc tgg att atc gat ttc gct gaa cta aaa gcg gcg ttt aaa cca 192
 Thr Gly Trp Ile Ile Asp Phe Ala Glu Leu Lys Ala Ala Phe Lys Pro
 50 55 60
 acc tac gag cgc ctc gat cac cat tat ctc aat gat att cca ggt ctg 240
 Thr Tyr Glu Arg Leu Asp His His Tyr Leu Asn Asp Ile Pro Gly Leu
 65 70 75 80
 gaa aac cca acc agc gag gtt tta gca aaa tgg att tgg gat cag gtt 288
 Glu Asn Pro Thr Ser Glu Val Leu Ala Lys Trp Ile Trp Asp Gln Val
 85 90 95
 aaa ccc gtt gtg ccg ctg tta agt gcg gtg atg gta aaa gaa acc tgc 336
 Lys Pro Val Val Pro Leu Leu Ser Ala Val Met Val Lys Glu Thr Cys
 100 105 110
 acc gca ggt tgt atc tat cgc ggc gaa tga 366
 Thr Ala Gly Cys Ile Tyr Arg Gly Glu *
 115 120

<210> 241
 <211> 1302
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1302)

<400> 241
 gtg ttg tgt tct gga tat ctg ggg cat gac atg gaa gac gac tgc gac 48
 Met Leu Cys Ser Gly Tyr Leu Gly His Asp Met Glu Asp Asp Cys Asp
 1 5 10 15
 att att att att ggt gcc ggt att gca ggc acc gct tgc gcg tta cgc 96
 Ile Ile Ile Ile Gly Ala Gly Ile Ala Gly Thr Ala Cys Ala Leu Arg

20	25	30	
tgc gcg cga gcg ggt tta tcc gtt ttg tta ctg gaa cgc gct gaa atc			144
Cys Ala Arg Ala Gly Leu Ser Val Leu Leu Leu Glu Arg Ala Glu Ile			
35	40	45	
ccc ggc agc aaa aat ctt tcc ggc ggg cgg tta tat acc cat gca ctc			192
Pro Gly Ser Lys Asn Leu Ser Gly Gly Arg Leu Tyr Thr His Ala Leu			
50	55	60	
gcg gaa ctc ctc ccg caa ttt cat ctg acc gcg cct ctt gaa cga cgc			240
Ala Glu Leu Leu Pro Gln Phe His Leu Thr Ala Pro Leu Glu Arg Arg			
65	70	75	80
atc act cac gaa agc ctt tcc ctg tta acg ccc gat ggc gta acg acg			288
Ile Thr His Glu Ser Leu Ser Leu Leu Thr Pro Asp Gly Val Thr Thr			
85	90	95	
ttt tcc agc tta cag ccc ggc ggt gaa tcc tgg agt gta tta cgt gca			336
Phe Ser Ser Leu Gln Pro Gly Gly Glu Ser Trp Ser Val Leu Arg Ala			
100	105	110	
cga ttc gat ccg tgg ctg gtt gcc gaa gcc gaa aaa gaa ggt gtc gaa			384
Arg Phe Asp Pro Trp Leu Val Ala Glu Ala Glu Lys Glu Gly Val Glu			
115	120	125	
tgc atc ccc gga gcg acg gtg gat gca ctg tat gaa gaa aac ggc aga			432
Cys Ile Pro Gly Ala Thr Val Asp Ala Leu Tyr Glu Glu Asn Gly Arg			
130	135	140	
gtc tgt ggc gtt att tgt ggt gac gat att ctc cgc gcc cgt tat gtg			480
Val Cys Gly Val Ile Cys Gly Asp Asp Ile Leu Arg Ala Arg Tyr Val			
145	150	155	160
gtg ctg gca gaa ggt gcc aac agc gtc ctg gct gaa cgt cac ggg tta			528
Val Leu Ala Glu Gly Ala Asn Ser Val Leu Ala Glu Arg His Gly Leu			
165	170	175	
gtg act cgt cct gct ggc gaa gcg atg gcg ttg ggg atc aaa gaa gtg			576
Val Thr Arg Pro Ala Gly Glu Ala Met Ala Leu Gly Ile Lys Glu Val			
180	185	190	
ctg tcg ctg gaa aca tcc gct att gaa gaa cgt ttt cat ctg gag aat			624
Leu Ser Leu Glu Thr Ser Ala Ile Glu Glu Arg Phe His Leu Glu Asn			
195	200	205	
aac gaa ggc gca gcg ttg ctg ttc agc ggc agg atc tgt gat gac tta			672
Asn Glu Gly Ala Ala Leu Leu Phe Ser Gly Arg Ile Cys Asp Asp Leu			
210	215	220	
ccc ggc ggc gca ttt ctt tat act aat caa caa acg ctc tcg tta ggg			720
Pro Gly Gly Ala Phe Leu Tyr Thr Asn Gln Gln Thr Leu Ser Leu Gly			
225	230	235	240
att gtt tgc ccg ctc tct tcc ctt acg caa agt cgt gtt ccg gca agc			768
Ile Val Cys Pro Leu Ser Ser Leu Thr Gln Ser Arg Val Pro Ala Ser			
245	250	255	
gag ctg ctg act cgc ttt aaa gcg cat ccg gca gtg cgc ccg ctt atc			816
Glu Leu Leu Thr Arg Phe Lys Ala His Pro Ala Val Arg Pro Leu Ile			

260	265	270	
aaa aac acg gaa tca ctg gag tat ggt gcg cat ctg gtg cca gaa ggt			864
Lys Asn Thr Glu Ser Leu Glu Tyr Gly Ala His Leu Val Pro Glu Gly			
275	280	285	
ggc ttg cac agt atg ccg gtg caa tac gcc ggt aac ggc tgg ctg ctg			912
Gly Leu His Ser Met Pro Val Gln Tyr Ala Gly Asn Gly Trp Leu Leu			
290	295	300	
gtg ggc gat gcg ttg cgc agt tgc gtc aat acc gga att tcc gtg cgc			960
Val Gly Asp Ala Leu Arg Ser Cys Val Asn Thr Gly Ile Ser Val Arg			
305	310	315	320
ggc atg gat atg gcg ctg act ggc gcg cag gcg gcg gca caa acg ctg			1008
Gly Met Asp Met Ala Leu Thr Gly Ala Gln Ala Ala Ala Gln Thr Leu			
325	330	335	
ata agc gcc tgc cag cac cgc gag ccg caa aat ctg ttt ccg ctt tat			1056
Ile Ser Ala Cys Gln His Arg Glu Pro Gln Asn Leu Phe Pro Leu Tyr			
340	345	350	
cat cac aac gta gag cgc agc ctg ctg tgg gat gtt cta cag cgt tat			1104
His His Asn Val Glu Arg Ser Leu Leu Trp Asp Val Leu Gln Arg Tyr			
355	360	365	
cag cat gtt ccg gcg ctt ttg caa cgc ccg gga tgg tac cgt acg tgg			1152
Gln His Val Pro Ala Leu Leu Gln Arg Pro Gly Trp Tyr Arg Thr Trp			
370	375	380	
cct gcg tta atg cag gat att tcc cgc gat tta tgg gat cag ggt gat			1200
Pro Ala Leu Met Gln Asp Ile Ser Arg Asp Leu Trp Asp Gln Gly Asp			
385	390	395	400
aaa cct gtt cca ccg ctg cgc cag tta ttc tgg cat cat tta cgt cgt			1248
Lys Pro Val Pro Pro Leu Arg Gln Leu Phe Trp His His Leu Arg Arg			
405	410	415	
cac ggc ctg tgg cat ctg gcg ggc gat gtt atc agg agt ctg cga tgt			1296
His Gly Leu Trp His Leu Ala Gly Asp Val Ile Arg Ser Leu Arg Cys			
420	425	430	
ctg tag			1302
Leu *			

<210> 242

<211> 297

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(297)

<400> 242

gtg gca tct ggc ggg cga tgt tat cag gag tct gcg atg tct gta gcc	48
Met Ala Ser Gly Gly Arg Cys Tyr Gln Glu Ser Ala Met Ser Val Ala	
1 5 10 15	

cgt aat ctc tgg cgc gtt gct gat gcg ccg cac att gtt ccg gct gac 96
 Arg Asn Leu Trp Arg Val Ala Asp Ala Pro His Ile Val Pro Ala Asp
 20 25 30

 tcc gtt gag cgc cag acg gca gaa cgg ttg att aac gcc tgt ccg gca 144
 Ser Val Glu Arg Gln Thr Ala Glu Arg Leu Ile Asn Ala Cys Pro Ala
 35 40 45

 ggt ctt ttt tcg ctc aca ccg gaa ggt aac tta cgt att gac tat cgc 192
 Gly Leu Phe Ser Leu Thr Pro Glu Gly Asn Leu Arg Ile Asp Tyr Arg
 50 55 60

 agt tgc ctg gag tgt ggc acc tgc cgt ttg ctg tgc gac gaa tca aca 240
 Ser Cys Leu Glu Cys Gly Thr Cys Arg Leu Leu Cys Asp Glu Ser Thr
 65 70 75 80

 cta caa cag tgg cgc tat ccg cct tcc gga ttc ggc atc acc tac cgc 288
 Leu Gln Gln Trp Arg Tyr Pro Pro Ser Gly Phe Gly Ile Thr Tyr Arg
 85 90 95

 ttt gga taa 297
 Phe Gly *

<210> 243
 <211> 576
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(576)

<400> 243
 atg ccc ctc tta cac ctg ctc cgc cag aat ccg gtg att gct gcc gtt 48
 Met Pro Leu Leu His Leu Leu Arg Gln Asn Pro Val Ile Ala Ala Val
 1 5 10 15

 aaa gat aat gcc agc ctg caa ctg gca atc gat tct gaa tgc caa ttt 96
 Lys Asp Asn Ala Ser Leu Gln Leu Ala Ile Asp Ser Glu Cys Gln Phe
 20 25 30

 att tcc gtg ttg tac ggc aat atc tgc acc atc agt aat atc gtt aaa 144
 Ile Ser Val Leu Tyr Gly Asn Ile Cys Thr Ile Ser Asn Ile Val Lys
 35 40 45

 aag att aag aac gcc ggg aaa tat gct ttt att cat gtt gat ttg ctg 192
 Lys Ile Lys Asn Ala Gly Lys Tyr Ala Phe Ile His Val Asp Leu Leu
 50 55 60

 gaa ggc gcg tca aat aaa gaa gtc gtt att cag ttt ttg aaa ctg gtg 240
 Glu Gly Ala Ser Asn Lys Glu Val Val Ile Gln Phe Leu Lys Leu Val
 65 70 75 80

 acc gag gcg gac ggc att atc agt acc aaa gcc tca atg ttg aaa gcg 288
 Thr Glu Ala Asp Gly Ile Ile Ser Thr Lys Ala Ser Met Leu Lys Ala
 85 90 95

gca aga gcg gaa ggt ttt ttc tgt att cat cgc ctg ttt att gtt gat 336
 Ala Arg Ala Glu Gly Phe Phe Cys Ile His Arg Leu Phe Ile Val Asp
 100 105 110

tca att tcg ttt cac aac att gat aag caa gtt gcg caa tcg aat ccg 384
 Ser Ile Ser Phe His Asn Ile Asp Lys Gln Val Ala Gln Ser Asn Pro
 115 120 125

gat tgt att gag atc ctg cca ggc tgt atg ccc aaa gtg ctg ggc tgg 432
 Asp Cys Ile Glu Ile Leu Pro Gly Cys Met Pro Lys Val Leu Gly Trp
 130 135 140

gtg aca gag aaa atc cgc caa ccg ctg att gcc ggt ggg ctg gtg tgc 480
 Val Thr Glu Lys Ile Arg Gln Pro Leu Ile Ala Gly Gly Leu Val Cys
 145 150 155 160

gat gaa gaa gat gcg cgt aat gcg att aac gcg ggt gtc gtg gcg ctt 528
 Asp Glu Glu Asp Ala Arg Asn Ala Ile Asn Ala Gly Val Val Ala Leu
 165 170 175

tcc acc acg aat acc ggg gtc tgg acg tta gcg aaa aaa tta ctt tga 576
 Ser Thr Thr Asn Thr Gly Val Trp Thr Leu Ala Lys Lys Leu Leu *
 180 185 190

<210> 244
 <211> 405
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(405)

<400> 244

atg ttc atg acc tgg gaa tat gcg cta att ggg tta gtc gtc ggc atc 48
 Met Phe Met Thr Trp Glu Tyr Ala Leu Ile Gly Leu Val Val Gly Ile
 1 5 10 15

att att ggt gct gtg gcc atg cgt ttt ggt aat cgt aaa cta cgc cag 96
 Ile Ile Gly Ala Val Ala Met Arg Phe Gly Asn Arg Lys Leu Arg Gln
 20 25 30

caa cag gcg ttg cag tac gaa ctg gaa aag aat aaa gct gaa ctg gac 144
 Gln Gln Ala Leu Gln Tyr Glu Leu Glu Lys Asn Lys Ala Glu Leu Asp
 35 40 45

gag tat cgc gaa gag ctg gtt agc cac ttt gcc cgc agc gcg gaa tta 192
 Glu Tyr Arg Glu Glu Leu Val Ser His Phe Ala Arg Ser Ala Glu Leu
 50 55 60

ctg gat acc atg gcg cac gac tat cgc cag ctg tat cag cac atg gca 240
 Leu Asp Thr Met Ala His Asp Tyr Arg Gln Leu Tyr Gln His Met Ala
 65 70 75 80

aaa agc tcc agc agc ctg ctg ccg gaa ctg lct gct gaa gca aac ccg 288
 Lys Ser Ser Ser Ser Leu Leu Pro Glu Leu Ser Ala Glu Ala Asn Pro
 85 90 95

ttc cgt aat cgt ctg gca gag tct gaa gcc agc aac gat cag gca ccg 336

Phe	Arg	Asn	Arg	Leu	Ala	Glu	Ser	Glu	Ala	Ser	Asn	Asp	Gln	Ala	Pro		
			100					105					110				
gtg	cag	atg	cct	cgc	gac	tat	tct	gaa	ggc	gca	tcc	ggc	ctg	ctg	cgt	384	
Val	Gln	Met	Pro	Arg	Asp	Tyr	Ser	Glu	Gly	Ala	Ser	Gly	Leu	Leu	Arg		
		115					120					125					
act	ggc	gcg	aag	cgc	gac	taa										405	
Thr	Gly	Ala	Lys	Arg	Asp	*											
		130															
<210> 245																	
<211> 1368																	
<212> DNA																	
<213> Escherichia coli																	
<220>																	
<221> CDS																	
<222> (1)...(1368)																	
<400> 245																	
atg	aaa	aaa	caa	acc	cag	ctg	ttg	agt	gca	tta	gcg	tta	agt	gtc	ggg	48	
Met	Lys	Lys	Gln	Thr	Gln	Leu	Leu	Ser	Ala	Leu	Ala	Leu	Ser	Val	Gly		
1				5					10					15			
tta	act	ctc	tcg	gcg	tca	ttt	cag	gcc	gtc	gcg	tcg	att	cca	ggc	cag	96	
Leu	Thr	Leu	Ser	Ala	Ser	Phe	Gln	Ala	Val	Ala	Ser	Ile	Pro	Gly	Gln		
			20					25					30				
gtt	gcc	gat	cag	gcc	cct	ctc	ccc	agt	ctg	gct	cca	atg	ctg	gaa	aaa	144	
Val	Ala	Asp	Gln	Ala	Pro	Leu	Pro	Ser	Leu	Ala	Pro	Met	Leu	Glu	Lys		
		35					40					45					
gtg	ctt	ccg	gca	gtg	gtg	agc	gta	cgg	gtg	gaa	gga	acg	gcc	agt	cag	192	
Val	Leu	Pro	Ala	Val	Val	Ser	Val	Arg	Val	Glu	Gly	Thr	Ala	Ser	Gln		
	50					55					60						
gga	cag	aaa	atc	ccg	gaa	gaa	ttc	aaa	aag	ttt	ttt	ggt	gat	gat	tta	240	
Gly	Gln	Lys	Ile	Pro	Glu	Glu	Phe	Lys	Lys	Phe	Phe	Gly	Asp	Asp	Leu		
65					70					75					80		
ccg	gat	caa	cct	gca	caa	ccc	ttc	gaa	ggt	tta	ggc	tcc	ggt	gtc	atc	288	
Pro	Asp	Gln	Pro	Ala	Gln	Pro	Phe	Glu	Gly	Leu	Gly	Ser	Gly	Val	Ile		
				85					90					95			
atc	aac	gcc	agt	aaa	ggc	tat	gtg	ctg	acc	aac	aac	cat	gtg	att	aat	336	
Ile	Asn	Ala	Ser	Lys	Gly	Tyr	Val	Leu	Thr	Asn	Asn	His	Val	Ile	Asn		
			100					105					110				
cag	gca	cag	aaa	atc	agt	att	cag	ctc	aat	gat	ggg	cgc	gag	ttt	gat	384	
Gln	Ala	Gln	Lys	Ile	Ser	Ile	Gln	Leu	Asn	Asp	Gly	Arg	Glu	Phe	Asp		
		115					120					125					
gca	aaa	ctg	att	ggt	agc	gat	gac	cag	agc	gat	atc	gcc	ctg	tta	caa	432	
Ala	Lys	Leu	Ile	Gly	Ser	Asp	Asp	Gln	Ser	Asp	Ile	Ala	Leu	Leu	Gln		
		130				135					140						
att	caa	aac	ccg	agc	aaa	tta	acg	caa	atc	gct	att	gcc	gac	tcc	gat	480	
Ile	Gln	Asn	Pro	Ser	Lys	Leu	Thr	Gln	Ile	Ala	Ile	Ala	Asp	Ser	Asp		

145	150	155	160	
aaa ttg cgc gtc ggt gat ttt gcc gta gcg gtc ggt aac cca ttt ggc				528
Lys Leu Arg Val Gly Asp Phe Ala Val Ala Val Gly Asn Pro Phe Gly				
165		170	175	
ctt ggg caa acc gcc acc tct ggc att gtt tcc gca tta ggc cgc agc				576
Leu Gly Gln Thr Ala Thr Ser Gly Ile Val Ser Ala Leu Gly Arg Ser				
180		185	190	
ggg ttg aat ctt gaa ggt ctg gaa aac ttt atc cag aca gat gct tcc				624
Gly Leu Asn Leu Glu Gly Leu Glu Asn Phe Ile Gln Thr Asp Ala Ser				
195		200	205	
att aac cgc ggt aac tcc ggc ggt gca cta tta aac ctt aac ggt gag				672
Ile Asn Arg Gly Asn Ser Gly Gly Ala Leu Leu Asn Leu Asn Gly Glu				
210		215	220	
tta att ggc atc aac act gca atc ctt gcg cct ggc ggc ggg agc gtc				720
Leu Ile Gly Ile Asn Thr Ala Ile Leu Ala Pro Gly Gly Gly Ser Val				
225		230	235	240
ggg att gga ttt gcc atc ccc agt aat atg gcg cga aca ctg gcg cag				768
Gly Ile Gly Phe Ala Ile Pro Ser Asn Met Ala Arg Thr Leu Ala Gln				
245		250	255	
cag ctt atc gac ttt ggt gaa atc aaa cgc ggt ttg tta ggc atc aaa				816
Gln Leu Ile Asp Phe Gly Glu Ile Lys Arg Gly Leu Leu Gly Ile Lys				
260		265	270	
ggc acc gag atg agt gcc gat atc gcc aaa gcc ttc aac ctt gac gtg				864
Gly Thr Glu Met Ser Ala Asp Ile Ala Lys Ala Phe Asn Leu Asp Val				
275		280	285	
cag cgt ggc gcg ttt gtc agc gaa gtg ttg cca ggt tct ggc tcg gca				912
Gln Arg Gly Ala Phe Val Ser Glu Val Leu Pro Gly Ser Gly Ser Ala				
290		295	300	
aaa gcg ggc gtc aaa gcg ggc gat att att acc agc ctc aac ggc aaa				960
Lys Ala Gly Val Lys Ala Gly Asp Ile Ile Thr Ser Leu Asn Gly Lys				
305		310	315	320
ccg ctg aat agc ttt gct gag ttg gcg tct cgt atc gcg acc acc gag				1008
Pro Leu Asn Ser Phe Ala Glu Leu Arg Ser Arg Ile Ala Thr Thr Glu				
325		330	335	
ccg ggc acg aaa gtg aag ctt ggc ctg ctg cgt aac ggc aaa cca ctg				1056
Pro Gly Thr Lys Val Lys Leu Gly Leu Leu Arg Asn Gly Lys Pro Leu				
340		345	350	
gaa gta gaa gtg acg ctc gat acc agc acc tct tcg tcg gcc agc gct				1104
Glu Val Glu Val Thr Leu Asp Thr Ser Thr Ser Ser Ser Ala Ser Ala				
355		360	365	
gaa atg atc acg cca gcg ctg gaa ggt gca acg ttg agc gat ggt cag				1152
Glu Met Ile Thr Pro Ala Leu Glu Gly Ala Thr Leu Ser Asp Gly Gln				
370		375	380	
cta aaa gat ggc ggc aaa ggt att aaa atc gat gaa gtt gtc aaa gga				1200
Leu Lys Asp Gly Gly Lys Gly Ile Lys Ile Asp Glu Val Val Lys Gly				

385	390	395	400	
agc cca gct gct	cag gct ggc ttg caa aaa	gac gat gtg atc att ggc		1248
Ser Pro Ala Ala	Gln Ala Gly Leu Gln Lys	Asp Asp Val Ile Ile Gly		
	405	410	415	
gtc aac cgc gat	cgg gtg aac tcg att gct	gaa atg cgt aaa gtg ctg		1296
Val Asn Arg Asp	Arg Val Asn Ser Ile Ala	Glu Met Arg Lys Val Leu		
	420	425	430	
gcg gca aaa ccg	gcc atc atc gcc ctg caa att	gta cgc ggc aat gaa		1344
Ala Ala Lys Pro	Ala Ile Ile Ala Leu Gln	Ile Val Arg Gly Asn Glu		
	435	440	445	
agc atc tat ctg	ctg atg cgt taa			1368
Ser Ile Tyr Leu	Leu Met Arg *			
	450	455		
<210> 246				
<211> 1068				
<212> DNA				
<213> Escherichia coli				
<220>				
<221> CDS				
<222> (1)...(1068)				
<400> 246				
atg ttt gtg aag	ctc tta cgt tcc gtt	gcg att gga tta att	gtc ggc	48
Met Phe Val Lys	Leu Leu Arg Ser Val	Ala Ile Gly Leu Ile	Val Gly	
1	5	10	15	
gct att ctg ctg	gtt gcc atg cct tcg	ctg cgc agc ctt aac	ccg ctt	96
Ala Ile Leu Leu	Val Ala Met Pro Ser	Leu Arg Ser Leu Asn	Pro Leu	
	20	25	30	
tcc act ccg caa	ttt gac agt acc gat	gag acg cct gcc agc	tat aat	144
Ser Thr Pro Gln	Phe Asp Ser Thr Asp	Glu Thr Pro Ala Ser	Tyr Asn	
	35	40	45	
ctg gcg gtt cgc	cgc gcc gcg cca gcg	gtg gtt aac gtt tac	aac cgt	192
Leu Ala Val Arg	Arg Ala Ala Pro Ala	Val Val Asn Val Tyr	Asn Arg	
	50	55	60	
ggc ttg aac acc	aac tct cac aac cag	ctt gag atc cgc acc	ctg gga	240
Gly Leu Asn Thr	Asn Ser His Asn Gln	Leu Glu Ile Arg Thr	Leu Gly	
	65	70	75	80
tcc ggt gta atc	atg gat caa cgc ggt	tat atc atc acc aat	aaa cac	288
Ser Gly Val Ile	Met Asp Gln Arg Gly	Tyr Ile Ile Thr Asn	Lys His	
	85	90	95	
gtc atc aac gac	gcc gat cag atc atc	gtc gcc tta cag gat	gga cgt	336
Val Ile Asn Asp	Ala Asp Gln Ile Ile	Val Ala Leu Gln Asp	Gly Arg	
	100	105	110	
gta ttt gaa gca	ttg ctg gtg gga tct	gac tct cta acc gat	ctg gcg	384
Val Phe Glu Ala	Leu Leu Val Gly Ser	Asp Ser Leu Thr Asp	Leu Ala	
	115	120	125	

gta ctt aaa att aat gcc act ggc ggt tta cct acc att cca att aat Val Leu Lys Ile Asn Ala Thr Gly Gly Leu Pro Thr Ile Pro Ile Asn 130 135 140	432
gca cgt cgc gta ccg cac att ggc gac gta gta ctg gcg atc ggt aac Ala Arg Arg Val Pro His Ile Gly Asp Val Val Leu Ala Ile Gly Asn 145 150 155 160	480
ccg tac aac ctc ggg cag acc att acc cag ggg att att agt gcc acg Pro Tyr Asn Leu Gly Gln Thr Ile Thr Gln Gly Ile Ile Ser Ala Thr 165 170 175	528
ggg cga atc ggt ctg aac ccg acc ggg cgg caa aac ttc ctc caa acc Gly Arg Ile Gly Leu Asn Pro Thr Gly Arg Gln Asn Phe Leu Gln Thr 180 185 190	576
gat gct tcc att aac cac ggt aac tct ggc ggc gcg ctg gtg aac tcg Asp Ala Ser Ile Asn His Gly Asn Ser Gly Gly Ala Leu Val Asn Ser 195 200 205	624
ctg ggc gaa ctg atg ggc att aat acg ctg tcg ttt gat aag agt aac Leu Gly Glu Leu Met Gly Ile Asn Thr Leu Ser Phe Asp Lys Ser Asn 210 215 220	672
gat ggc gaa acg ccg gaa ggt atc ggc ttt gcg att cct ttc cag tta Asp Gly Glu Thr Pro Glu Gly Ile Gly Phe Ala Ile Pro Phe Gln Leu 225 230 235 240	720
gca acc aaa att atg gat aag ctg atc cgc gat ggt cgc gtg atc cgc Ala Thr Lys Ile Met Asp Lys Leu Ile Arg Asp Gly Arg Val Ile Arg 245 250 255	768
ggc tac att ggt atc ggc gga cgt gag atc gca cca ctg cac gcg cag Gly Tyr Ile Gly Ile Gly Gly Arg Glu Ile Ala Pro Leu His Ala Gln 260 265 270	816
ggc ggt ggt ata gat caa ctg caa ggg atc gtg gtt aat gaa gtg tca Gly Gly Gly Ile Asp Gln Leu Gln Gly Ile Val Val Asn Glu Val Ser 275 280 285	864
cct gac ggc ccg gcg gcg aat gcg ggt att cag gtc aac gat ctg att Pro Asp Gly Pro Ala Ala Asn Ala Gly Ile Gln Val Asn Asp Leu Ile 290 295 300	912
att tcg gtg gat aac aaa ccg gcc atc tct gct ctg gag acg atg gat Ile Ser Val Asp Asn Lys Pro Ala Ile Ser Ala Leu Glu Thr Met Asp 305 310 315 320	960
cag gtg gcg gaa att cgc cct ggt tcg gtg atc cct gta gta gtg atg Gln Val Ala Glu Ile Arg Pro Gly Ser Val Ile Pro Val Val Val Met 325 330 335	1008
cgt gat gat aag cag tta acg ctg cag gtc acc att cag gaa tat ccg Arg Asp Asp Lys Gln Leu Thr Leu Gln Val Thr Ile Gln Glu Tyr Pro 340 345 350	1056
gca acc aat taa Ala Thr Asn *	1068
355	

<210> 247
 <211> 357
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(357)

<400> 247
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 Met Ala Arg Ile Ala Gly Ile Asn Ile Pro Asp His Lys His Ala Val
 1 5 10 15
 atc gca tta act tcg att tat ggc gtc ggc aag acc cgt tct aaa gcc 96
 Ile Ala Leu Thr Ser Ile Tyr Gly Val Gly Lys Thr Arg Ser Lys Ala
 20 25 30
 atc ctg gct gca gcg ggt atc gct gaa gat gtt aag atc agt gag ctg 144
 Ile Leu Ala Ala Ala Gly Ile Ala Glu Asp Val Lys Ile Ser Glu Leu
 35 40 45
 tct gaa gga caa atc gac acg ctg cgt gac gaa gtt gcc aaa ttt gtc 192
 Ser Glu Gly Gln Ile Asp Thr Leu Arg Asp Glu Val Ala Lys Phe Val
 50 55 60
 gtt gaa ggt gat ctg cgc cgt gaa atc agc atg agc atc aag cgc ctg 240
 Val Glu Gly Asp Leu Arg Arg Glu Ile Ser Met Ser Ile Lys Arg Leu
 65 70 75 80
 atg gat ctt ggt tgc tat cgc ggt ttg cgt cat cgt cgt ggt ctc ccg 288
 Met Asp Leu Gly Cys Tyr Arg Gly Leu Arg His Arg Arg Gly Leu Pro
 85 90 95
 gtt cgc ggt cag cgt acc aag acc aac gca cgt acc cgt aag ggt ccg 336
 Val Arg Gly Gln Arg Thr Lys Thr Asn Ala Arg Thr Arg Lys Gly Pro
 100 105 110
 cgc aaa ccg atc aag aaa taa 357
 Arg Lys Pro Ile Lys Lys *
 115

<210> 248
 <211> 390
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(390)

<400> 248
 atg gca aag gca cca att cgt gca cgt aaa cgt gta aga aaa caa gtc 48
 Met Ala Lys Ala Pro Ile Arg Ala Arg Lys Arg Val Arg Lys Gln Val
 1 5 10 15
 tct gac ggc gtg gct cat atc cat gct tct ttc aac aac acc atc gtg 96

Ser Asp Gly Val Ala His Ile His Ala Ser Phe Asn Asn Thr Ile Val
 20 25 30

act atc act gat cgt cag ggt aac gcg ttg ggt tgg gca aca gcc ggt 144
 Thr Ile Thr Asp Arg Gln Gly Asn Ala Leu Gly Trp Ala Thr Ala Gly
 35 40 45

ggg tcc ggt ttc cgt ggt tct cgc aaa tcc act ccg ttt gca gct cag 192
 Gly Ser Gly Phe Arg Gly Ser Arg Lys Ser Thr Pro Phe Ala Ala Gln
 50 55 60

gtt gca gca gag cgt tgc gct gac gcc gtg aaa gaa tac ggc atc aag 240
 Val Ala Ala Glu Arg Cys Ala Asp Ala Val Lys Glu Tyr Gly Ile Lys
 65 70 75 80

aat ctg gaa gtt atg gtt aaa ggt ccg ggt cca ggc cgc gaa tct act 288
 Asn Leu Glu Val Met Val Lys Gly Pro Gly Pro Gly Arg Glu Ser Thr
 85 90 95

att cgt gct ctg aac gcc gca ggt ttc cgc atc act aac att act gat 336
 Ile Arg Ala Leu Asn Ala Ala Gly Phe Arg Ile Thr Asn Ile Thr Asp
 100 105 110

gtg act ccg atc cct cat aac ggt tgt cgt ccg ccg aaa aaa cgt cgc 384
 Val Thr Pro Ile Pro His Asn Gly Cys Arg Pro Pro Lys Lys Arg Arg
 115 120 125

gta taa 390
 Val *

<210> 249

<211> 621

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(621)

<400> 249

atg gca aga tat ttg ggt cct aag ctc aag ctg agc cgt cgt gag ggc 48
 Met Ala Arg Tyr Leu Gly Pro Lys Leu Lys Leu Ser Arg Arg Glu Gly
 1 5 10 15

acc gac tta ttc ctt aag tct ggc gtt cgc gcg atc gat acc aag tgt 96
 Thr Asp Leu Phe Leu Lys Ser Gly Val Arg Ala Ile Asp Thr Lys Cys
 20 25 30

aaa att gaa caa gct cct ggc cag cac ggt gcg cgt aaa ccg cgt ctg 144
 Lys Ile Glu Gln Ala Pro Gly Gln His Gly Ala Arg Lys Pro Arg Leu
 35 40 45

tct gac tat ggt gtg cag ttg cgt gaa aag caa aaa gtt cgc cgt atc 192
 Ser Asp Tyr Gly Val Gln Leu Arg Glu Lys Gln Lys Val Arg Arg Ile
 50 55 60

tat ggt gtg ctg gag cgt cag ttc cgt aac tac tac aaa gaa gca gca 240
 Tyr Gly Val Leu Glu Arg Gln Phe Arg Asn Tyr Tyr Lys Glu Ala Ala

65	70	75	80	
cgt ctg aaa ggc aac acc ggt gaa aac	ctg ttg gct ctg ctg gaa ggt	288		
Arg Leu Lys Gly Asn Thr Gly Glu Asn	Leu Leu Ala Leu Leu Glu Gly			
85	90	95		
cgt ctg gac aac gtt gta tac cgt atg ggc ttc ggt gcc act cgt gca	336			
Arg Leu Asp Asn Val Val Tyr Arg Met Gly Phe Gly Ala Thr Arg Ala				
100	105	110		
gaa gca cgt cag ctg gtt agc cat aaa gca att atg gta aac ggt cgt	384			
Glu Ala Arg Gln Leu Val Ser His Lys Ala Ile Met Val Asn Gly Arg				
115	120	125		
gtt gtt aac atc gct tct tat cag gtt agt ccg aat gac gtt gta agc	432			
Val Val Asn Ile Ala Ser Tyr Gln Val Ser Pro Asn Asp Val Val Ser				
130	135	140		
att cgt gag aaa gcg aag aag cag tct cgc gtg aaa gcc gct ctg gag	480			
Ile Arg Glu Lys Ala Lys Lys Gln Ser Arg Val Lys Ala Ala Leu Glu				
145	150	155	160	
ctg gct gag cag cgt gaa aag cca acc tgg ctg gaa gtt gat gct ggc	528			
Leu Ala Glu Gln Arg Glu Lys Pro Thr Trp Leu Glu Val Asp Ala Gly				
165	170	175		
aag atg gaa ggt acg ttt aag cgt aag ccg gag cgt tct gat ctg tct	576			
Lys Met Glu Gly Thr Phe Lys Arg Lys Pro Glu Arg Ser Asp Leu Ser				
180	185	190		
gcg gac att aac gaa cac ctg atc gtc gag ctt tac tcc aag taa	621			
Ala Asp Ile Asn Glu His Leu Ile Val Glu Leu Tyr Ser Lys *				
195	200	205		
<210> 250				
<211> 990				
<212> DNA				
<213> Escherichia coli				
<220>				
<221> CDS				
<222> (1)... (990)				
<400> 250				
atg cag ggt tct gtg aca gag ttt cta aaa ccg cgc ctg gtt gat atc	48			
Met Gln Gly Ser Val Thr Glu Phe Leu Lys Pro Arg Leu Val Asp Ile				
1	5	10	15	
gag caa gtg agt tcg acg cac gcc aag gtg acc ctt gag cct tta gag	96			
Glu Gln Val Ser Ser Thr His Ala Lys Val Thr Leu Glu Pro Leu Glu				
20	25	30		
cgt ggc ttt ggc cat act ctg ggt aac gca ctg cgc cgt att ctg ctc	144			
Arg Gly Phe Gly His Thr Leu Gly Asn Ala Leu Arg Arg Ile Leu Leu				
35	40	45		
tca tcg atg ccg ggt tgc gcg gtg acc gag gtt gag att gat ggt gta	192			
Ser Ser Met Pro Gly Cys Ala Val Thr Glu Val Glu Ile Asp Gly Val				
50	55	60		

cta cat gag tac agc acc aaa gaa ggc gtt cag gaa gat atc ctg gaa Leu His Glu Tyr Ser Thr Lys Glu Gly Val Gln Glu Asp Ile Leu Glu 65 70 75 80	240
atc ctg ctc aac ctg aaa ggg ctg gcg gtg aga gtt cag ggc aaa gat Ile Leu Leu Asn Leu Lys Gly Leu Ala Val Arg Val Gln Gly Lys Asp 85 90 95	288
gaa gtt att ctt acc ttg aat aaa tct ggc att ggc cct gtg act gca Glu Val Ile Leu Thr Leu Asn Lys Ser Gly Ile Gly Pro Val Thr Ala 100 105 110	336
gcc gat atc acc cac gac ggt gat gtc gaa atc gtc aag ccg cag cac Ala Asp Ile Thr His Asp Gly Asp Val Glu Ile Val Lys Pro Gln His 115 120 125	384
gtg atc tgc cac ctg acc gat gag aac gcg tct att agc atg cgt atc Val Ile Cys His Leu Thr Asp Glu Asn Ala Ser Ile Ser Met Arg Ile 130 135 140	432
aaa gtt cag cgc ggt cgt ggt tat gtg ccg gct tct acc cga att cat Lys Val Gln Arg Gly Arg Gly Tyr Val Pro Ala Ser Thr Arg Ile His 145 150 155 160	480
tcg gaa gaa gat gag cgc cca atc ggc cgt ctg ctg gtc gac gca tgc Ser Glu Glu Asp Glu Arg Pro Ile Gly Arg Leu Leu Val Asp Ala Cys 165 170 175	528
tac agc cct gtg gag cgt att gcc tac aat gtt gaa gca gcg cgt gta Tyr Ser Pro Val Glu Arg Ile Ala Tyr Asn Val Glu Ala Ala Arg Val 180 185 190	576
gaa cag cgt acc gac ctg gac aag ctg gtc atc gaa atg gaa acc aac Glu Gln Arg Thr Asp Leu Asp Lys Leu Val Ile Glu Met Glu Thr Asn 195 200 205	624
ggc aca atc gat cct gaa gag gcg att cgt cgt gcg gca acc att ctg Gly Thr Ile Asp Pro Glu Glu Ala Ile Arg Arg Ala Ala Thr Ile Leu 210 215 220	672
gct gaa caa ctg gaa gct ttc gtt gac tta cgt gat gta cgt cag cct Ala Glu Gln Leu Glu Ala Phe Val Asp Leu Arg Asp Val Arg Gln Pro 225 230 235 240	720
gaa gtg aaa gaa gag aaa cca gag ttc gat ccg atc ctg ctg cgc cct Glu Val Lys Glu Glu Lys Pro Glu Phe Asp Pro Ile Leu Leu Arg Pro 245 250 255	768
gtt gac gat ctg gaa ttg act gtc cgc tct gct aac tgc ctt aaa gca Val Asp Asp Leu Glu Leu Thr Val Arg Ser Ala Asn Cys Leu Lys Ala 260 265 270	816
gaa gct atc cac tat atc ggt gat ctg gta cag cgt acc gag gtt gag Glu Ala Ile His Tyr Ile Gly Asp Leu Val Gln Arg Thr Glu Val Glu 275 280 285	864
ctc ctt aaa acg cct aac ctt ggt aaa aaa tct ctt act gag att aaa Leu Leu Lys Thr Pro Asn Leu Gly Lys Lys Ser Leu Thr Glu Ile Lys 290 295 300	912

gac gtg ctg gct tcc cgt gga ctg tct ctg ggc atg cgc ctg gaa aac 960
 Asp Val Leu Ala Ser Arg Gly Leu Ser Leu Gly Met Arg Leu Glu Asn
 305 310 315 320

tgg cca ccg gca agc atc gct gac gag taa 990
 Trp Pro Pro Ala Ser Ile Ala Asp Glu *
 325

<210> 251

<211> 384

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(384)

<400> 251

atg cgc cat cgt aag agt ggt cgt caa ctg aac cgc aac agc agc cat 48
 Met Arg His Arg Lys Ser Gly Arg Gln Leu Asn Arg Asn Ser Ser His
 1 5 10 15

cgc cag gct atg ttc cgc aat atg gca ggt tca ctg gtt cgt cat gaa 96
 Arg Gln Ala Met Phe Arg Asn Met Ala Gly Ser Leu Val Arg His Glu
 20 25 30

atc atc aag acg act ctg cct aaa gcg aaa gag ctg cgc cgc gta gtt 144
 Ile Ile Lys Thr Thr Leu Pro Lys Ala Lys Glu Leu Arg Arg Val Val
 35 40 45

gag ccg ctg att act ctt gcc aag act gat agc gtt gct aat cgt cgt 192
 Glu Pro Leu Ile Thr Leu Ala Lys Thr Asp Ser Val Ala Asn Arg Arg
 50 55 60

ctg gca ttc gcc cgt act cgt gat aac gag atc gtg gca aaa ctg ttt 240
 Leu Ala Phe Ala Arg Thr Arg Asp Asn Glu Ile Val Ala Lys Leu Phe
 65 70 75 80

aac gaa ctg ggc ccg cgt ttc gcg agc cgt gcc ggt ggt tac act cgt 288
 Asn Glu Leu Gly Pro Arg Phe Ala Ser Arg Ala Gly Gly Tyr Thr Arg
 85 90 95

att ctg aag tgt ggc ttc cgt gca ggc gac aac gcg ccg atg gct tac 336
 Ile Leu Lys Cys Gly Phe Arg Ala Gly Asp Asn Ala Pro Met Ala Tyr
 100 105 110

atc gag ctg gtt gat cgt tca gag aaa gca gaa gct gct gca gag taa 384
 Ile Glu Leu Val Asp Arg Ser Glu Lys Ala Glu Ala Ala Ala Glu *
 115 120 125

<210> 252

<211> 141

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(141)

<400> 252

atg aaa cgc act ttt caa ccg tct gta ctg aag cgc aac cgt tct cac 48
 Met Lys Arg Thr Phe Gln Pro Ser Val Leu Lys Arg Asn Arg Ser His
 1 5 10 15

ggc ttc cgt gct cgt atg gct act aaa aat ggt cgt cag gtt ctg gca 96
 Gly Phe Arg Ala Arg Met Ala Thr Lys Asn Gly Arg Gln Val Leu Ala
 20 25 30

cgt cgt cgt gct aaa ggc cgc gct cgt ctg acc gtt tct aag taa 141
 Arg Arg Arg Ala Lys Gly Arg Ala Arg Leu Thr Val Ser Lys *
 35 40 45

<210> 253

<211> 360

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(360)

<400> 253

gtg gtt aag ctc gca ttt ccc agg gag tta cgc ttg tta act ccc agt 48
 Met Val Lys Leu Ala Phe Pro Arg Glu Leu Arg Leu Leu Thr Pro Ser
 1 5 10 15

caa ttc aca ttc gtc ttc cag cag cca caa cgg gct ggc acg ccg caa 96
 Gln Phe Thr Phe Val Phe Gln Gln Pro Gln Arg Ala Gly Thr Pro Gln
 20 25 30

att acc att ctc ggc cgc ctg aat tcg ctg ggg cat ccc cgt atc ggt 144
 Ile Thr Ile Leu Gly Arg Leu Asn Ser Leu Gly His Pro Arg Ile Gly
 35 40 45

ctt aca gtc gcc aag aaa aac gtt cga cgc gcc cat gaa cgc aat cgg 192
 Leu Thr Val Ala Lys Lys Asn Val Arg Arg Ala His Glu Arg Asn Arg
 50 55 60

att aaa cgt ctg acg cgt gaa agc ttc cgt ctg cgc caa cat gaa ctc 240
 Ile Lys Arg Leu Thr Arg Glu Ser Phe Arg Leu Arg Gln His Glu Leu
 65 70 75 80

ccg gct atg gat ttc gtg gtg gtg gcg aaa aaa ggg gtt gcc gac ctc 288
 Pro Ala Met Asp Phe Val Val Val Ala Lys Lys Gly Val Ala Asp Leu
 85 90 95

gat aac cgt gct ctc tcg gaa gcg ttg gaa aaa tta tgg cgc cgc cac 336
 Asp Asn Arg Ala Leu Ser Glu Ala Leu Glu Lys Leu Trp Arg Arg His
 100 105 110

tgt cgc ctg gct cgc ggg tcc tga 360
 Cys Arg Leu Ala Arg Gly Ser *
 115

<210> 254

<211> 1776

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1776)

<400> 254

gtg	atc	gaa	aaa	ttg	cgt	aat	atc	gcc	atc	atc	gcg	cac	gta	gac	cat	48
Met	Ile	Glu	Lys	Leu	Arg	Asn	Ile	Ala	Ile	Ile	Ala	His	Val	Asp	His	
1				5				10						15		

ggt	aaa	acc	acc	ctg	gta	gac	aag	ctg	ctc	caa	caa	tcc	ggt	acg	ttc	96
Gly	Lys	Thr	Thr	Leu	Val	Asp	Lys	Leu	Leu	Gln	Gln	Ser	Gly	Thr	Phe	
			20					25					30			

gac	tct	cgt	gcc	gaa	acc	caa	gag	cgc	gtg	atg	gac	tcc	aac	gat	ttg	144
Asp	Ser	Arg	Ala	Glu	Thr	Gln	Glu	Arg	Val	Met	Asp	Ser	Asn	Asp	Leu	
		35					40					45				

gag	aaa	gag	cgt	ggg	att	acc	atc	ctc	gcg	aaa	aac	acc	gct	atc	aaa	192
Glu	Lys	Glu	Arg	Gly	Ile	Thr	Ile	Leu	Ala	Lys	Asn	Thr	Ala	Ile	Lys	
	50					55					60					

tgg	aat	gat	tac	cgt	atc	aac	atc	gtt	gat	acc	ccg	ggg	cac	gcc	gac	240
Trp	Asn	Asp	Tyr	Arg	Ile	Asn	Ile	Val	Asp	Thr	Pro	Gly	His	Ala	Asp	
65				70					75					80		

ttc	ggt	ggt	gaa	gtt	gaa	cgt	gta	atg	tcc	atg	gta	gac	tca	gtg	ctg	288
Phe	Gly	Gly	Glu	Val	Glu	Arg	Val	Met	Ser	Met	Val	Asp	Ser	Val	Leu	
			85					90						95		

ctg	gtg	gtt	gac	gca	ttt	gac	ggc	ccg	atg	ccg	caa	acg	cgc	ttc	gta	336
Leu	Val	Val	Asp	Ala	Phe	Asp	Gly	Pro	Met	Pro	Gln	Thr	Arg	Phe	Val	
			100				105						110			

acc	aaa	aaa	gcg	ttt	gct	tac	ggc	ctg	aag	ccg	att	gtt	gtt	atc	aac	384
Thr	Lys	Lys	Ala	Phe	Ala	Tyr	Gly	Leu	Lys	Pro	Ile	Val	Val	Ile	Asn	
		115					120					125				

aaa	gtt	gac	cgc	cct	ggc	gcg	cgt	cct	gat	tgg	gtt	gtg	gat	cag	gta	432
Lys	Val	Asp	Arg	Pro	Gly	Ala	Arg	Pro	Asp	Trp	Val	Val	Asp	Gln	Val	
	130					135				140						

ttc	gat	ctg	ttc	gtt	aac	ctc	gac	gcg	acc	gac	gag	cag	ctg	gac	ttc	480
Phe	Asp	Leu	Phe	Val	Asn	Leu	Asp	Ala	Thr	Asp	Glu	Gln	Leu	Asp	Phe	
145					150				155					160		

ccg	atc	gtt	tac	gct	tct	gcg	ctg	aac	ggt	atc	gcg	ggt	ctg	gac	cac	528
Pro	Ile	Val	Tyr	Ala	Ser	Ala	Leu	Asn	Gly	Ile	Ala	Gly	Leu	Asp	His	
			165					170					175			

gaa	gat	atg	gcg	gaa	gac	atg	acc	ccg	ctg	tac	cag	gcg	att	gtt	gac	576
Glu	Asp	Met	Ala	Glu	Asp	Met	Thr	Pro	Leu	Tyr	Gln	Ala	Ile	Val	Asp	
			180					185					190			

cac	gtt	cct	gcg	ccg	gac	gtt	gac	ctt	gac	ggt	ccg	ttc	cag	atg	cag	624
His	Val	Pro	Ala	Pro	Asp	Val	Asp	Leu	Asp	Gly	Pro	Phe	Gln	Met	Gln	
		195				200						205				

att tct cag ctc gat tac aac agc tat gtt ggc gtt atc ggc att ggc Ile Ser Gln Leu Asp Tyr Asn Ser Tyr Val Gly Val Ile Gly Ile Gly 210 215 220	672
cgc atc aag cgc ggt aaa gtg aag ccg aac cag cag gtc act atc atc Arg Ile Lys Arg Gly Lys Val Lys Pro Asn Gln Gln Val Thr Ile Ile 225 230 235 240	720
gat agc gaa ggc aaa acc cgc aac gcg aaa gtc ggt aaa gtg ctg ggc Asp Ser Glu Gly Lys Thr Arg Asn Ala Lys Val Gly Lys Val Leu Gly 245 250 255	768
cac ctc ggt ctg gaa cgt atc gaa acc gat ctg gcg gaa gct ggc gat His Leu Gly Leu Glu Arg Ile Glu Thr Asp Leu Ala Glu Ala Gly Asp 260 265 270	816
atc gtt gcg atc acg ggc ctt ggc gaa ctg aac att tct gac acc gtt Ile Val Ala Ile Thr Gly Leu Gly Glu Leu Asn Ile Ser Asp Thr Val 275 280 285	864
tgc gac acg caa aac gtt gaa gcg ctg ccg gca ctc tcc gtt gat gag Cys Asp Thr Gln Asn Val Glu Ala Leu Pro Ala Leu Ser Val Asp Glu 290 295 300	912
ccg acc gtt tct atg ttc ttc tgc gtt aac acc tcg ccg ttc tgc ggt Pro Thr Val Ser Met Phe Phe Cys Val Asn Thr Ser Pro Phe Cys Gly 305 310 315 320	960
aaa gaa ggt aag ttc gta acg tct cgt cag atc ctg gat cgt ctg aac Lys Glu Gly Lys Phe Val Thr Ser Arg Gln Ile Leu Asp Arg Leu Asn 325 330 335	1008
aaa gaa ctg gta cac aac gtt gcg ctg cgc gta gaa gaa acc gaa gac Lys Glu Leu Val His Asn Val Ala Leu Arg Val Glu Glu Thr Glu Asp 340 345 350	1056
gcc gat gcg ttc cgc gtt tct ggt cgt ggc gaa ctg cac ctg tct gtt Ala Asp Ala Phe Arg Val Ser Gly Arg Gly Glu Leu His Leu Ser Val 355 360 365	1104
ctg atc gaa aac atg cgt cgt gaa ggt ttc gaa ctg gcg gta tcc cgt Leu Ile Glu Asn Met Arg Arg Glu Gly Phe Glu Leu Ala Val Ser Arg 370 375 380	1152
ccg aaa gtt atc ttc cgt gaa atc gac ggt cgt aaa caa gag ccg tat Pro Lys Val Ile Phe Arg Glu Ile Asp Gly Arg Lys Gln Glu Pro Tyr 385 390 395 400	1200
gaa aac gtg act ctg gac gtt gaa gaa cag cat cag ggt tct gta atg Glu Asn Val Thr Leu Asp Val Glu Glu Gln His Gln Gly Ser Val Met 405 410 415	1248
cag gcg ctg ggc gaa cgt aaa ggc gac ctg aaa aac atg aat cca gac Gln Ala Leu Gly Glu Arg Lys Gly Asp Leu Lys Asn Met Asn Pro Asp 420 425 430	1296
ggg aaa ggc cgc gta cgt ctc gac tac gtg atc cca agc cgt ggt ctg Gly Lys Gly Arg Val Arg Leu Asp Tyr Val Ile Pro Ser Arg Gly Leu 435 440 445	1344

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att ggc ttc cgt tct gag ttc atg acc atg act tcc ggt act ggt ctg      1392
Ile Gly Phe Arg Ser Glu Phe Met Thr Met Thr Ser Gly Thr Gly Leu
   450                               455                               460

ctg tac tcc acc ttc agc cac tac gac gac gta cgt ccg ggt gaa gtg      1440
Leu Tyr Ser Thr Phe Ser His Tyr Asp Asp Val Arg Pro Gly Glu Val
   465                               470                               475                               480

ggt cag cgt cag aac ggc gta ctg atc tct aac ggt cag ggt aaa gcg      1488
Gly Gln Arg Gln Asn Gly Val Leu Ile Ser Asn Gly Gln Gly Lys Ala
                               485                               490                               495

gtc gcg ttc gcg ctg ttc ggt ctg cag gat cgc ggt aag ctg ttc ctc      1536
Val Ala Phe Ala Leu Phe Gly Leu Gln Asp Arg Gly Lys Leu Phe Leu
                               500                               505                               510

ggt cac ggt gca gaa gtt tac gaa ggt cag att atc ggt att cat agc      1584
Gly His Gly Ala Glu Val Tyr Glu Gly Gln Ile Ile Gly Ile His Ser
                               515                               520                               525

cgc tct aac gac ctg act gta aac tgc ctg acc ggt aag aaa ctg acc      1632
Arg Ser Asn Asp Leu Thr Val Asn Cys Leu Thr Gly Lys Lys Leu Thr
   530                               535                               540

aac atg cgt gct tcc ggt act gac gaa gcc gtt gtt ctg gtt ccg cct      1680
Asn Met Arg Ala Ser Gly Thr Asp Glu Ala Val Val Leu Val Pro Pro
   545                               550                               555                               560

atc cgc atg act ctg gaa caa gct ctg gag ttc atc gat gat gac gaa      1728
Ile Arg Met Thr Leu Glu Gln Ala Leu Glu Phe Ile Asp Asp Asp Glu
                               565                               570                               575

ctg gta gaa gtg act ccg acc tct atc cgt att cgt aaa cgt cac tga      1776
Leu Val Glu Val Thr Pro Thr Ser Ile Arg Ile Arg Lys Arg His *
                               580                               585                               590

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<210> 255
 <211> 2271
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(2271)

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<400> 255
atg atg aaa gta tta att gtt gaa agc gag ttt ctc cat caa gac acc      48
Met Met Lys Val Leu Ile Val Glu Ser Glu Phe Leu His Gln Asp Thr
   1                               5                               10                               15

tgg gtc ggt aac gcc gtt gag cgt ctg gca gat gct tta agc cag caa      96
Trp Val Gly Asn Ala Val Glu Arg Leu Ala Asp Ala Leu Ser Gln Gln
                               20                               25                               30

aat gtt acc gtg att aaa tcc acc tcc ttt gat gat ggt ttt gcc att      144
Asn Val Thr Val Ile Lys Ser Thr Ser Phe Asp Asp Gly Phe Ala Ile
   35                               40                               45

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ctc tct tca aac gaa gcc att gac tgc ctg atg ttc agc tat caa atg Leu Ser Ser Asn Glu Ala Ile Asp Cys Leu Met Phe Ser Tyr Gln Met 50 55 60	192
gaa cat ccg gac gaa cat caa aac gtc aga caa ttg atc ggt aag ctt Glu His Pro Asp Glu His Gln Asn Val Arg Gln Leu Ile Gly Lys Leu 65 70 75 80	240
cat gag cgc caa caa aac gtg ccg gtc ttc ctg ttg ggc gat cgg gaa His Glu Arg Gln Gln Asn Val Pro Val Phe Leu Leu Gly Asp Arg Glu 85 90 95	288
aaa gcc ctc gcc gca atg gat cgc gac ctg ctg gag ctt gtc gat gaa Lys Ala Leu Ala Ala Met Asp Arg Asp Leu Leu Glu Leu Val Asp Glu 100 105 110	336
ttc gcc tgg att ctg gaa gat acc gcc gac ttt atc gcc gga cgc gcc Phe Ala Trp Ile Leu Glu Asp Thr Ala Asp Phe Ile Ala Gly Arg Ala 115 120 125	384
gtt gcc gcg atg acc cgc tac cgc cag cag ctg ttg ccg cca ctg ttc Val Ala Ala Met Thr Arg Tyr Arg Gln Gln Leu Leu Pro Pro Leu Phe 130 135 140	432
agc gcg ctg atg aaa tat agt gac atc cat gaa tat tcc tgg gca gcg Ser Ala Leu Met Lys Tyr Ser Asp Ile His Glu Tyr Ser Trp Ala Ala 145 150 155 160	480
cca gcc cac cag ggc ggc gtt ggt ttt acc aaa aca ccc gcc gga cgt Pro Gly His Gln Gly Gly Val Gly Phe Thr Lys Thr Pro Ala Gly Arg 165 170 175	528
ttc tac cat gac tac tat ggt gaa aat ctg ttc cgc acc gac atg ggc Phe Tyr His Asp Tyr Tyr Gly Glu Asn Leu Phe Arg Thr Asp Met Gly 180 185 190	576
atc gaa cga act tcc ctc ggt tct ttg ctt gac cat act ggc gca ttt Ile Glu Arg Thr Ser Leu Gly Ser Leu Leu Asp His Thr Gly Ala Phe 195 200 205	624
ggc gaa agc gaa aaa tat gcc gca cgc gta ttt ggt gcc gat cgc tcc Gly Glu Ser Glu Lys Tyr Ala Ala Arg Val Phe Gly Ala Asp Arg Ser 210 215 220	672
tgg tcg gta gtc gtc ggt act tcc gcc tct aac cgc acc atc atg cag Trp Ser Val Val Val Gly Thr Ser Gly Ser Asn Arg Thr Ile Met Gln 225 230 235 240	720
gct tgc atg acc gat aac gat gtc gtg gtc gtt gac cgt aac tgc cat Ala Cys Met Thr Asp Asn Asp Val Val Val Val Asp Arg Asn Cys His 245 250 255	768
aaa tcc atc gaa caa ggt ttg atg ctg aca ggc gcg aaa ccg gtc tat Lys Ser Ile Glu Gln Gly Leu Met Leu Thr Gly Ala Lys Pro Val Tyr 260 265 270	816
atg gtg cca agc cgc aac cgc tac gcc att atc ggg cca atc tat ccg Met Val Pro Ser Arg Asn Arg Tyr Gly Ile Ile Gly Pro Ile Tyr Pro 275 280 285	864

cag gaa atg caa cct gaa acc ttg cag aag aaa atc agt gaa agc ccg Gln Glu Met Gln Pro Glu Thr Leu Gln Lys Lys Ile Ser Glu Ser Pro 290 295 300	912
ctg acc aaa gac aaa gcc ggg caa aaa ccg tct tac tgc gtg gtg acc Leu Thr Lys Asp Lys Ala Gly Gln Lys Pro Ser Tyr Cys Val Val Thr 305 310 315 320	960
aac tgc acc tat gac ggc gtg tgt tat aac gct aaa gaa gcg cag gat Asn Cys Thr Tyr Asp Gly Val Cys Tyr Asn Ala Lys Glu Ala Gln Asp 325 330 335	1008
ctg ctg gaa aaa acc tcc gat cgt ctg cac ttt gac gaa gcc tgg tac Leu Leu Glu Lys Thr Ser Asp Arg Leu His Phe Asp Glu Ala Trp Tyr 340 345 350	1056
ggc tat gca cgt ttc aac ccg atc tat gcc gat cac tat gcc atg cgc Gly Tyr Ala Arg Phe Asn Pro Ile Tyr Ala Asp His Tyr Ala Met Arg 355 360 365	1104
ggc gaa cct ggc gat cac aac ggt cct acc gtt ttc gcc acc cac tcc Gly Glu Pro Gly Asp His Asn Gly Pro Thr Val Phe Ala Thr His Ser 370 375 380	1152
acc cac aaa ctg ctg aat gcg ctg tca cag gct tct tat att cat gta Thr His Lys Leu Leu Asn Ala Leu Ser Gln Ala Ser Tyr Ile His Val 385 390 395 400	1200
cgt gaa ggt cgt ggg gcg att aac ttc tcc cgc ttc aac cag gcc tac Arg Glu Gly Arg Gly Ala Ile Asn Phe Ser Arg Phe Asn Gln Ala Tyr 405 410 415	1248
atg atg cat gcc acc acc tcc ccg ctg tat gcc atc tgc gca tcc aac Met Met His Ala Thr Thr Ser Pro Leu Tyr Ala Ile Cys Ala Ser Asn 420 425 430	1296
gac gtg gcg gtg tcg atg atg gac ggc aac agc ggc ctg tca ctg aca Asp Val Ala Val Ser Met Met Asp Gly Asn Ser Gly Leu Ser Leu Thr 435 440 445	1344
cag gaa gtg att gac gaa gcg gtt gat ttc cgt cag gcg atg gcg cgg Gln Glu Val Ile Asp Glu Ala Val Asp Phe Arg Gln Ala Met Ala Arg 450 455 460	1392
cta tat aaa gag ttc acc gct gac ggt agc tgg ttc ttc aaa ccg tgg Leu Tyr Lys Glu Phe Thr Ala Asp Gly Ser Trp Phe Phe Lys Pro Trp 465 470 475 480	1440
aac aaa gaa gtc gtc acc gac cca caa acc ggc aaa acc tat gac ttt Asn Lys Glu Val Val Thr Asp Pro Gln Thr Gly Lys Thr Tyr Asp Phe 485 490 495	1488
gct gac gca cca acc aaa ctg ctg acc acc gtt cag gac tgc tgg gta Ala Asp Ala Pro Thr Lys Leu Leu Thr Thr Val Gln Asp Cys Trp Val 500 505 510	1536
atg cat ccg ggc gaa agc tgg cac ggc ttc aaa gat att ccg gat aac Met His Pro Gly Glu Ser Trp His Gly Phe Lys Asp Ile Pro Asp Asn 515 520 525	1584

tgg agt atg ctc gac ccg att aaa gtc agc atc ctt gct ccg gga atg Trp Ser Met Leu Asp Pro Ile Lys Val Ser Ile Leu Ala Pro Gly Met 530 535 540	1632
ggt gaa gat ggt gaa ctg gaa gaa acc ggt gtt ccg gcg gcg ctg gtc Gly Glu Asp Gly Glu Leu Glu Glu Thr Gly Val Pro Ala Ala Leu Val 545 550 555 560	1680
act gcc tgg ctt ggt cgc cac ggc att gta cct acc cgc acc act gac Thr Ala Trp Leu Gly Arg His Gly Ile Val Pro Thr Arg Thr Thr Asp 565 570 575	1728
ttc caa att atg ttc ctg ttc tct atg ggc gta acc cgt ggg aaa tgg Phe Gln Ile Met Phe Leu Phe Ser Met Gly Val Thr Arg Gly Lys Trp 580 585 590	1776
gga act ctg gtt aac acc ctt tgc tcc ttc aaa cgc cac tat gac gcc Gly Thr Leu Val Asn Thr Leu Cys Ser Phe Lys Arg His Tyr Asp Ala 595 600 605	1824
aac aca ccg ctg gcg cag gtg atg ccg gaa ctt gtt gaa caa tat cct Asn Thr Pro Leu Ala Gln Val Met Pro Glu Leu Val Glu Gln Tyr Pro 610 615 620	1872
gac act tac gcg aac atg ggg att cac gat ctg ggt gac acc atg ttt Asp Thr Tyr Ala Asn Met Gly Ile His Asp Leu Gly Asp Thr Met Phe 625 630 635 640	1920
gcc tgg ctg aaa gaa aac aac cct ggc gca cgg ttg aac gaa gcc tat Ala Trp Leu Lys Glu Asn Asn Pro Gly Ala Arg Leu Asn Glu Ala Tyr 645 650 655	1968
tcc ggc ctg ccg gtg gcg gaa gtc acc ccg cgt gaa gcg tac aac gcg Ser Gly Leu Pro Val Ala Glu Val Thr Pro Arg Glu Ala Tyr Asn Ala 660 665 670	2016
att gtc gac aac aat gtc gaa ctg gta tcc att gaa aat ctg cca gga Ile Val Asp Asn Asn Val Glu Leu Val Ser Ile Glu Asn Leu Pro Gly 675 680 685	2064
cgc atc gcg gca aac tca gtt atc ccg tat ccg cca gga atc ccg atg Arg Ile Ala Ala Asn Ser Val Ile Pro Tyr Pro Pro Gly Ile Pro Met 690 695 700	2112
ctg ctg tct ggt gaa aac ttc ggc gat aaa aac agt ccg caa gta agt Leu Leu Ser Gly Glu Asn Phe Gly Asp Lys Asn Ser Pro Gln Val Ser 705 710 715 720	2160
tat tta cgc tcg ctg caa tcc tgg gac cac cat ttc cct gga ttt gaa Tyr Leu Arg Ser Leu Gln Ser Trp Asp His His Phe Pro Gly Phe Glu 725 730 735	2208
cac gaa act gaa ggg act gaa att att gac ggt att tac cac gtt atg His Glu Thr Glu Gly Thr Glu Ile Ile Asp Gly Ile Tyr His Val Met 740 745 750	2256
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1				5					10					15		

gat	gtc	tgg	ata	agg	gtg	aat	ggg	aaa	gaa	cct	att	agc	ctt	aaa	gct	96
Asp	Val	Trp	Ile	Arg	Val	Asn	Gly	Lys	Glu	Pro	Ile	Ser	Leu	Lys	Ala	
			20					25					30			

aac	cat	atg	gcg	tta	tta	aat	tgt	gaa	aat	aat	att	atc	gac	gtc	tcc	144
Asn	His	Met	Ala	Leu	Leu	Asn	Cys	Glu	Asn	Asn	Ile	Ile	Asp	Val	Ser	
		35					40					45				

tct	ctt	aac	aac	act	ttg	gtt	gct	cat	att	agt	cac	gac	atc	atc	aaa	192
Ser	Leu	Asn	Asn	Thr	Leu	Val	Ala	His	Ile	Ser	His	Asp	Ile	Ile	Lys	
	50					55					60					

gat	tac	ctc	cgg	ttt	ctg	aat	aaa	gat	ctc	tcg	caa	ata	cca	gta	tgg	240
Asp	Tyr	Leu	Arg	Phe	Leu	Asn	Lys	Asp	Leu	Ser	Gln	Ile	Pro	Val	Trp	
65					70					75					80	

caa	cgt	agc	gct	acg	ccc	ata	ctc	acc	ctg	cca	tgc	ctg	acg	cca	gac	288
Gln	Arg	Ser	Ala	Thr	Pro	Ile	Leu	Thr	Leu	Pro	Cys	Leu	Thr	Pro	Asp	
				85					90					95		

gtc	ttt	cgc	gtt	gcc	gcg	caa	cac	agc	atg	atg	ccc	gca	gaa	act	gag	336
Val	Phe	Arg	Val	Ala	Ala	Gln	His	Ser	Met	Met	Pro	Ala	Glu	Thr	Glu	
			100					105					110			

tca	gaa	aag	gaa	cga	aca	cgc	gca	tta	tta	ttc	acg	gtg	cta	tcc	cgt	384
Ser	Glu	Lys	Glu	Arg	Thr	Arg	Ala	Leu	Leu	Phe	Thr	Val	Leu	Ser	Arg	
		115					120					125				

ttt	ctc	gac	agt	aaa	aaa	ttc	gtt	tca	tta	atg	atg	tat	atg	tta	cgt	432
Phe	Leu	Asp	Ser	Lys	Lys	Phe	Val	Ser	Leu	Met	Met	Tyr	Met	Leu	Arg	
	130					135					140					

aat	tgt	gta	agt	gac	agc	gtt	tat	caa	att	att	gaa	agc	gat	att	cac	480
Asn	Cys	Val	Ser	Asp	Ser	Val	Tyr	Gln	Ile	Ile	Glu	Ser	Asp	Ile	His	
145					150					155					160	

aaa	gac	tgg	aat	ctt	agt	atg	gta	gcc	agt	tgt	tta	lgt	ctt	agc	cca	528
Lys	Asp	Trp	Asn	Leu	Ser	Met	Val	Ala	Ser	Cys	Leu	Cys	Leu	Ser	Pro	
			165						170					175		

agt	ctg	tta	aag	aaa	aag	ttg	aaa	agc	gaa	aac	acc	agt	tat	agc	caa	576
Ser	Leu	Leu	Lys	Lys	Lys	Leu	Lys	Ser	Glu	Asn	Thr	Ser	Tyr	Ser	Gln	
			180					185					190			

ata	atc	acc	acc	tgc	cgc	atg	cgt	tat	gcc	gta	aat	gaa	tta	atg	atg	624
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Ile Ile Thr Thr Cys Arg Met Arg Tyr Ala Val Asn Glu Leu Met Met	
195 200 205	
gac ggt aaa aat atc tct cag gta tca cag tcc tgc ggc tac aac agt	672
Asp Gly Lys Asn Ile Ser Gln Val Ser Gln Ser Cys Gly Tyr Asn Ser	
210 215 220	
acg tcg tac ttt att tct gtc ttt aaa gac ttc tac ggt atg acg ccg	720
Thr Ser Tyr Phe Ile Ser Val Phe Lys Asp Phe Tyr Gly Met Thr Pro	
225 230 235 240	
ctg cat tat gtt agt cag cac aga gaa cgc act gtc gcc tga	762
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cag gaa aca aat atg gca aca gca tgg tat aaa caa gtt aat cca cca	96
Gln Glu Thr Asn Met Ala Thr Ala Trp Tyr Lys Gln Val Asn Pro Pro	
20 25 30	
caa cgg aaa gct ctt ttt tcc gca tgg ctt gga tat gta ttt gat ggc	144
Gln Arg Lys Ala Leu Phe Ser Ala Trp Leu Gly Tyr Val Phe Asp Gly	
35 40 45	
ttt gat ttt atg atg ata ttt tac att ctt cat att ata aaa gca gat	192
Phe Asp Phe Met Met Ile Phe Tyr Ile Leu His Ile Ile Lys Ala Asp	
50 55 60	
ctt ggc att acg gat att cag gct act tta ata ggg aca gtg gcc ttc	240
Leu Gly Ile Thr Asp Ile Gln Ala Thr Leu Ile Gly Thr Val Ala Phe	
65 70 75 80	
ata gcc aga cct att gga ggt ggt ttt ttt ggt gcc atg gct gat aaa	288
Ile Ala Arg Pro Ile Gly Gly Gly Phe Phe Gly Ala Met Ala Asp Lys	
85 90 95	
tat ggt cgt aag cca atg atg atg tgg gca att ttc att tac tca gtc	336
Tyr Gly Arg Lys Pro Met Met Met Trp Ala Ile Phe Ile Tyr Ser Val	
100 105 110	
gga aca ggc ctt agc ggt att gct aca aac tta tat atg ctc gca gtt	384
Gly Thr Gly Leu Ser Gly Ile Ala Thr Asn Leu Tyr Met Leu Ala Val	
115 120 125	
tgc cgt ttt att gtt ggc tta ggg atg tct ggt gaa tat gca tgt gct	432
Cys Arg Phe Ile Val Gly Leu Gly Met Ser Gly Glu Tyr Ala Cys Ala	

130	135	140	
tca act tat gcg gta gaa agt tgg cct aaa aat ctt caa tct aaa gct			480
Ser Thr Tyr Ala Val Glu Ser Trp Pro Lys Asn Leu Gln Ser Lys Ala			
145	150	155	160
agt gct ttt ttg gta agt ggt ttt tct gtt gga aat att att gcg gca			528
Ser Ala Phe Leu Val Ser Gly Phe Ser Val Gly Asn Ile Ile Ala Ala			
	165	170	175
caa ata atc cct cag ttt gct gaa gta tat gga tgg aga aac tct ttt			576
Gln Ile Ile Pro Gln Phe Ala Glu Val Tyr Gly Trp Arg Asn Ser Phe			
	180	185	190
ttt ata ggc ctg tta cca gtt tta cta gtt ctt tgg atc aga aaa agt			624
Phe Ile Gly Leu Leu Pro Val Leu Leu Val Leu Trp Ile Arg Lys Ser			
	195	200	205
gct cca gaa agt cag gag tgg att gaa gat aaa tat aag gat aaa tca			672
Ala Pro Glu Ser Gln Glu Trp Ile Glu Asp Lys Tyr Lys Asp Lys Ser			
	210	215	220
aca ttt ttg tct gtc ttc aga aaa cca cat ctt tca atc tct atg atc			720
Thr Phe Leu Ser Val Phe Arg Lys Pro His Leu Ser Ile Ser Met Ile			
	225	230	235
gtt ttc ctc gtc tgt ttt tgt cta ttt ggt gca aac tgg ccg ata aac			768
Val Phe Leu Val Cys Phe Cys Leu Phe Gly Ala Asn Trp Pro Ile Asn			
	245	250	255
gga cta ctt cct tcc tac ctg gca gat aat gga gtt aat aca gtg gtc			816
Gly Leu Leu Pro Ser Tyr Leu Ala Asp Asn Gly Val Asn Thr Val Val			
	260	265	270
att tca act ctg atg aca ata gca ggt tta gga aca ctg aca ggt aca			864
Ile Ser Thr Leu Met Thr Ile Ala Gly Leu Gly Thr Leu Thr Gly Thr			
	275	280	285
ata ttt ttt ggt ttt gtt ggt gat aag att ggt gta aaa aaa gcc ttt			912
Ile Phe Phe Gly Phe Val Gly Asp Lys Ile Gly Val Lys Lys Ala Phe			
	290	295	300
gta gtc ggt cta ata act tca ttt att ttc ctt tgt cct ctt ttt ttt			960
Val Val Gly Leu Ile Thr Ser Phe Ile Phe Leu Cys Pro Leu Phe Phe			
	305	310	315
att tct gtg aaa aac tct tct ctt ata gga tta tgt ctc ttt gga tta			1008
Ile Ser Val Lys Asn Ser Ser Leu Ile Gly Leu Cys Leu Phe Gly Leu			
	325	330	335
atg ttt aca aat tta ggt att gca ggg ttg gtt cca aaa ttt ata tat			1056
Met Phe Thr Asn Leu Gly Ile Ala Gly Leu Val Pro Lys Phe Ile Tyr			
	340	345	350
gat tac ttt cca aca aaa tta aga gga tta ggg acc ggt ctt att tat			1104
Asp Tyr Phe Pro Thr Lys Leu Arg Gly Leu Gly Thr Gly Leu Ile Tyr			
	355	360	365
aac tta ggg gca act gga gga atg gcc gca cct gta tta gct aca tac			1152
Asn Leu Gly Ala Thr Gly Gly Met Ala Ala Pro Val Leu Ala Thr Tyr			

370	375	380	
att tca gga tat tat ggc tta ggt gtt tca tta ttc att gtt acg gtt			1200
Ile Ser Gly Tyr Tyr Gly Leu Gly Val Ser Leu Phe Ile Val Thr Val			
385	390	395	400
gca ttc tct gcc tta tta att ttg tta gtt ggt ttt gat att cca ggt			1248
Ala Phe Ser Ala Leu Leu Ile Leu Leu Val Gly Phe Asp Ile Pro Gly			
	405	410	415
aaa att tat aaa cta tcc gtg gct aaa tga			1278
Lys Ile Tyr Lys Leu Ser Val Ala Lys *			
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1	5	10	15
ttt ggc gct gaa tta gct cgt ttt atg aat atg cat gat aat gca aaa			96
Phe Gly Ala Glu Leu Ala Arg Phe Met Asn Met His Asp Asn Ala Lys			
	20	25	30
att aca tgt gta tac gat cct gaa aat gga gaa aat att gcc cgt gaa			144
Ile Thr Cys Val Tyr Asp Pro Glu Asn Gly Glu Asn Ile Ala Arg Glu			
	35	40	45
ttg cag tgt atc aat atg tca agc ttg gat gct tta gtc tca agt aaa			192
Leu Gln Cys Ile Asn Met Ser Ser Leu Asp Ala Leu Val Ser Ser Lys			
	50	55	60
tta gtc gat tgc gtg atc gta gcc acc cca aat tat ctg cat aaa gaa			240
Leu Val Asp Cys Val Ile Val Ala Thr Pro Asn Tyr Leu His Lys Glu			
	65	70	75
cca gta att aaa gca gca aag aat aag aag cat gtt ttt tgt gaa aaa			288
Pro Val Ile Lys Ala Ala Lys Asn Lys Lys His Val Phe Cys Glu Lys			
	85	90	95
cca att gca tta agt tat gaa gat tgt gtg gat atg gtc aaa gcg tgt			336
Pro Ile Ala Leu Ser Tyr Glu Asp Cys Val Asp Met Val Lys Ala Cys			
	100	105	110
aaa gaa gct ggt gtg acc ttt atg gcc ggg cat att atg aat ttt ttc			384
Lys Glu Ala Gly Val Thr Phe Met Ala Gly His Ile Met Asn Phe Phe			
	115	120	125
aat ggg gtt caa tat gca cgg aag tta att aaa gaa ggt gtt atc ggc			432
Asn Gly Val Gln Tyr Ala Arg Lys Leu Ile Lys Glu Gly Val Ile Gly			
	130	135	140

gaa ata tta tca tgt cat act aag aga aat ggc tgg gaa aac aaa caa	480
Glu Ile Leu Ser Cys His Thr Lys Arg Asn Gly Trp Glu Asn Lys Gln	
145 150 155 160	
gag aga ctt tcc tgg aaa aag atg aaa gaa caa tct ggt gga cat cta	528
Glu Arg Leu Ser Trp Lys Lys Met Lys Glu Gln Ser Gly Gly His Leu	
165 170 175	
tat cat cat ata cat gag tta gat tgt gtt cag cat tta ctt gga gaa	576
Tyr His His Ile His Glu Leu Asp Cys Val Gln His Leu Leu Gly Glu	
180 185 190	
ata cca gag acg gtt act atg att ggt gga aat ttg gcc cat tct ggt	624
Ile Pro Glu Thr Val Thr Met Ile Gly Gly Asn Leu Ala His Ser Gly	
195 200 205	
cca gga ttt ggc aat gaa gat gat atg tta ttt atg acc ttg gaa ttc	672
Pro Gly Phe Gly Asn Glu Asp Asp Met Leu Phe Met Thr Leu Glu Phe	
210 215 220	
ccg tca gga aaa cta gca acc tta gag tgg ggg agt gca ttt aac tgg	720
Pro Ser Gly Lys Leu Ala Thr Leu Glu Trp Gly Ser Ala Phe Asn Trp	
225 230 235 240	
ccg gaa cat tat gtc atc atc aat gga act aaa ggc tct att aaa att	768
Pro Glu His Tyr Val Ile Ile Asn Gly Thr Lys Gly Ser Ile Lys Ile	
245 250 255	
gat atg caa gaa aca gca ggg tca ctt agg att ggc ggt cag aca aag	816
Asp Met Gln Glu Thr Ala Gly Ser Leu Arg Ile Gly Gly Gln Thr Lys	
260 265 270	
cat ttt ttg gtc cat gaa aca caa gaa gaa gat gat gat cgt cgg aaa	864
His Phe Leu Val His Glu Thr Gln Glu Glu Asp Asp Arg Arg Lys	
275 280 285	
ggc aat atg acc tca gaa atg gat ggc gct ata gca tat ggt cat cca	912
Gly Asn Met Thr Ser Glu Met Asp Gly Ala Ile Ala Tyr Gly His Pro	
290 295 300	
gga aaa aaa aca cca tta tgg ctt gcc agt tta ata aga aag gag acg	960
Gly Lys Lys Thr Pro Leu Trp Leu Ala Ser Leu Ile Arg Lys Glu Thr	
305 310 315 320	
tta ttc ctc cat aat atc ctc tgt ggt gca aaa cct gaa gaa gat tat	1008
Leu Phe Leu His Asn Ile Leu Cys Gly Ala Lys Pro Glu Glu Asp Tyr	
325 330 335	
att gac ctt ctc aat ggt gag gcg gcc atg tcg gcg att gct act gct	1056
Ile Asp Leu Leu Asn Gly Glu Ala Ala Met Ser Ala Ile Ala Thr Ala	
340 345 350	
gat gct gcc act ctt tca aga tcg cag gac agg aaa gtg aaa atc agt	1104
Asp Ala Ala Thr Leu Ser Arg Ser Gln Asp Arg Lys Val Lys Ile Ser	
355 360 365	
gag atc att aaa cat aca tca gta atg taa	1134
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 acg gtc aca act cta atc cga gga gta acg tat aaa aaa gag cag gca 96
 Thr Val Thr Thr Leu Ile Arg Gly Val Thr Tyr Lys Lys Glu Gln Ala
 20 25 30
 ata aat tat cta aaa gat gat tat ttg cct ctt atc cgt gcg aac aat 144
 Ile Asn Tyr Leu Lys Asp Asp Tyr Leu Pro Leu Ile Arg Ala Asn Asn
 35 40 45
 att cag aat ggc aag ttt gat act acg gac ttg gtt ttt gtt cct aaa 192
 Ile Gln Asn Gly Lys Phe Asp Thr Thr Asp Leu Val Phe Val Pro Lys
 50 55 60
 aat ctt gtt aaa gaa agt caa aaa ata tct cct gaa gat att gtt att 240
 Asn Leu Val Lys Glu Ser Gln Lys Ile Ser Pro Glu Asp Ile Val Ile
 65 70 75 80
 gca atg tca tca ggg agc aaa tcc gta gtt ggt aaa tcc gca cat cag 288
 Ala Met Ser Ser Gly Ser Lys Ser Val Val Gly Lys Ser Ala His Gln
 85 90 95
 cat cta cca ttt gaa tgt agt ttc ggc gca ttt tgc ggt gta tta cgt 336
 His Leu Pro Phe Glu Cys Ser Phe Gly Ala Phe Cys Gly Val Leu Arg
 100 105 110
 cct gaa aaa ctt ata ttt tct ggt ttt att gct cat ttc aca aaa tct 384
 Pro Glu Lys Leu Ile Phe Ser Gly Phe Ile Ala His Phe Thr Lys Ser
 115 120 125
 tct ctt tat cga aac aaa att tca tca ctt tct gct ggt gca aat att 432
 Ser Leu Tyr Arg Asn Lys Ile Ser Ser Leu Ser Ala Gly Ala Asn Ile
 130 135 140
 aat aat att aag ccg gca agc ttt gat ttg ata aat ata cca atc cca 480
 Asn Asn Ile Lys Pro Ala Ser Phe Asp Leu Ile Asn Ile Pro Ile Pro
 145 150 155 160
 cca ctt gcc gaa caa aaa atc atc gct gaa aaa ctc gat acg ctg ctg 528
 Pro Leu Ala Glu Gln Lys Ile Ile Ala Glu Lys Leu Asp Thr Leu Leu
 165 170 175
 gcg cag gta gac agc acc aaa gca cgt ttt gag caa atc cca caa atc 576
 Ala Gln Val Asp Ser Thr Lys Ala Arg Phe Glu Gln Ile Pro Gln Ile
 180 185 190

ctg aaa cgt ttt cgt caa gcg gta ttg ggg ggc gca gtt aat gga aaa Leu Lys Arg Phe Arg Gln Ala Val Leu Gly Gly Ala Val Asn Gly Lys 195 200 205	624
ttg aca gaa aaa tgg cgt aat ttt gag ccg caa cat tct gta ttt aag Leu Thr Glu Lys Trp Arg Asn Phe Glu Pro Gln His Ser Val Phe Lys 210 215 220	672
aag tta aat ttt gaa tct atc tta act gaa tta cgt aat ggt ctt tca Lys Leu Asn Phe Glu Ser Ile Leu Thr Glu Leu Arg Asn Gly Leu Ser 225 230 235 240	720
tca aag cca aat gaa agt ggt gtt ggt cat cca ata cta cgc att agt Ser Lys Pro Asn Glu Ser Gly Val Gly His Pro Ile Leu Arg Ile Ser 245 250 255	768
tct gta cgt gct ggc cat gta gat caa aac gat att cgg ttt cta gaa Ser Val Arg Ala Gly His Val Asp Gln Asn Asp Ile Arg Phe Leu Glu 260 265 270	816
tgt tca gaa agt gaa cta aac cgc cac aaa tta caa gat gga gat ctt Cys Ser Glu Ser Glu Leu Asn Arg His Lys Leu Gln Asp Gly Asp Leu 275 280 285	864
tta ttt act cgc tat aac gga agt tta gaa ttt gtt ggt gtt tgt ggg Leu Phe Thr Arg Tyr Asn Gly Ser Leu Glu Phe Val Gly Val Cys Gly 290 295 300	912
tta ttg aaa aaa tta caa cat caa aat ttg cta tat cct gat aaa ctt Leu Leu Lys Lys Leu Gln His Gln Asn Leu Leu Tyr Pro Asp Lys Leu 305 310 315 320	960
att cga gct cga tta acc aaa gat gct tta cca gaa tat atc gaa ata Ile Arg Ala Arg Leu Thr Lys Asp Ala Leu Pro Glu Tyr Ile Glu Ile 325 330 335	1008
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aca act tct ggt caa aaa ggt att tca gga aaa gat atc aaa tcc caa Thr Thr Ser Gly Gln Lys Gly Ile Ser Gly Lys Asp Ile Lys Ser Gln 355 360 365	1104
gtt gtt tta tta cct cca gta aaa gaa caa gcc gaa atc gtt cgc cgc Val Val Leu Leu Pro Pro Val Lys Glu Gln Ala Glu Ile Val Arg Arg 370 375 380	1152
gtc gag caa ctc ttc gcc tac gcc gac acc ata gaa aaa cag gtc aac Val Glu Gln Leu Phe Ala Tyr Ala Asp Thr Ile Glu Lys Gln Val Asn 385 390 395 400	1200
aac gcc tta gcc cgc gtc aac aac ctg acg caa tcc atc ctg gca aaa Asn Ala Leu Ala Arg Val Asn Asn Leu Thr Gln Ser Ile Leu Ala Lys 405 410 415	1248
gcg ttc cgt ggt gaa ctt acc gcc cag tgg cgg gcc gaa aac ccg gat Ala Phe Arg Gly Glu Leu Thr Ala Gln Trp Arg Ala Glu Asn Pro Asp 420 425 430	1296

ttg atc agc gga gaa aac agc gcc gcc gcg ttg ctg gaa aaa atc aaa 1344
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 435 440 445

gct gaa cgc gca gct agc ggg ggt aaa aaa gcc tca cgt aaa aaa tcc 1392
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tga 1395
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<400> 260

atg aac aat aac gat ctg gtc gcg aag ctg tgg aag ctg tgc gac aac 48
 Met Asn Asn Asn Asp Leu Val Ala Lys Leu Trp Lys Leu Cys Asp Asn
 1 5 10 15

ctg cgc gat ggc ggc gtt tcc tat caa aac tac gtc aat gaa ctc gcc 96
 Leu Arg Asp Gly Gly Val Ser Tyr Gln Asn Tyr Val Asn Glu Leu Ala
 20 25 30

tcg ctg ctg ttt ttg aaa atg tgt aaa gag acc ggt cag gaa gcg gaa 144
 Ser Leu Leu Phe Leu Lys Met Cys Lys Glu Thr Gly Gln Glu Ala Glu
 35 40 45

tac ctg ccg gaa ggt tac cgc tgg gat gac ctg aaa tcc cgc atc ggc 192
 Tyr Leu Pro Glu Gly Tyr Arg Trp Asp Asp Leu Lys Ser Arg Ile Gly
 50 55 60

cag gag cag ttg cag ttc tac cga aaa atg ctc gtg cat tta ggc gaa 240
 Gln Glu Gln Leu Gln Phe Tyr Arg Lys Met Leu Val His Leu Gly Glu
 65 70 75 80

gat gac aaa aag ctg gta cag gca gtt ttt cat aat gtt agt acc acc 288
 Asp Asp Lys Lys Leu Val Gln Ala Val Phe His Asn Val Ser Thr Thr
 85 90 95

atc acc gag ccg aaa caa ata acc gca ctg gtc agc aat atg gat tcg 336
 Ile Thr Glu Pro Lys Gln Ile Thr Ala Leu Val Ser Asn Met Asp Ser
 100 105 110

ctg gac tgg tac aac ggc gcg cac ggt aag tcg cgc gat gac ttc ggc 384
 Leu Asp Trp Tyr Asn Gly Ala His Gly Lys Ser Arg Asp Asp Phe Gly
 115 120 125

gat atg tac gaa ggg ctg ttg cag aag aac gcg aat gaa acc aag tct 432
 Asp Met Tyr Glu Gly Leu Leu Gln Lys Asn Ala Asn Glu Thr Lys Ser
 130 135 140

ggt gca ggc cag tac ttc acc ccg cgt ccg ctg att aaa acc att att 480

Gly 145	Ala	Gly	Gln	Tyr	Phe 150	Thr	Pro	Arg	Pro	Leu 155	Ile	Lys	Thr	Ile 160	Ile		
cat	ctg	ctg	aaa	ccg	cag	ccg	cgt	gaa	gtg	gtg	cag	gac	ccg	gcg	gca	528	
His	Leu	Leu	Lys	Pro	Gln	Pro	Arg	Glu	Val	Val	Gln	Asp	Pro	Ala	Ala	175	
ggt	acg	gcg	ggc	ttt	ttg	att	gaa	gcc	gac	cgc	tat	gtt	aag	tcg	caa	576	
Gly	Thr	Ala	Gly	Phe	Leu	Ile	Glu	Ala	Asp	Arg	Tyr	Val	Lys	Ser	Gln	190	
acc	aat	gat	ctg	gac	gac	ctt	gat	ggc	gac	acg	cag	gat	ttc	cag	atc	624	
Thr	Asn	Asp	Leu	Asp	Asp	Leu	Asp	Gly	Asp	Thr	Gln	Asp	Phe	Gln	Ile	205	
cac	cgc	gcg	ttt	atc	ggc	ctc	gaa	ctg	gtg	ccc	ggc	acc	cgt	cgt	ctg	672	
His	Arg	Ala	Phe	Ile	Gly	Leu	Glu	Leu	Val	Pro	Gly	Thr	Arg	Arg	Leu	220	
gca	ctg	atg	aac	tgc	ctg	ctg	cac	gat	att	gaa	ggc	aac	ctc	gac	cac	720	
Ala	Leu	Met	Asn	Cys	Leu	Leu	His	Asp	Ile	Glu	Gly	Asn	Leu	Asp	His	240	
ggc	ggc	gca	atc	cgt	ctg	ggc	aac	act	ctg	ggt	agc	gac	ggt	gaa	aac	768	
Gly	Gly	Ala	Ile	Arg	Leu	Gly	Asn	Thr	Leu	Gly	Ser	Asp	Gly	Glu	Asn	255	
ctg	ccg	aag	gcg	cat	att	gtc	gcc	act	aac	ccg	ccg	ttt	ggc	agc	gcc	816	
Leu	Pro	Lys	Ala	His	Ile	Val	Ala	Thr	Asn	Pro	Pro	Phe	Gly	Ser	Ala	270	
gca	ggc	acc	aac	att	acc	cgc	acc	ttt	gtt	cac	ccg	acc	agc	aac	aaa	864	
Ala	Gly	Thr	Asn	Ile	Thr	Arg	Thr	Phe	Val	His	Pro	Thr	Ser	Asn	Lys	285	
cag	ttg	tgc	ttt	atg	cag	cat	att	atc	gaa	acg	ctg	cat	ccc	ggc	ggt	912	
Gln	Leu	Cys	Phe	Met	Gln	His	Ile	Ile	Glu	Thr	Leu	His	Pro	Gly	Gly	300	
cgt	gcg	gcg	gtg	gtg	gtg	ccg	gat	aac	gtg	ctg	ttt	gaa	ggc	ggc	aaa	960	
Arg	Ala	Ala	Val	Val	Val	Pro	Asp	Asn	Val	Leu	Phe	Glu	Gly	Gly	Lys	320	
ggc	acc	gac	att	cgt	cgt	gac	ctg	atg	gat	aag	tgt	cat	ctg	cac	acc	1008	
Gly	Thr	Asp	Ile	Arg	Arg	Asp	Leu	Met	Asp	Lys	Cys	His	Leu	His	Thr	335	
att	ctg	cgt	ctg	ccg	acc	ggt	att	ttt	tac	gct	cag	ggc	gtg	aag	acc	1056	
Ile	Leu	Arg	Leu	Pro	Thr	Gly	Ile	Phe	Tyr	Ala	Gln	Gly	Val	Lys	Thr	350	
aac	gtg	ctg	ttc	ttt	acc	aaa	ggg	acg	gtg	gcg	aac	ccg	aat	cag	gat	1104	
Asn	Val	Leu	Phe	Phe	Thr	Lys	Gly	Thr	Val	Ala	Asn	Pro	Asn	Gln	Asp	365	
aag	aac	tgt	acc	gat	gat	gtg	tgg	gtg	tat	gac	ctg	cgt	acc	aat	atg	1152	
Lys	Asn	Cys	Thr	Asp	Asp	Val	Trp	Val	Tyr	Asp	Leu	Arg	Thr	Asn	Met	380	
ccg	agt	ttc	ggc	aag	cgc	aca	ccg	ttt	acc	gac	gag	cat	ttg	cag	ccg	1200	

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<400> 261
atg aaa aaa gag aac tat tca ttc aag caa gct tgt gct gtt gtc ggt      48
Met Lys Lys Glu Asn Tyr Ser Phe Lys Gln Ala Cys Ala Val Val Gly
  1                      5                      10                      15

ggg caa tca gca atg gct agg ctt tta ggt gta tca cct cca agc gta      96
Gly Gln Ser Ala Met Ala Arg Leu Leu Gly Val Ser Pro Pro Ser Val
          20                      25                      30

aat caa tgg atc aaa ggg gta cgt caa ttg cct gcc gag aga tgt cca     144
Asn Gln Trp Ile Lys Gly Val Arg Gln Leu Pro Ala Glu Arg Cys Pro

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35	40	45	
gca att gaa cgt gca aca aga ggt gag gtt ctg tgc gaa gaa ctt cgt			192
Ala Ile Glu Arg Ala Thr Arg Gly Glu Val Leu Cys Glu Glu Leu Arg			
50	55	60	
cct gat att gac tgg tca tat tta cga cgt tcg gca tgt tgt tcg cag			240
Pro Asp Ile Asp Trp Ser Tyr Leu Arg Arg Ser Ala Cys Cys Ser Gln			
65	70	75	80
aat atg tca gtg aag caa cta aat gac agt aac aaa tcc tca ttt gat			288
Asn Met Ser Val Lys Gln Leu Asn Asp Ser Asn Lys Ser Ser Phe Asp			
85	90	95	
cat acc tga			297
His Thr *			
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<211> 423			
<212> DNA			
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<220>			
<221> CDS			
<222> (1)...(423)			
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Met Lys Ile Lys His Glu His Ile Glu Ser Val Leu Phe Ala Leu Ala			
1	5	10	15
gcc gaa aaa ggg cag gca tgg gta gcc aat gca att act gaa gaa tat			96
Ala Glu Lys Gly Gln Ala Trp Val Ala Asn Ala Ile Thr Glu Glu Tyr			
20	25	30	
ctg cgc cag ggg ggc ggc gaa ttg ccc ctg gtt cca ggc aag gac tgg			144
Leu Arg Gln Gly Gly Gly Glu Leu Pro Leu Val Pro Gly Lys Asp Trp			
35	40	45	
aac aat cag cag aat atc tat cac cgt tgg ttg aaa ggt gaa acg aaa			192
Asn Asn Gln Gln Asn Ile Tyr His Arg Trp Leu Lys Gly Glu Thr Lys			
50	55	60	
acg caa aga gaa aaa att cag aag ctg atc cca gca att ctg gca atc			240
Thr Gln Arg Glu Lys Ile Gln Lys Leu Ile Pro Ala Ile Leu Ala Ile			
65	70	75	80
ctt ccg cgc gag ctg cgt cac cga ctc tgc atc ttc gat acc ctg gaa			288
Leu Pro Arg Glu Leu Arg His Arg Leu Cys Ile Phe Asp Thr Leu Glu			
85	90	95	
cgc cgt gca tta ctg gcg gcg cag gaa gcg tta agt acg gca att gat			336
Arg Arg Ala Leu Leu Ala Ala Gln Glu Ala Leu Ser Thr Ala Ile Asp			
100	105	110	
gcg cat gat gat gca gtc caa gcc gtt tac cgg aaa gcg cat ttc agc			384
Ala His Asp Asp Ala Val Gln Ala Val Tyr Arg Lys Ala His Phe Ser			
115	120	125	

ggc ggc ggt tct tcc gac gat tct gtc att gtt cat taa 423
 Gly Gly Gly Ser Ser Asp Asp Ser Val Ile Val His *
 130 135 140

<210> 263
 <211> 858
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(858)

<400> 263
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 Met Leu Phe Val Leu Ile Leu Ser His Arg Ala Ala Ser Tyr Gly Ala
 1 5 10 15

att atg gcc gca tta cca tac atg caa ctg tac ata gct gat tac ctg 96
 Ile Met Ala Ala Leu Pro Tyr Met Gln Leu Tyr Ile Ala Asp Tyr Leu
 20 25 30

gct gac acc atg cat ttg tca gca gag gag cat ggt gcg tat ttg ttg 144
 Ala Asp Thr Met His Leu Ser Ala Glu Glu His Gly Ala Tyr Leu Leu
 35 40 45

ctg atg ttc aat tac tgg caa aca gga aag cca ata cct aaa aac agg 192
 Leu Met Phe Asn Tyr Trp Gln Thr Gly Lys Pro Ile Pro Lys Asn Arg
 50 55 60

ctg gca aaa att gcc cgt ctg act aac gag cga tgg gct gat gtt gaa 240
 Leu Ala Lys Ile Ala Arg Leu Thr Asn Glu Arg Trp Ala Asp Val Glu
 65 70 75 80

cca tcc ttg cag gag ttt ttt tgc gat aac ggc gag gaa tgg gtg cat 288
 Pro Ser Leu Gln Glu Phe Phe Cys Asp Asn Gly Glu Glu Trp Val His
 85 90 95

ctt cgg att gag gaa gat ctg gca tca gtc agg gaa aaa tta acc aaa 336
 Leu Arg Ile Glu Glu Asp Leu Ala Ser Val Arg Glu Lys Leu Thr Lys
 100 105 110

aaa tca gcc gca gga aaa gca tct gtt cag gcc aga aga agc aga aag 384
 Lys Ser Ala Ala Gly Lys Ala Ser Val Gln Ala Arg Arg Ser Arg Lys
 115 120 125

gaa gca gat gtt caa aca aaa caa gag aga aat tta aca ggt gtt caa 432
 Glu Ala Asp Val Gln Thr Lys Gln Glu Arg Asn Leu Thr Gly Val Gln
 130 135 140

aca gat gtt gaa gtg gtg ttt gaa cat gat gtc aac aca aag gca act 480
 Thr Asp Val Glu Val Val Phe Glu His Asp Val Asn Thr Lys Ala Thr
 145 150 155 160

aat aaa gat aca gat aaa gat cta aaa aca gat ccc ccc cta aat ccc 528
 Asn Lys Asp Thr Asp Lys Asp Leu Lys Thr Asp Pro Pro Leu Asn Pro
 165 170 175

ccc cgg ggg aat cga ggt gtc aaa aag ttt gac cct ctg gat att act 576
 Pro Arg Gly Asn Arg Gly Val Lys Lys Phe Asp Pro Leu Asp Ile Thr
 180 185 190

ttg ccg aac tgg att tct gtc tcg ctt tgg cgt gag tgg gtt gaa ttt 624
 Leu Pro Asn Trp Ile Ser Val Ser Leu Trp Arg Glu Trp Val Glu Phe
 195 200 205

cgc cag gca ttg cga aaa ccg att cga acg gag cag ggc gct aac ggg 672
 Arg Gln Ala Leu Arg Lys Pro Ile Arg Thr Glu Gln Gly Ala Asn Gly
 210 215 220

gcg ata ccg gag ctg gaa aaa ttc cgc cag cag ggt ttt tca cct gag 720
 Ala Ile Arg Glu Leu Glu Lys Phe Arg Gln Gln Gly Phe Ser Pro Glu
 225 230 235 240

cag gtg att cga cac agc atc gcc aat gaa tac cag ggc ttg ttc gcg 768
 Gln Val Ile Arg His Ser Ile Ala Asn Glu Tyr Gln Gly Leu Phe Ala
 245 250 255

ccg aaa ggt gtt cga cct gag acg tta ctc cga cag gtt aac acc gtc 816
 Pro Lys Gly Val Arg Pro Glu Thr Leu Leu Arg Gln Val Asn Thr Val
 260 265 270

tcg tta ccg gat agt gcg atc ccg cca ggc ttc agg ggg taa 858
 Ser Leu Pro Asp Ser Ala Ile Pro Pro Gly Phe Arg Gly *
 275 280 285

<210> 264
 <211> 747
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(747)

<400> 264

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 Met Lys Asn Ile Ala Thr Gly Asp Val Leu Glu Arg Ile Arg Arg Leu
 1 5 10 15

gcc ccg tca cat gta acc gcg cca ttc aag acg gta gcg gag tgg cgc 96
 Ala Pro Ser His Val Thr Ala Pro Phe Lys Thr Val Ala Glu Trp Arg
 20 25 30

gag tgg caa ctt tcc gaa ggc cag aaa cgt tgt gag gag atc aac cgt 144
 Glu Trp Gln Leu Ser Glu Gly Gln Lys Arg Cys Glu Glu Ile Asn Arg
 35 40 45

cag aat cgt cag ttg ccg gtg gaa aaa att ctg aat cgc tct ggc atc 192
 Gln Asn Arg Gln Leu Arg Val Glu Lys Ile Leu Asn Arg Ser Gly Ile
 50 55 60

cag cca ttg cac cgc aaa tgc tcg ttt tcg aat tac cag gtg cag aac 240
 Gln Pro Leu His Arg Lys Cys Ser Phe Ser Asn Tyr Gln Val Gln Asn
 65 70 75 80

gaa ggg cag cga tac gcg ttg agt cag gcg aaa tcc atc gct gat gaa 288

Glu Gly Gln Arg Tyr Ala Leu Ser Gln Ala Lys Ser Ile Ala Asp Glu	
85 90 95	
ctg atg acc ggg tgt aca aat ttt gcg ttc agc gga aaa cct ggt acc	336
Leu Met Thr Gly Cys Thr Asn Phe Ala Phe Ser Gly Lys Pro Gly Thr	
100 105 110	
ggg aag aac cac tta gcg gca gct atc ggg aat cgc ctg ctg aaa gac	384
Gly Lys Asn His Leu Ala Ala Ile Gly Asn Arg Leu Leu Lys Asp	
115 120 125	
ggt cag aca gtg att gtg gtt acc gtg gct gat gtt atg agt gcc ctg	432
Gly Gln Thr Val Ile Val Val Thr Val Ala Asp Val Met Ser Ala Leu	
130 135 140	
cac gcc agc tat gac gat ggg cag tca ggc gaa aaa ttt ttg cgg gaa	480
His Ala Ser Tyr Asp Asp Gly Gln Ser Gly Glu Lys Phe Leu Arg Glu	
145 150 155 160	
ctg tgc gaa gtg gat ctg ctg gtt ctt gat gaa att ggc att cag cgc	528
Leu Cys Glu Val Asp Leu Leu Val Leu Asp Glu Ile Gly Ile Gln Arg	
165 170 175	
gag acg aaa aac gag cag gtg gta ctg cac cag att gtt gat cgc cgg	576
Glu Thr Lys Asn Glu Gln Val Val Leu His Gln Ile Val Asp Arg Arg	
180 185 190	
aca gcg tcg atg cgc agc gtg ggg atg ctg aca aac ctg aac tat gag	624
Thr Ala Ser Met Arg Ser Val Gly Met Leu Thr Asn Leu Asn Tyr Glu	
195 200 205	
gcc atg aaa aca ttg ctc ggc gag cgg att atg gat cgc atg acc atg	672
Ala Met Lys Thr Leu Leu Gly Glu Arg Ile Met Asp Arg Met Thr Met	
210 215 220	
aac ggc ggg cga tgg gtg aat ttt aac tgg gag agc tgg cgt ccg aat	720
Asn Gly Gly Arg Trp Val Asn Phe Asn Trp Glu Ser Trp Arg Pro Asn	
225 230 235 240	
gtc gtc cag cca gga att gcg aag taa	747
Val Val Gln Pro Gly Ile Ala Lys *	
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<400> 265	
atg tcg tcc agc cag gaa ttg cga agt aat ttt tac cgg gag aaa aat	48
Met Ser Ser Ser Gln Glu Leu Arg Ser Asn Phe Tyr Arg Glu Lys Asn	
1 5 10 15	
tta atg gag act gtt ttt gac gca ctg aaa gca atg gga aaa gcc aca	96
Leu Met Glu Thr Val Phe Asp Ala Leu Lys Ala Met Gly Lys Ala Thr	

20	25	30	
tcc ata gaa ctt gct gcg cga ctt gat atc agt cgt gaa gaa gtg ctg			144
Ser Ile Glu Leu Ala Ala Arg Leu Asp Ile Ser Arg Glu Glu Val Leu			
35	40	45	
aac gaa cta tgg gaa ctg aaa aag gct ggt ttt gtt gat aaa agc gcg			192
Asn Glu Leu Trp Glu Leu Lys Lys Ala Gly Phe Val Asp Lys Ser Ala			
50	55	60	
tac acc tgg cgt gtg gct gat aac aat gtt cag cag gaa cag cca gcg			240
Tyr Thr Trp Arg Val Ala Asp Asn Asn Val Gln Gln Glu Gln Pro Ala			
65	70	75	80
cag gca gaa ctg ccg gaa gaa atc acc aca gca aca gta gcg aaa atc			288
Gln Ala Glu Leu Pro Glu Glu Ile Thr Thr Ala Thr Val Ala Lys Ile			
85	90	95	
tca gag tgc gat tta acc gcg acg att gaa caa cga gga cca caa acg			336
Ser Glu Cys Asp Leu Thr Ala Thr Ile Glu Gln Arg Gly Pro Gln Thr			
100	105	110	
gct gat gag ctg gct aca ttg ttt ggt acc aca tca cgc aaa gtg gct			384
Ala Asp Glu Leu Ala Thr Leu Phe Gly Thr Thr Ser Arg Lys Val Ala			
115	120	125	
tca acg ctg gca atg gca atc agc aaa ggt cgt ctg att cgc gta aat			432
Ser Thr Leu Ala Met Ala Ile Ser Lys Gly Arg Leu Ile Arg Val Asn			
130	135	140	
cag ggc ggt aaa ttt cgt tac tgc ata ccg ggc gat aat tta cca gca			480
Gln Gly Gly Lys Phe Arg Tyr Cys Ile Pro Gly Asp Asn Leu Pro Ala			
145	150	155	160
gag ccg aaa gca gca tcg gta tct ccg ctc tgg tta tct gca tcg tcg			528
Glu Pro Lys Ala Ala Ser Val Ser Pro Leu Trp Leu Ser Ala Ser Ser			
165	170	175	
tct gcc tgt cat ggg gtg tta atc att acc gtg ata acg cca tcg cct			576
Ser Ala Cys His Gly Val Leu Ile Ile Thr Val Ile Thr Pro Ser Pro			
180	185	190	
aca aag aac agc gcg aca aaa atg cca gag aac tga			612
Thr Lys Asn Ser Ala Thr Lys Met Pro Glu Asn *			
195	200		
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<211> 306			
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<222> (1)...(306)			
<400> 266			
atg cag atg cgt cag cgt gat gtt gct gcg ctc gat gca aaa tac acg			48
Met Gln Met Arg Gln Arg Asp Val Ala Ala Leu Asp Ala Lys Tyr Thr			
1	5	10	15


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aag gag tta gct gat gcg aaa gct gaa aat gat gct ctg cgt gat gat      96
Lys Glu Leu Ala Asp Ala Lys Ala Glu Asn Asp Ala Leu Arg Asp Asp
      20                      25                      30

gtt gcc gct ggt cgt cgt cgg ttg cac atc aaa gca gtc tgt cag tca      144
Val Ala Ala Gly Arg Arg Arg Leu His Ile Lys Ala Val Cys Gln Ser
      35                      40                      45

gtg cgt gaa gcc acc acc gcc tcc ggc gtg gat aat gca gcc tcc ccc      192
Val Arg Glu Ala Thr Thr Ala Ser Gly Val Asp Asn Ala Ala Ser Pro
      50                      55                      60

cga ctg gca gac acc gct gaa cgg gat tat ttc acc ctc cgg gaa cga      240
Arg Leu Ala Asp Thr Ala Glu Arg Asp Tyr Phe Thr Leu Arg Glu Arg
      65                      70                      75                      80

ctg gta atg atg cag gcc caa ctt gaa ggt gct cag caa tac ata acc      288
Leu Val Met Met Gln Ala Gln Leu Glu Gly Ala Gln Gln Tyr Ile Thr
      85                      90                      95

gag cag tgt tta aag taa      306
Glu Gln Cys Leu Lys *
      100

<210> 267
<211> 879
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(879)

<400> 267
atg aaa ctg gga ttt att ggc tta ggc att atg ggt aca ccg atg gcc      48
Met Lys Leu Gly Phe Ile Gly Leu Gly Ile Met Gly Thr Pro Met Ala
      1                      5                      10                      15

att aat ctg gcg cgt gcc ggt cat caa tta cat gtc acg acc att gga      96
Ile Asn Leu Ala Arg Ala Gly His Gln Leu His Val Thr Thr Ile Gly
      20                      25                      30

ccg gtt gct gat gaa tta ctg tca ctg ggt gcc gtc agt gtt gaa act      144
Pro Val Ala Asp Glu Leu Leu Ser Leu Gly Ala Val Ser Val Glu Thr
      35                      40                      45

gct cgc cag gta acg gaa gca tcg gac atc att ttt att atg gtg ccg      192
Ala Arg Gln Val Thr Glu Ala Ser Asp Ile Ile Phe Ile Met Val Pro
      50                      55                      60

gac aca cct cag gtt gaa gaa gtt ctg ttc ggt gaa aat ggt tgt acc      240
Asp Thr Pro Gln Val Glu Glu Val Leu Phe Gly Glu Asn Gly Cys Thr
      65                      70                      75                      80

aaa gcc tcg ctg aag ggc aaa acc att gtt gat atg agc tcc att tcc      288
Lys Ala Ser Leu Lys Gly Lys Thr Ile Val Asp Met Ser Ser Ile Ser
      85                      90                      95

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ccg att gaa act aag cgt ttc gct cgt cag gtg aat gaa ctg ggc ggc Pro Ile Glu Thr Lys Arg Phe Ala Arg Gln Val Asn Glu Leu Gly Gly 100 105 110	336
gat tat ctc gat gcg cca gtc tcc ggc ggt gaa atc ggt gcg cgt gaa Asp Tyr Leu Asp Ala Pro Val Ser Gly Gly Glu Ile Gly Ala Arg Glu 115 120 125	384
ggg acg ttg tcg att atg gtt ggc ggt gat gaa gcg gta ttt gaa cgt Gly Thr Leu Ser Ile Met Val Gly Gly Asp Glu Ala Val Phe Glu Arg 130 135 140	432
gtt aaa ccg ctg ttt gaa ctg ctc ggt aaa aat atc acc ctc gtg ggc Val Lys Pro Leu Phe Glu Leu Leu Gly Lys Asn Ile Thr Leu Val Gly 145 150 155 160	480
ggt aac ggc gat ggt caa acc tgc aaa gtg gca aat cag att atc gtg Gly Asn Gly Asp Gly Gln Thr Cys Lys Val Ala Asn Gln Ile Ile Val 165 170 175	528
gcg ctc aat att gaa gcg gtt tct gaa gcc ctg cta ttt gct tca aaa Ala Leu Asn Ile Glu Ala Val Ser Glu Ala Leu Leu Phe Ala Ser Lys 180 185 190	576
gcc ggt gcg gac ccg gta cgt gtg cgc cag gcg ctg atg ggc ggc ttt Ala Gly Ala Asp Pro Val Arg Val Arg Gln Ala Leu Met Gly Gly Phe 195 200 205	624
gct tcc tca cgt att ctg gaa gtt cat ggc gag cgt atg att aaa cgc Ala Ser Ser Arg Ile Leu Glu Val His Gly Glu Arg Met Ile Lys Arg 210 215 220	672
acc ttt aat ccg ggc ttc aaa atc gct ctg cac cag aaa gat ctc aac Thr Phe Asn Pro Gly Phe Lys Ile Ala Leu His Gln Lys Asp Leu Asn 225 230 235 240	720
ctg gca ctg caa agt gcg aaa gca ctt gcg ctg aac ctg cca aac act Leu Ala Leu Gln Ser Ala Lys Ala Leu Ala Leu Asn Leu Pro Asn Thr 245 250 255	768
gcg acc tgc cag gag tta ttt aat acc tgt gcg gca aac ggt ggc agc Ala Thr Cys Gln Glu Leu Phe Asn Thr Cys Ala Ala Asn Gly Gly Ser 260 265 270	816
cag ttg gat cac tct gcg tta gtg cag gcg ctg gaa tta atg gct aac Gln Leu Asp His Ser Ala Leu Val Gln Ala Leu Glu Leu Met Ala Asn 275 280 285	864
cat aaa ctg gcc tga His Lys Leu Ala *	879
290	

<210> 268

<211> 279

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(279)

<400> 268

atg aat cgg cca gca ata tta aaa aag aaa gca gcc aaa gat gtt gct	48
Met Asn Arg Pro Ala Ile Leu Lys Lys Lys Ala Ala Lys Asp Val Ala	
1 5 10 15	
tca gta tta aaa ata ata ttt tta ttt tat ttg ttc ctc ata gct aga	96
Ser Val Leu Lys Ile Ile Phe Leu Phe Tyr Leu Phe Leu Ile Ala Arg	
20 25 30	
tta aaa caa cgt tat tcg ata cgt gaa att aag agg gat tta tgg aac	144
Leu Lys Gln Arg Tyr Ser Ile Arg Glu Ile Lys Arg Asp Leu Trp Asn	
35 40 45	
atc aga gaa aac tat tcc agc aac gcg gct ata gcg aag atc tat tgc	192
Ile Arg Glu Asn Tyr Ser Ser Asn Ala Ala Ile Ala Lys Ile Tyr Cys	
50 55 60	
cga aaa cgc aaa gcc agc gga cct gga aaa cat tta act att tta cct	240
Arg Lys Arg Lys Ala Ser Gly Pro Gly Lys His Leu Thr Ile Leu Pro	
65 70 75 80	
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ctg gca att atc ctc agc gcc ttt ttc att gcc gcg gta atg gta tta	96
Leu Ala Ile Ile Leu Ser Ala Phe Phe Ile Ala Ala Val Met Val Leu	
20 25 30	
aac ggt gct gcg ggc agt aaa tac ggt gtg cct ttt gcc atg atc ctg	144
Asn Gly Ala Ala Gly Ser Lys Tyr Gly Val Pro Phe Ala Met Ile Leu	
35 40 45	
cgt gct tct tac ggt gta cgt ggt gca ctg ttt ccc gga tta tta agg	192
Arg Ala Ser Tyr Gly Val Arg Gly Ala Leu Phe Pro Gly Leu Leu Arg	
50 55 60	
ggc gga att gcc gcc atc atg tgg ttt ggt ttg caa tgt tac gcg ggg	240
Gly Gly Ile Ala Ala Ile Met Trp Phe Gly Leu Gln Cys Tyr Ala Gly	
65 70 75 80	
tca ctg gcc tgc ttg att ctg att ggc aaa atc tgg ccg gga ttt tta	288
Ser Leu Ala Cys Leu Ile Leu Ile Gly Lys Ile Trp Pro Gly Phe Leu	

85						90						95						
act	ctc	ggt	ggt	gat	ttc	act	ctg	tta	ggc	ctt	tct	cta	ccg	ggc	tta	336		
Thr	Leu	Gly	Gly	Asp	Phe	Thr	Leu	Leu	Gly	Leu	Ser	Leu	Pro	Gly	Leu			
			100					105					110					
att	act	ttc	tta	atc	ttc	tgg	ctg	gtc	aac	ggt	ggt	ata	ggt	ttt	ggc	384		
Ile	Thr	Phe	Leu	Ile	Phe	Trp	Leu	Val	Asn	Val	Gly	Ile	Gly	Phe	Gly			
		115					120					125						
ggt	ggc	aaa	ggt	tta	aat	aaa	ttc	act	gcc	att	ctt	aac	ccg	tgc	atc	432		
Gly	Gly	Lys	Val	Leu	Asn	Lys	Phe	Thr	Ala	Ile	Leu	Asn	Pro	Cys	Ile			
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tat	atc	ggt	ttc	ggc	ggt	atg	gcg	att	tgg	gcg	att	tca	ctg	gtc	ggg	480		
Tyr	Ile	Val	Phe	Gly	Gly	Met	Ala	Ile	Trp	Ala	Ile	Ser	Leu	Val	Gly			
145					150					155					160			
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Ile	Gly	Pro	Ile	Phe	Asp	Tyr	Ile	Pro	Ser	Gly	Ile	Gln	Lys	Ala	Glu			
				165				170						175				
aac	ggt	ggc	ttc	ctg	ttc	ctg	gtg	gtg	att	aac	gcg	gta	ggt	gcg	gtc	576		
Asn	Gly	Gly	Phe	Leu	Phe	Leu	Val	Val	Ile	Asn	Ala	Val	Val	Ala	Val			
			180					185					190					
tgg	gcg	gca	ccg	gcg	gtg	agc	gca	tcc	gac	ttt	acg	caa	aac	gcc	cac	624		
Trp	Ala	Ala	Pro	Ala	Val	Ser	Ala	Ser	Asp	Phe	Thr	Gln	Asn	Ala	His			
		195					200					205						
tcg	ttt	cgt	gag	cag	gcg	ctg	ggg	caa	acg	ctg	ggt	tta	ggt	gtg	gcc	672		
Ser	Phe	Arg	Glu	Gln	Ala	Leu	Gly	Gln	Thr	Leu	Gly	Leu	Val	Val	Ala			
	210					215					220							
tat	att	ctg	ttt	gcg	gtc	gcc	ggg	gta	tgt	att	att	gcc	gga	gcc	agt	720		
Tyr	Ile	Leu	Phe	Ala	Val	Ala	Gly	Val	Cys	Ile	Ile	Ala	Gly	Ala	Ser			
225					230					235					240			
att	cac	tac	ggc	gct	gat	acc	tgg	aac	gtg	ctg	gat	att	ggt	cag	cgt	768		
Ile	His	Tyr	Gly	Ala	Asp	Thr	Trp	Asn	Val	Leu	Asp	Ile	Val	Gln	Arg			
			245					250						255				
tgg	gac	agc	ctg	ttc	gcc	tcg	ttc	ttt	gcg	gta	ctg	ggt	att	ctg	atg	816		
Trp	Asp	Ser	Leu	Phe	Ala	Ser	Phe	Phe	Ala	Val	Leu	Val	Ile	Leu	Met			
			260					265					270					
aca	act	atc	tcc	act	aac	gcg	acc	ggt	aat	att	att	cca	gcc	ggt	tat	864		
Thr	Thr	Ile	Ser	Thr	Asn	Ala	Thr	Gly	Asn	Ile	Ile	Pro	Ala	Gly	Tyr			
		275					280					285						
cag	att	gcc	gcc	att	gca	ccg	aca	aaa	ctg	acc	tat	aaa	aac	ggc	gta	912		
Gln	Ile	Ala	Ala	Ile	Ala	Pro	Thr	Lys	Leu	Thr	Tyr	Lys	Asn	Gly	Val			
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ctg	att	gcc	agt	att	atc	agc	ttg	ctg	atc	tgc	ccg	tgg	aaa	tta	atg	960		
Leu	Ile	Ala	Ser	Ile	Ile	Ser	Leu	Leu	Ile	Cys	Pro	Trp	Lys	Leu	Met			
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gaa	aat	cag	gac	agc	att	tat	ctt	ttc	ctc	gat	att	atc	ggc	gga	atg	1008		
Glu	Asn	Gln	Asp	Ser	Ile	Tyr	Leu	Phe	Leu	Asp	Ile	Ile	Gly	Gly	Met			

325	330	335	
ctt ggt ccg gta att ggt gtc atg atg gcg cat tat ttt gtg gtg atg Leu Gly Pro Val Ile Gly Val Met Met Ala His Tyr Phe Val Val Met 340 345 350			1056
cgc gga caa att aat ctt gat gaa ctg tat acc gca cct ggc gat tat Arg Gly Gln Ile Asn Leu Asp Glu Leu Tyr Thr Ala Pro Gly Asp Tyr 355 360 365			1104
aaa tat tac gat aac ggt ttt aac ctc act gcg ttt tca gta act ctg Lys Tyr Tyr Asp Asn Gly Phe Asn Leu Thr Ala Phe Ser Val Thr Leu 370 375 380			1152
gtg gcc gtt att tta tct ctt ggc ggt aag ttt att cac ttt atg gaa Val Ala Val Ile Leu Ser Leu Gly Gly Lys Phe Ile His Phe Met Glu 385 390 395 400			1200
ccg tta tcg cgt gtt tca tgg ttt gtc ggc gtc atc gtc gcc ttt gcg Pro Leu Ser Arg Val Ser Trp Phe Val Gly Val Ile Val Ala Phe Ala 405 410 415			1248
gcc tac gcc tta tta aag aaa cgt aca aca gca gaa aaa aca gga gag Ala Tyr Ala Leu Leu Lys Lys Arg Thr Thr Ala Glu Lys Thr Gly Glu 420 425 430			1296
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gct aca cta gta tca ttc cgc gaa acg ttt cag gaa gag aaa ctc tta Ala Thr Leu Val Ser Phe Arg Glu Thr Phe Gln Glu Glu Lys Leu Leu 35 40 45	144
acg atg aaa ggt agt tat aaa tcc cgt tgg gta atc gta atc gtg gtg Thr Met Lys Gly Ser Tyr Lys Ser Arg Trp Val Ile Val Ile Val Val 50 55 60	192
gtt atc gcc gcc atc gcc gca ttc tgg ttc tgg caa ggc cgc aat gac Val Ile Ala Ala Ile Ala Ala Phe Trp Phe Trp Gln Gly Arg Asn Asp 65 70 75 80	240

tcc cgg agt gca gcc cca ggg gcg acg aaa caa gcg cag caa tcg cca	288
Ser Arg Ser Ala Ala Pro Gly Ala Thr Lys Gln Ala Gln Gln Ser Pro	
85 90 95	
gcg ggt ggt cga cgt ggt atg cgt tcc ggc cca tta gcc ccg gtt cag	336
Ala Gly Gly Arg Arg Gly Met Arg Ser Gly Pro Leu Ala Pro Val Gln	
100 105 110	
gcg gcg acc gcc gta gaa cag gca gtt ccg cgt tac ctc acc ggg ctt	384
Ala Ala Thr Ala Val Glu Gln Ala Val Pro Arg Tyr Leu Thr Gly Leu	
115 120 125	
ggc acc att acc gcc gct aat acc gtt acg gtg cgc agc cgc gtg gac	432
Gly Thr Ile Thr Ala Ala Asn Thr Val Thr Val Arg Ser Arg Val Asp	
130 135 140	
ggc caa ctg ata gcg tta cat ttc cag gaa ggc cag cag gtc aaa gca	480
Gly Gln Leu Ile Ala Leu His Phe Gln Glu Gly Gln Gln Val Lys Ala	
145 150 155 160	
ggc gat tta ctg gca gaa att gac ccc agc cag ttc aaa gtt gca tta	528
Gly Asp Leu Leu Ala Glu Ile Asp Pro Ser Gln Phe Lys Val Ala Leu	
165 170 175	
gca caa gcc cag gcc caa ctg gca aaa gat aaa gcc acg ctt gcc aac	576
Ala Gln Ala Gln Gly Gln Leu Ala Lys Asp Lys Ala Thr Leu Ala Asn	
180 185 190	
gcc cgc cgt gac ctg gcg cgt tat caa caa ctg gca aaa acc aat ctc	624
Ala Arg Arg Asp Leu Ala Arg Tyr Gln Gln Leu Ala Lys Thr Asn Leu	
195 200 205	
gtt tcc cgc cag gag ctg gat gcc caa cag gcg ctg gtc agt gaa acc	672
Val Ser Arg Gln Glu Leu Asp Ala Gln Gln Ala Leu Val Ser Glu Thr	
210 215 220	
gaa ggc acc att aag gct gat gaa gca agc gtt gcc agc gcg cag ctg	720
Glu Gly Thr Ile Lys Ala Asp Glu Ala Ser Val Ala Ser Ala Gln Leu	
225 230 235 240	
caa ctc gac tgg agc cgg att acc gca cca gtc gat ggt cgc gtt ggt	768
Gln Leu Asp Trp Ser Arg Ile Thr Ala Pro Val Asp Gly Arg Val Gly	
245 250 255	
ctc aag cag gtt gat gtt ggt aac caa atc tcc agt ggt gat acc acc	816
Leu Lys Gln Val Asp Val Gly Asn Gln Ile Ser Ser Gly Asp Thr Thr	
260 265 270	
ggg atc gtg gtg atc acc cag acg cat cct atc gat tta gtc ttt acc	864
Gly Ile Val Val Ile Thr Gln Thr His Pro Ile Asp Leu Val Phe Thr	
275 280 285	
ctg ccg gaa agc gat atc gct acc gta gtg cag gcg cag aaa gcc gga	912
Leu Pro Glu Ser Asp Ile Ala Thr Val Val Gln Ala Gln Lys Ala Gly	
290 295 300	
aaa ccg ctg gtg gta gaa gcc tgg gat cgc acc aac tcg aag aaa tta	960
Lys Pro Leu Val Val Glu Ala Trp Asp Arg Thr Asn Ser Lys Lys Leu	
305 310 315 320	

agt gaa ggc acg ctg tta agt cta gat aac caa atc gat gcc act acc 1008
 Ser Glu Gly Thr Leu Leu Ser Leu Asp Asn Gln Ile Asp Ala Thr Thr
 325 330 335

 ggt acg att aaa gtg aaa gca cgc ttt aat aat cag gat gat gcg ctg 1056
 Gly Thr Ile Lys Val Lys Ala Arg Phe Asn Asn Gln Asp Asp Ala Leu
 340 345 350

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 Phe Pro Asn Gln Phe Val Asn Ala Arg Met Leu Val Asp Thr Glu Gln
 355 360 365

 aac gcc gta gtg atc cca aca gcc gcc ctg caa atg ggc aat gaa ggc 1152
 Asn Ala Val Val Ile Pro Thr Ala Ala Leu Gln Met Gly Asn Glu Gly
 370 375 380

 cat ttt gtc tgg gtg ctg aat agc gaa aac aag gtc agc aaa cat ctg 1200
 His Phe Val Trp Val Leu Asn Ser Glu Asn Lys Val Ser Lys His Leu
 385 390 395 400

 gtg acg ccg ggc att cag gac agt cag aaa gtg gtg atc cgt gca ggt 1248
 Val Thr Pro Gly Ile Gln Asp Ser Gln Lys Val Val Ile Arg Ala Gly
 405 410 415

 att tct gcg ggc gat cgc gtg gtg aca gac ggc att gat cgc ctg acc 1296
 Ile Ser Ala Gly Asp Arg Val Val Thr Asp Gly Ile Asp Arg Leu Thr
 420 425 430

 gaa ggg gcg aaa gtg gaa gtg gtg gaa gcc cag agc gcc act act ccg 1344
 Glu Gly Ala Lys Val Glu Val Val Glu Ala Gln Ser Ala Thr Thr Pro
 435 440 445

 gaa gag aaa gcc acc agc cgc gaa tac gcg aaa aaa gga gca cgc tcc 1392
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 att atg cgt cct gtg gcc acc acg ctg ctg atg gtg gcg atc tta ctc 96
 Ile Met Arg Pro Val Ala Thr Thr Leu Leu Met Val Ala Ile Leu Leu
 20 25 30

gcc ggg att atc ggt tat cgc gcc ctg ccc gtt tcg gcg ctg ccg gaa Ala Gly Ile Ile Gly Tyr Arg Ala Leu Pro Val Ser Ala Leu Pro Glu 35 40 45	144
gtg gac tat ccg acc att cag gtg gtc acg ctc tac cca ggt gcc agc Val Asp Tyr Pro Thr Ile Gln Val Val Thr Leu Tyr Pro Gly Ala Ser 50 55 60	192
ccg gat gtc atg acc tct gcc gtt acc gcg ccg cta gaa cgc cag ttc Pro Asp Val Met Thr Ser Ala Val Thr Ala Pro Leu Glu Arg Gln Phe 65 70 75 80	240
ggg cag atg tct ggc ctg aaa cag atg tcg tcg caa agt tcc ggc ggt Gly Gln Met Ser Gly Leu Lys Gln Met Ser Ser Gln Ser Ser Gly Gly 85 90 95	288
gcg tca gtt atc act ttg cag ttc cag cta aca tta ccg ctc gat gtc Ala Ser Val Ile Thr Leu Gln Phe Gln Leu Thr Leu Pro Leu Asp Val 100 105 110	336
gcc gag cag gaa gtg cag gcc gcg att aac gct gcg acc aac ttg ttg Ala Glu Gln Glu Val Gln Ala Ala Ile Asn Ala Ala Thr Asn Leu Leu 115 120 125	384
ccg agc gat ctg cct aac ccg ccg gtt tac agc aaa gtg aac ccg gca Pro Ser Asp Leu Pro Asn Pro Pro Val Tyr Ser Lys Val Asn Pro Ala 130 135 140	432
gat ccg ccg atc atg acg ctc gcc gtc acc tca acc gcc atg ccg atg Asp Pro Pro Ile Met Thr Leu Ala Val Thr Ser Thr Ala Met Pro Met 145 150 155 160	480
acg caa gtg gaa gat atg gtg gaa acc cgc gtc gcg cag aaa atc tcg Thr Gln Val Glu Asp Met Val Glu Thr Arg Val Ala Gln Lys Ile Ser 165 170 175	528
cag att tcc ggc gtc ggc ctg gtg acg ctt tcc ggc ggt cag cgt ccg Gln Ile Ser Gly Val Gly Leu Val Thr Leu Ser Gly Gly Gln Arg Pro 180 185 190	576
gct gtt cgc gtc aaa ctt aac gct cag gcg att gcc gcc ctc ggc ctg Ala Val Arg Val Lys Leu Asn Ala Gln Ala Ile Ala Ala Leu Gly Leu 195 200 205	624
acc agc gaa acc gtg cgc acc gcc att acc ggc gct aac gtt aac tcg Thr Ser Glu Thr Val Arg Thr Ala Ile Thr Gly Ala Asn Val Asn Ser 210 215 220	672
gca aaa ggt agc ctc gac ggc cct tcc cgt gcg gtc acg ctt tcc gcg Ala Lys Gly Ser Leu Asp Gly Pro Ser Arg Ala Val Thr Leu Ser Ala 225 230 235 240	720
aac gac cag atg caa tcc gcc gaa gag tat cgc cag cta atc atc gcc Asn Asp Gln Met Gln Ser Ala Glu Glu Tyr Arg Gln Leu Ile Ile Ala 245 250 255	768
tac cag aac ggc gcg cca att cgt ctg ggc gat gtc gca act gta gag Tyr Gln Asn Gly Ala Pro Ile Arg Leu Gly Asp Val Ala Thr Val Glu 260 265 270	816

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gcc att gtg atg aat gtt cag cgc cag ccc ggt gct aac att atc tcc Ala Ile Val Met Asn Val Gln Arg Gln Pro Gly Ala Asn Ile Ile Ser 290 295 300	912
acc gcc gac agc att cgg cag atg ctg cca cag ctc act gag agt ctg Thr Ala Asp Ser Ile Arg Gln Met Leu Pro Gln Leu Thr Glu Ser Leu 305 310 315 320	960
ccg aaa tcg gtg aag gtg aca gtg ctt tcc gat cgc acc acc aat atc Pro Lys Ser Val Lys Val Thr Val Leu Ser Asp Arg Thr Thr Asn Ile 325 330 335	1008
cgc gca tcc gtc gat gat act cag ttt gaa ttg atg atg gct atc gcg Arg Ala Ser Val Asp Asp Thr Gln Phe Glu Leu Met Met Ala Ile Ala 340 345 350	1056
ctg gta gtc atg att atc tac ctg ttt ttg cgc aat att ccg gcg acc Leu Val Val Met Ile Ile Tyr Leu Phe Leu Arg Asn Ile Pro Ala Thr 355 360 365	1104
atc att ccc ggt gtt gct gta ccg ctg tcg tta atc ggc act ttc gcg Ile Ile Pro Gly Val Ala Val Pro Leu Ser Leu Ile Gly Thr Phe Ala 370 375 380	1152
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ttc ttc ccg gta cag gac aat ggc att att cag ggc act ttg cag gca Phe Phe Pro Val Gln Asp Asn Gly Ile Ile Gln Gly Thr Leu Gln Ala 565 570 575	1728
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ctc ggc att ctg tac gag agc ttt att cac ccg atc acc att ctc tcg Leu Gly Ile Leu Tyr Glu Ser Phe Ile His Pro Ile Thr Ile Leu Ser 885 890 895	2688
acg cta ccc acc gca ggg gtt ggc gca ctg ctg gcg ttg ctg att gct Thr Leu Pro Thr Ala Gly Val Gly Ala Leu Leu Ala Leu Leu Ile Ala 900 905 910	2736
ggc agc gaa ctg gat gtg att gcg att atc ggc att att ttg ctg atc Gly Ser Glu Leu Asp Val Ile Ala Ile Ile Gly Ile Ile Leu Leu Ile 915 920 925	2784
ggc atc gtg aag aag aac gcc atc atg atg atc gac ttc gcg ctg gct Gly Ile Val Lys Lys Asn Ala Ile Met Met Ile Asp Phe Ala Leu Ala 930 935 940	2832
gct gag cgc gag caa ggc atg tcg ccg cgc gag gca atc tac cag gct Ala Glu Arg Glu Gln Gly Met Ser Pro Arg Glu Ala Ile Tyr Gln Ala 945 950 955 960	2880
tgt ctg ttg cgt ttt cgt ccg atc ctg atg acc act ctg gcg gct ctg Cys Leu Leu Arg Phe Arg Pro Ile Leu Met Thr Thr Leu Ala Ala Leu 965 970 975	2928
ctt ggc gcg ctg ccg ctg atg ttg agt acc ggg gtc ggc gcg gaa ctg Leu Gly Ala Leu Pro Leu Met Leu Ser Thr Gly Val Gly Ala Glu Leu 980 985 990	2976

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cgt cgt ccg tta ggt atc ggc atg gtc ggc ggt ctg att gtc agc cag      3024
Arg Arg Pro Leu Gly Ile Gly Met Val Gly Gly Leu Ile Val Ser Gln
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Val Leu Thr Leu Phe Thr Thr Pro Val Ile Tyr Leu Leu Phe Asp Arg
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Leu Ser Val Ala Ile Thr Leu Cys Gly Ile Leu Gly Phe Arg Met Leu
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ccg gtc gcc ccg ctg ccg cag gtc gat ttt ccg gtg att atc gtc agc      144
Pro Val Ala Pro Leu Pro Gln Val Asp Phe Pro Val Ile Ile Val Ser
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Ala Ser Leu Pro Gly Ala Ser Pro Glu Thr Met Ala Ser Ser Val Ala
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acc tcc agc agt tcg ctc ggc agc acg cgt att att ttg cag ttt gat      288
Thr Ser Ser Ser Ser Leu Gly Ser Thr Arg Ile Ile Leu Gln Phe Asp
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Phe Asp Arg Asp Ile Asn Gly Ala Ala Arg Asp Val Gln Ala Ala Ile
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aac gct gca caa agt ttg ctg ccc agt ggg atg ccc agc cgc ccg acc      384
Asn Ala Ala Gln Ser Leu Leu Pro Ser Gly Met Pro Ser Arg Pro Thr
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tat cgc aaa gcg aac ccg tcg gat gcg cca att atg atc ctc acg ctg      432
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Ala	Leu	Phe	Asn	Gln	Gly	Val	Ser	Leu	Asp	Asp	Val	Arg	Thr	Ala	Val		
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Gln	Asp	Arg	Ser	Pro	Thr	Ile	Arg	Ala	Ser	Leu	Glu	Glu	Val	Glu	Gln		
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Thr	Leu	Ile	Ile	Ser	Val	Ala	Leu	Val	Ile	Leu	Val	Val	Phe	Leu	Phe		
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Phe	Thr	Val	Leu	Ser	Met	Ser	Leu	Ser	Leu	Val	Ala	Val	Phe	Leu	Pro	
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Thr	Val	Arg	Gly	Ser	Phe	Ala	Gly	Thr	Ala	Gln	Val	Phe	Gln	Glu	Thr		
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Asp	Arg	Leu	Arg	Leu	Arg	Phe	Ser	Arg	Lys	Pro	Lys	Gln	Thr	Val	Thr	
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Leu Pro Ser Met Ala Gln Ser Leu Gly Glu Ser Pro Leu His Met His				
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Met Val Ile Val Ser Tyr Val Leu Thr Val Ala Val Met Leu Pro Ala				
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Ser Gly Trp Leu Ala Asp Lys Val Gly Val Arg Asn Ile Phe Phe Thr				
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gcc atc gtg ctg ttt act ctc ggt tca ctg ttt tgc gcg ctt tcc gcc				288
Ala Ile Val Leu Phe Thr Leu Gly Ser Leu Phe Cys Ala Leu Ser Gly				
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Thr Leu Asn Glu Leu Leu Leu Ala Arg Ala Leu Gln Gly Val Gly Gly				
100		105	110	
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Ala Met Met Val Pro Val Gly Arg Leu Thr Val Met Lys Ile Val Pro				
115		120	125	
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Arg Glu Gln Tyr Met Ala Ala Met Thr Phe Val Thr Leu Pro Gly Gln				
130		135	140	
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Val Gly Pro Leu Leu Gly Pro Ala Leu Gly Gly Leu Leu Val Glu Tyr				
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Gly Ala Ile Ala Thr Leu Leu Leu Met Pro Asn Tyr Thr Met Gln Thr				
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Val Leu Thr Leu Ala Leu Asp Gly Ser Lys Gly Thr Gly Leu Ser Pro				
210		215	220	
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Leu Thr Ile Ala Gly Leu Val Ala Val Gly Val Val Ala Leu Val Leu				
225		230	235	240
tat ctg ctg cac gcc aga aat aac aac cgt gcc ctg ttc agt ctg aaa				768
Tyr Leu Leu His Ala Arg Asn Asn Asn Arg Ala Leu Phe Ser Leu Lys				

245										250					255					
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Pro	Met	Val	Leu	Gly	Ser	Met	Gly	Met	Lys	Arg	Ile	Val	Val	Gln	Val					
305					310					315					320					
gtg	aat	cgc	ttt	ggt	tat	cgt	cgg	gta	ctg	gta	gcg	acc	acg	ctg	ggt	1008				
Val	Asn	Arg	Phe	Gly	Tyr	Arg	Arg	Val	Leu	Val	Ala	Thr	Thr	Leu	Gly					
				325				330						335						
ctg	tcg	ctg	gtc	acc	ctg	ttg	ttt	atg	act	acc	gcc	ctg	ctg	ggc	tgg	1056				
Leu	Ser	Leu	Val	Thr	Leu	Leu	Phe	Met	Thr	Thr	Ala	Leu	Leu	Gly	Trp					
			340					345					350							
tac	tac	gtt	ttg	ccg	ttc	gtc	ctg	ttt	tta	caa	ggg	atg	gtc	aac	tcg	1104				
Tyr	Tyr	Val	Leu	Pro	Phe	Val	Leu	Phe	Leu	Gln	Gly	Met	Val	Asn	Ser					
		355					360					365								
acg	cgt	ttc	tcc	tcc	atg	aac	acc	ctg	acg	ctg	aaa	gat	ctc	ccg	gac	1152				
Thr	Arg	Phe	Ser	Ser	Met	Asn	Thr	Leu	Thr	Leu	Lys	Asp	Leu	Pro	Asp					
		370				375					380									
aat	ctg	gcg	agc	agc	ggc	aac	agc	ctg	ctg	tcg	atg	att	atg	caa	ttg	1200				
Asn	Leu	Ala	Ser	Ser	Gly	Asn	Ser	Leu	Leu	Ser	Met	Ile	Met	Gln	Leu					
385					390					395					400					
tcg	atg	agt	atc	ggc	gtc	act	atc	gcc	ggg	ctg	ttg	ctg	gga	ctt	ttt	1248				
Ser	Met	Ser	Ile	Gly	Val	Thr	Ile	Ala	Gly	Leu	Leu	Leu	Gly	Leu	Phe					
				405				410					415							
ggt	tca	cag	cat	gtc	agc	gtc	gac	agc	ggc	acc	aca	caa	acc	gtc	ttt	1296				
Gly	Ser	Gln	His	Val	Ser	Val	Asp	Ser	Gly	Thr	Thr	Gln	Thr	Val	Phe					
			420					425					430							
atg	tac	acc	tgg	ctt	agc	atg	gcg	ttg	atc	atc	gcc	ctt	ccg	gcg	ttc	1344				
Met	Tyr	Thr	Trp	Leu	Ser	Met	Ala	Leu	Ile	Ile	Ala	Leu	Pro	Ala	Phe					
		435					440					445								
atc	ttt	gcc	aga	gtg	ccg	aac	gat	acg	cat	caa	aat	gta	gct	att	tcg	1392				
Ile	Phe	Ala	Arg	Val	Pro	Asn	Asp	Thr	His	Gln	Asn	Val	Ala	Ile	Ser					
		450				455					460									
cgg	cga	aaa	agg	agc	gcg	caa	tga									1416				
Arg	Arg	Lys	Arg	Ser	Ala	Gln	*													
465					470															

<210> 274

<211> 417
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(417)

<400> 274
 gtg att gcg ttt gaa gtg ttg aag tgg gca ggc gcg gct tac ttg att 48
 Met Ile Ala Phe Glu Val Leu Lys Trp Ala Gly Ala Ala Tyr Leu Ile
 1 5 10 15
 tgg ctg gga atc cag cag tgg cgc gcc gct ggt gca att gac ctt aaa 96
 Trp Leu Gly Ile Gln Gln Trp Arg Ala Ala Gly Ala Ile Asp Leu Lys
 20 25 30
 tcg ctg gcc tct act caa tcg cgt cga cat ttg ttc cag cgc gca gtt 144
 Ser Leu Ala Ser Thr Gln Ser Arg Arg His Leu Phe Gln Arg Ala Val
 35 40 45
 ttt gtg aat ctc acc aat ccc aaa agt att gtg ttt ctg gcg gcg cta 192
 Phe Val Asn Leu Thr Asn Pro Lys Ser Ile Val Phe Leu Ala Ala Leu
 50 55 60
 ttt ccg caa ttc atc atg ccg caa cag ccg caa ctg atg cag tat atc 240
 Phe Pro Gln Phe Ile Met Pro Gln Gln Pro Gln Leu Met Gln Tyr Ile
 65 70 75 80
 gtg ctc ggc gtc acc act att gtg gtc gat att att gtg atg atc ggt 288
 Val Leu Gly Val Thr Thr Ile Val Val Asp Ile Ile Val Met Ile Gly
 85 90 95
 tac gcc acc ctt gct caa cgg att gct cta tgg att aaa gga cca aag 336
 Tyr Ala Thr Leu Ala Gln Arg Ile Ala Leu Trp Ile Lys Gly Pro Lys
 100 105 110
 cag atg aag gcg ctg aat aag att ttc ggc tcg ttg ttt atg ctg gtg 384
 Gln Met Lys Ala Leu Asn Lys Ile Phe Gly Ser Leu Phe Met Leu Val
 115 120 125
 gga gcg ctg tta gca tcg gcg agg cat gcg tga 417
 Gly Ala Leu Leu Ala Ser Ala Arg His Ala *
 130 135

<210> 275
 <211> 774
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(774)

<400> 275
 atg gct cgt aaa tgg ttg aac ttg ttt gcc ggg gcg gca ctc tct ttc 48
 Met Ala Arg Lys Trp Leu Asn Leu Phe Ala Gly Ala Ala Leu Ser Phe
 1 5 10 15

gct gtt gct ggc aat gca ctg gca gat gaa ggg aaa atc acg gtg ttc Ala Val Ala Gly Asn Ala Leu Ala Asp Glu Gly Lys Ile Thr Val Phe 20 25 30	96
gcc gcc gca tca ctg act aac gca atg cag gac att gct acg cag ttt Ala Ala Ala Ser Leu Thr Asn Ala Met Gln Asp Ile Ala Thr Gln Phe 35 40 45	144
aaa aaa gag aaa ggc gtg gat gtg gtt tct tct ttc gct tcg tca tct Lys Lys Glu Lys Gly Val Asp Val Val Ser Ser Phe Ala Ser Ser Ser 50 55 60	192
act ctc gcc cgt cag att gaa gcg ggt gcg cct gcg gat ctg ttt att Thr Leu Ala Arg Gln Ile Glu Ala Gly Ala Pro Ala Asp Leu Phe Ile 65 70 75 80	240
tct gcc gat cag aaa tgg atg gat tat gcg gtt gat aaa aaa gcg atc Ser Ala Asp Gln Lys Trp Met Asp Tyr Ala Val Asp Lys Lys Ala Ile 85 90 95	288
gat aca gct acg cgt cag aca ctg ctc ggc aat agc ctg gtc gtt gta Asp Thr Ala Thr Arg Gln Thr Leu Leu Gly Asn Ser Leu Val Val Val 100 105 110	336
gca ccg aaa gcc agc gtg cag aaa gat ttc acc atc gac agc aaa acc Ala Pro Lys Ala Ser Val Gln Lys Asp Phe Thr Ile Asp Ser Lys Thr 115 120 125	384
aac tgg act tca ctg ctg aat ggc ggt cgc ctg gcg gtt ggc gat ccg Asn Trp Thr Ser Leu Leu Asn Gly Gly Arg Leu Ala Val Gly Asp Pro 130 135 140	432
gaa cat gtt ccc gct ggc att tat gca aaa gaa gca ctg caa aaa ctg Glu His Val Pro Ala Gly Ile Tyr Ala Lys Glu Ala Leu Gln Lys Leu 145 150 155 160	480
ggc gca tgg gat acg ctc tct ccg aaa ctg gcc cca gcg gaa gat gtt Gly Ala Trp Asp Thr Leu Ser Pro Lys Leu Ala Pro Ala Glu Asp Val 165 170 175	528
cgt ggg gcg ctg gcg ctg gtc gaa cgt aac gaa gcg cct ctg ggc att Arg Gly Ala Leu Ala Leu Val Glu Arg Asn Glu Ala Pro Leu Gly Ile 180 185 190	576
gtc tac ggt tct gac gca gtt gcc agc aaa ggg gta aaa gtg gtt gcc Val Tyr Gly Ser Asp Ala Val Ala Ser Lys Gly Val Lys Val Val Ala 195 200 205	624
acc ttc ccg gaa gat tca cat aaa aaa gtg gaa tat ccg gtt gct gtt Thr Phe Pro Glu Asp Ser His Lys Lys Val Glu Tyr Pro Val Ala Val 210 215 220	672
gtg gaa ggg cat aac aat gcg aca gtg aaa gca ttt tat gat tat ctg Val Glu Gly His Asn Asn Ala Thr Val Lys Ala Phe Tyr Asp Tyr Leu 225 230 235 240	720
aag gga ccg cag gca gcg gaa atc ttt aaa cgt tac gga ttt aca atc Lys Gly Pro Gln Ala Ala Glu Ile Phe Lys Arg Tyr Gly Phe Thr Ile 245 250 255	768

aag taa
Lys *

774

<210> 276
<211> 690
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(690)

<400> 276
atg ata ctg acc gat cca gaa tgg cag gca gtt tta tta agc ctg aaa 48
Met Ile Leu Thr Asp Pro Glu Trp Gln Ala Val Leu Leu Ser Leu Lys
1 5 10 15
gtt tct tcc ctg gct gtg ctg ttt agc ctg ccg ttt ggg atc ttt ttt 96
Val Ser Ser Leu Ala Val Leu Phe Ser Leu Pro Phe Gly Ile Phe Phe
20 25 30
gcc tgg tta ctg gtg cgt tgc acg ttt ccg ggc aaa gct ctg ctc gac 144
Ala Trp Leu Leu Val Arg Cys Thr Phe Pro Gly Lys Ala Leu Leu Asp
35 40 45
agc gta ctg cat cta ccg ctg gtg tta ccg ccc gtg gtc gtc ggt tac 192
Ser Val Leu His Leu Pro Leu Val Leu Pro Pro Val Val Val Gly Tyr
50 55 60
tta tta tta gtt tcg atg gga cgg cgc gga ttt atc ggt gaa cgt ctg 240
Leu Leu Leu Val Ser Met Gly Arg Arg Gly Phe Ile Gly Glu Arg Leu
65 70 75 80
tat gac tgg ttt ggt att acc ttc gcc ttt agc tgg cgc ggc gcg gtt 288
Tyr Asp Trp Phe Gly Ile Thr Phe Ala Phe Ser Trp Arg Gly Ala Val
85 90 95
ctc gct gcc gcc gtc atg tcg ttt ccg ctg atg gtg cgg gca att cgt 336
Leu Ala Ala Ala Val Met Ser Phe Pro Leu Met Val Arg Ala Ile Arg
100 105 110
ctg gcg ctg gaa ggg gtt gat gtc aaa ctg gaa cag gcc gca aga aca 384
Leu Ala Leu Glu Gly Val Asp Val Lys Leu Glu Gln Ala Ala Arg Thr
115 120 125
ctg ggg gcc ggg cgc tgg cgc gtt ttc ttt act atc acg tta ccg ctg 432
Leu Gly Ala Gly Arg Trp Arg Val Phe Phe Thr Ile Thr Leu Pro Leu
130 135 140
acc tta ccg gga att att gtt ggt acg gta ctg gct ttt gct cgt tct 480
Thr Leu Pro Gly Ile Ile Val Gly Thr Val Leu Ala Phe Ala Arg Ser
145 150 155 160
ctc ggt gag ttt ggt gca acc atc acc ttt gtg tcg aac att cct ggt 528
Leu Gly Glu Phe Gly Ala Thr Ile Thr Phe Val Ser Asn Ile Pro Gly
165 170 175
gaa acg cga acc att cct tct gcc atg tat acc ctg atc cag acc ccc 576

Glu Thr Arg Thr Ile Pro Ser Ala Met Tyr Thr Leu Ile Gln Thr Pro	
180 185 190	
ggc ggg gaa agt gga gcg gcg aga ctg tgc att att tct att gcg ctg	624
Gly Gly Glu Ser Gly Ala Ala Arg Leu Cys Ile Ile Ser Ile Ala Leu	
195 200 205	
gcg atg atc tcc ctg ttg att tca gaa tgg ctg gcc aga atc agc cgt	672
Ala Met Ile Ser Leu Leu Ile Ser Glu Trp Leu Ala Arg Ile Ser Arg	
210 215 220	
gaa cgg gcg ggg cgc taa	690
Glu Arg Ala Gly Arg *	
225	
<210> 277	
<211> 1059	
<212> DNA	
<213> Escherichia coli	
<220>	
<221> CDS	
<222> (1)...(1059)	
<400> 277	
atg ctg gaa ctg aat ttt tcc cag acg ttg ggc aac cat tgc ctg act	48
Met Leu Glu Leu Asn Phe Ser Gln Thr Leu Gly Asn His Cys Leu Thr	
1 5 10 15	
att aat gaa acg ctg ccc gcc aat ggc atc act gct atc ttt ggc gtc	96
Ile Asn Glu Thr Leu Pro Ala Asn Gly Ile Thr Ala Ile Phe Gly Val	
20 25 30	
tcc ggt gcc gga aaa act tcg ctg att aac gcc atc agt gga ctg acg	144
Ser Gly Ala Gly Lys Thr Ser Leu Ile Asn Ala Ile Ser Gly Leu Thr	
35 40 45	
cgc ccg caa aaa ggg cgg att gtc ctc aat ggg cgg gta cta aat gat	192
Arg Pro Gln Lys Gly Arg Ile Val Leu Asn Gly Arg Val Leu Asn Asp	
50 55 60	
gcc gaa aaa ggt atc tgc ctg acg ccg gaa aag cgt cgc gtt gcc tat	240
Ala Glu Lys Gly Ile Cys Leu Thr Pro Glu Lys Arg Arg Val Gly Tyr	
65 70 75 80	
gtt ttt cag gat gcg cgg ctg ttc ccg cat tac aaa gtg cgt ggc aat	288
Val Phe Gln Asp Ala Arg Leu Phe Pro His Tyr Lys Val Arg Gly Asn	
85 90 95	
ctg cgc tac ggc atg tcg aaa agt atg gtc gat cag ttc gat aag ctg	336
Leu Arg Tyr Gly Met Ser Lys Ser Met Val Asp Gln Phe Asp Lys Leu	
100 105 110	
gtg gcg ctt tta ggc att gaa ccg ttg ctt gac cgt tta cca ggc agc	384
Val Ala Leu Leu Gly Ile Glu Pro Leu Leu Asp Arg Leu Pro Gly Ser	
115 120 125	
ctg tcc gga ggc gaa aaa cag cgc gtg gcg att ggt cgg gct ttg ctg	432
Leu Ser Gly Gly Glu Lys Gln Arg Val Ala Ile Gly Arg Ala Leu Leu	

130	135	140	
aca gca ccg gaa ttg ctg ttg ctg gat gaa ccg ctg gcg tca ctg gat			480
Thr Ala Pro Glu Leu Leu Leu Leu Asp Glu Pro Leu Ala Ser Leu Asp			
145	150	155	160
att ccg cgt aaa cgc gaa ctg ttg cct tat ctg caa cgg ctg aca cgg			528
Ile Pro Arg Lys Arg Glu Leu Leu Pro Tyr Leu Gln Arg Leu Thr Arg			
	165	170	175
gaa atc aac att ccg atg ttg tat gtc agc cat tcg ctg gat gag atc			576
Glu Ile Asn Ile Pro Met Leu Tyr Val Ser His Ser Leu Asp Glu Ile			
	180	185	190
ctc cat ctg gca gac aga gtg atg gta ctg gaa aac ggt cag gtg aaa			624
Leu His Leu Ala Asp Arg Val Met Val Leu Glu Asn Gly Gln Val Lys			
	195	200	205
gcc ttt ggc gcg ctg gag gaa gtg tgg ggc agt agc gtg atg aat ccg			672
Ala Phe Gly Ala Leu Glu Glu Val Trp Gly Ser Ser Val Met Asn Pro			
	210	215	220
tgg ctg ccg aaa gag caa caa agt agc att ctg aaa gtg acg gtg ctt			720
Trp Leu Pro Lys Glu Gln Gln Ser Ser Ile Leu Lys Val Thr Val Leu			
	225	230	240
gag cat cat ccg cat tac gcg atg acc gcg ctg gcg ctg ggc gat cag			768
Glu His His Pro His Tyr Ala Met Thr Ala Leu Ala Leu Gly Asp Gln			
	245	250	255
cat ttg tgg gtc aat aag ctg gac gaa ccg ctg caa gct gcg cta cgt			816
His Leu Trp Val Asn Lys Leu Asp Glu Pro Leu Gln Ala Ala Leu Arg			
	260	265	270
atc cgc att cag gct tcc gat gtt tct ctg gtt tta caa ccg ccg cag			864
Ile Arg Ile Gln Ala Ser Asp Val Ser Leu Val Leu Gln Pro Pro Gln			
	275	280	285
caa acc agc att cgt aac gta ttg ccg gca aaa gtt gtt aat agt tat			912
Gln Thr Ser Ile Arg Asn Val Leu Arg Ala Lys Val Val Asn Ser Tyr			
	290	295	300
gac gac aac ggc cag gtg gaa gtg gaa ctg gaa gtc ggc ggt aaa acg			960
Asp Asp Asn Gly Gln Val Glu Val Glu Leu Glu Val Gly Gly Lys Thr			
	305	310	315
ctg tgg gcg cgt atc agc ccg tgg gcc agg gat gaa ctg gcg atc aaa			1008
Leu Trp Ala Arg Ile Ser Pro Trp Ala Arg Asp Glu Leu Ala Ile Lys			
	325	330	335
cct ggc ctg tgg ctg tac gcg caa att aaa agt gtg tcg ata acc gcc			1056
Pro Gly Leu Trp Leu Tyr Ala Gln Ile Lys Ser Val Ser Ile Thr Ala			
	340	345	350
tga			1059
*			

<210> 278

<211> 507
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(507)

<400> 278
 gtg aac tcc gtc att aca caa aaa gtg tca tct ggc gtt aca ctt tat 48
 Met Asn Ser Val Ile Thr Gln Lys Val Ser Ser Gly Val Thr Leu Tyr
 1 5 10 15
 gcg gat act aaa aca gga ggt ttt atg aac aga acg att ctt gtc cct 96
 Ala Asp Thr Lys Thr Gly Gly Phe Met Asn Arg Thr Ile Leu Val Pro
 20 25 30
 atc gat att tcc gat tca gaa tta act caa cgc gtg att agc cac gtt 144
 Ile Asp Ile Ser Asp Ser Glu Leu Thr Gln Arg Val Ile Ser His Val
 35 40 45
 gag gaa gag gca aag att gat gat gca gag gtt cat ttc ctg acg gta 192
 Glu Glu Glu Ala Lys Ile Asp Asp Ala Glu Val His Phe Leu Thr Val
 50 55 60
 ata cct tca ctg ccc tac tat gcc tct ctg ggt tta gcg tat tcc gca 240
 Ile Pro Ser Leu Pro Tyr Tyr Ala Ser Leu Gly Leu Ala Tyr Ser Ala
 65 70 75 80
 gaa tta ccg gca atg gat gac ctg aaa gcg gaa gcc aaa tcg caa ctg 288
 Glu Leu Pro Ala Met Asp Asp Leu Lys Ala Glu Ala Lys Ser Gln Leu
 85 90 95
 gaa gag atc att aaa aaa ttt aaa ctg cca acc gac aga gtg cat gtc 336
 Glu Glu Ile Ile Lys Lys Phe Lys Leu Pro Thr Asp Arg Val His Val
 100 105 110
 cat gtt gag gaa ggc tcg ccc aaa gac cgc att ctg gaa ttg gcg aag 384
 His Val Glu Glu Gly Ser Pro Lys Asp Arg Ile Leu Glu Leu Ala Lys
 115 120 125
 aag atc ccc gct cat atg atc atc att gct tcc cat cga ccg gat atc 432
 Lys Ile Pro Ala His Met Ile Ile Ile Ala Ser His Arg Pro Asp Ile
 130 135 140
 acc act tat ctg ctc ggt tcc aac gcc gca gct gta gtg cgt cac gca 480
 Thr Thr Tyr Leu Leu Gly Ser Asn Ala Ala Val Val Arg His Ala
 145 150 155 160
 gag tgc tcc gtg ctg gtt gtg cgc tga 507
 Glu Cys Ser Val Leu Val Val Arg *
 165

<210> 279
 <211> 1134
 <212> DNA
 <213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1134)

<400> 279

atg	aaa	agc	aaa	gta	ctg	gca	ctt	tta	att	cct	gcc	ctg	ctc	gcc	gca	48
Met	Lys	Ser	Lys	Val	Leu	Ala	Leu	Leu	Ile	Pro	Ala	Leu	Leu	Ala	Ala	
1				5					10					15		

ggt	gct	gca	cat	gca	gcc	gaa	gtt	tat	aat	aaa	gac	ggc	aac	aaa	tta	96
Gly	Ala	Ala	His	Ala	Ala	Glu	Val	Tyr	Asn	Lys	Asp	Gly	Asn	Lys	Leu	
			20					25					30			

gat	ctg	tat	ggc	aaa	gtt	gat	ggc	ctg	cat	tat	ttt	tct	gat	aat	tca	144
Asp	Leu	Tyr	Gly	Lys	Val	Asp	Gly	Leu	His	Tyr	Phe	Ser	Asp	Asn	Ser	
			35				40					45				

gcg	aaa	gat	ggc	gac	cag	agc	tat	gcg	cgt	ctg	ggt	ttt	aaa	ggc	gaa	192
Ala	Lys	Asp	Gly	Asp	Gln	Ser	Tyr	Ala	Arg	Leu	Gly	Phe	Lys	Gly	Glu	
	50					55					60					

acc	caa	att	aac	gat	caa	ctc	act	ggc	tac	ggt	caa	tgg	gaa	tac	aat	240
Thr	Gln	Ile	Asn	Asp	Gln	Leu	Thr	Gly	Tyr	Gly	Gln	Trp	Glu	Tyr	Asn	
65					70					75					80	

att	cag	gca	aac	aac	act	gaa	tct	tca	aaa	aac	cag	tca	tgg	acc	cgt	288
Ile	Gln	Ala	Asn	Asn	Thr	Glu	Ser	Ser	Lys	Asn	Gln	Ser	Trp	Thr	Arg	
			85						90					95		

ctg	gca	ttt	gcc	ggg	ctg	aaa	ttt	gca	gat	tac	ggt	tct	ttc	gat	tac	336
Leu	Ala	Phe	Ala	Gly	Leu	Lys	Phe	Ala	Asp	Tyr	Gly	Ser	Phe	Asp	Tyr	
			100					105					110			

gga	cgt	aat	tat	ggc	gta	atg	tac	gac	atc	gaa	ggc	tgg	acc	gat	atg	384
Gly	Arg	Asn	Tyr	Gly	Val	Met	Tyr	Asp	Ile	Glu	Gly	Trp	Thr	Asp	Met	
		115					120					125				

ctg	cct	gaa	ttt	ggc	ggt	gac	tct	tat	acc	aat	gca	gac	aac	ttt	atg	432
Leu	Pro	Glu	Phe	Gly	Gly	Asp	Ser	Tyr	Thr	Asn	Ala	Asp	Asn	Phe	Met	
	130					135					140					

act	ggt	cga	gcc	aat	ggc	gtc	gcg	act	tat	cgt	aat	act	gat	ttc	ttc	480
Thr	Gly	Arg	Ala	Asn	Gly	Val	Ala	Thr	Tyr	Arg	Asn	Thr	Asp	Phe	Phe	
145					150					155					160	

ggt	ctg	gta	aat	ggt	ctg	aac	ttc	gcg	gtg	cag	tat	caa	ggt	aac	aac	528
Gly	Leu	Val	Asn	Gly	Leu	Asn	Phe	Ala	Val	Gln	Tyr	Gln	Gly	Asn	Asn	
			165					170					175			

gaa	gga	gcc	agt	aat	ggt	cag	gaa	ggc	acc	aac	aac	gga	cgt	gat	gtt	576
Glu	Gly	Ala	Ser	Asn	Gly	Gln	Glu	Gly	Thr	Asn	Asn	Gly	Arg	Asp	Val	
			180					185					190			

cgc	cat	gaa	aac	ggt	gac	ggc	tgg	ggt	ctt	tcc	aca	aca	tat	gat	tta	624
Arg	His	Glu	Asn	Gly	Asp	Gly	Trp	Gly	Leu	Ser	Thr	Thr	Tyr	Asp	Leu	
		195					200					205				

ggc	atg	ggc	ttt	agc	gct	ggt	gcg	gca	tac	acc	tct	tct	gac	cgc	acc	672
Gly	Met	Gly	Phe	Ser	Ala	Gly	Ala	Ala	Tyr	Thr	Ser	Ser	Asp	Arg	Thr	
	210					215					220					

aat gac cag gtt aac cat act gcg gcg ggt ggt gat aaa gca gac gcg Asn Asp Gln Val Asn His Thr Ala Ala Gly Gly Asp Lys Ala Asp Ala 225 230 235 240	720
tgg act gct ggg cta aaa tac gat gct aac aat att tac ctg gca acc Trp Thr Ala Gly Leu Lys Tyr Asp Ala Asn Asn Ile Tyr Leu Ala Thr 245 250 255	768
atg tat tca gaa acg cgt aat atg acc ccg ttt ggc gac agc gat tat Met Tyr Ser Glu Thr Arg Asn Met Thr Pro Phe Gly Asp Ser Asp Tyr 260 265 270	816
gct gtg gca aac aaa acc cag aat ttt gaa gtc act gca cag tac cag Ala Val Ala Asn Lys Thr Gln Asn Phe Glu Val Thr Ala Gln Tyr Gln 275 280 285	864
ttt gat ttt ggt ctg cgt ccg gca gtc tct ttc ctg atg tct aaa ggc Phe Asp Phe Gly Leu Arg Pro Ala Val Ser Phe Leu Met Ser Lys Gly 290 295 300	912
cgt gac ctg cac gct gcg ggt ggt gca gac aac ccg gca ggt gtt gat Arg Asp Leu His Ala Ala Gly Gly Ala Asp Asn Pro Ala Gly Val Asp 305 310 315 320	960
gat aaa gat ctg gtt aaa tac gcc gat att ggc gcg act tac tat ttc Asp Lys Asp Leu Val Lys Tyr Ala Asp Ile Gly Ala Thr Tyr Tyr Phe 325 330 335	1008
aat aaa aac atg tcc acc tac gtt gac tat aaa atc aac ctg ttg gat Asn Lys Asn Met Ser Thr Tyr Val Asp Tyr Lys Ile Asn Leu Leu Asp 340 345 350	1056
gaa gat gac agc ttc tac gct gcc aat ggc atc tct acc gat gat att Glu Asp Asp Ser Phe Tyr Ala Ala Asn Gly Ile Ser Thr Asp Asp Ile 355 360 365	1104
gtc gct tta ggt ctg gtt tat cag ttc taa Val Ala Leu Gly Leu Val Tyr Gln Phe *	1134
<210> 280	
<211> 3369	
<212> DNA	
<213> Escherichia coli	
<220>	
<221> CDS	
<222> (1)...(3369)	
<400> 280	
atg tta agg gtc tac cat tcc aat cgt ctg gac gtg ctg gaa gcg ttg Met Leu Arg Val Tyr His Ser Asn Arg Leu Asp Val Leu Glu Ala Leu 1 5 10 15	48
atg gag ttt att gtc gaa cgc gaa cgg ctg gac gat cct ttc gaa cca Met Glu Phe Ile Val Glu Arg Glu Arg Leu Asp Asp Pro Phe Glu Pro 20 25 30	96
gag atg att ctg gtg caa agt acc ggt atg gca cag tgg ctg caa atg	144

Glu Met Ile Leu Val Gln Ser Thr Gly Met Ala Gln Trp Leu Gln Met	
35 40 45	
acc ctg tcg caa aag ttt ggt att gcg gca aac att gat ttt ccg ctg	192
Thr Leu Ser Gln Lys Phe Gly Ile Ala Ala Asn Ile Asp Phe Pro Leu	
50 55 60	
cca gcg agc ttt atc tgg gat atg ttc gtc cgg gtg tta ccg gaa atc	240
Pro Ala Ser Phe Ile Trp Asp Met Phe Val Arg Val Leu Pro Glu Ile	
65 70 75 80	
ccc aaa gag agc gcc ttt aac aaa cag agc atg agc tgg aaa ctg atg	288
Pro Lys Glu Ser Ala Phe Asn Lys Gln Ser Met Ser Trp Lys Leu Met	
85 90 95	
act ctg ctg ccg caa ttg ctg gag cgc gaa gac ttt acc ctg ttg cgg	336
Thr Leu Leu Pro Gln Leu Leu Glu Arg Glu Asp Phe Thr Leu Leu Arg	
100 105 110	
cat tat ctg act gac gat agc gac aag cga aaa ctg ttc cag ctt tcc	384
His Tyr Leu Thr Asp Asp Ser Asp Lys Arg Lys Leu Phe Gln Leu Ser	
115 120 125	
tca aaa gcg gcg gac ctg ttt gac cag tat ctg gtc tat cgt ccg gac	432
Ser Lys Ala Ala Asp Leu Phe Asp Gln Tyr Leu Val Tyr Arg Pro Asp	
130 135 140	
tgg ctg gca cag tgg gaa aca gga cat ttg gtt gaa ggg ctg gga gaa	480
Trp Leu Ala Gln Trp Glu Thr Gly His Leu Val Glu Gly Leu Gly Glu	
145 150 155 160	
gca cag gcc tgg caa gcc ccg ttg tgg aag gcg ctg gtg gaa tat acc	528
Ala Gln Ala Trp Gln Ala Pro Leu Trp Lys Ala Leu Val Glu Tyr Thr	
165 170 175	
cat caa ctc ggg caa ccg cgc tgg cac cgc gcc aat ctc tat cag cgc	576
His Gln Leu Gly Gln Pro Arg Trp His Arg Ala Asn Leu Tyr Gln Arg	
180 185 190	
ttt atc gaa acg ctg gag tcc gcg acg acc tgc ccg ccg ggg tta cct	624
Phe Ile Glu Thr Leu Glu Ser Ala Thr Thr Cys Pro Pro Gly Leu Pro	
195 200 205	
tcg cgc gtc ttt ata tgc ggt att tcc gcg tta ccg cct gtt tat ctc	672
Ser Arg Val Phe Ile Cys Gly Ile Ser Ala Leu Pro Pro Val Tyr Leu	
210 215 220	
cag gcg cta cag gcg ctg ggt aaa cat att gaa atc cat ctc ctg ttt	720
Gln Ala Leu Gln Ala Leu Gly Lys His Ile Glu Ile His Leu Leu Phe	
225 230 235 240	
acc aac ccc tgc cgt tat tac tgg ggc gat att aaa gat cct gct tat	768
Thr Asn Pro Cys Arg Tyr Tyr Trp Gly Asp Ile Lys Asp Pro Ala Tyr	
245 250 255	
ctg gcg aaa ctg ctg acc cgt cag cgt cga cac agt ttt gaa gat cgc	816
Leu Ala Lys Leu Leu Thr Arg Gln Arg Arg His Ser Phe Glu Asp Arg	
260 265 270	
gaa ttg ccg cta ttt cgt gat agc gaa aat gcc ggg cag ctc ttt aac	864

Glu	Leu	Pro	Leu	Phe	Arg	Asp	Ser	Glu	Asn	Ala	Gly	Gln	Leu	Phe	Asn		
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agc	gat	ggg	gaa	cag	gat	gtc	ggc	aac	ccg	ctg	ctg	gct	tca	tgg	ggg	912	
Ser	Asp	Gly	Glu	Gln	Asp	Val	Gly	Asn	Pro	Leu	Leu	Ala	Ser	Trp	Gly		
		290				295					300						
aag	ctt	ggg	cgc	gac	tac	att	tat	ctc	ctt	tct	gac	ctg	gag	agc	agc	960	
Lys	Leu	Gly	Arg	Asp	Tyr	Ile	Tyr	Leu	Leu	Ser	Asp	Leu	Glu	Ser	Ser		
		305			310					315					320		
cag	gag	ctg	gac	gcc	ttt	gtc	gat	gtc	acg	cca	gat	aac	ctg	ctg	cat	1008	
Gln	Glu	Leu	Asp	Ala	Phe	Val	Asp	Val	Thr	Pro	Asp	Asn	Leu	Leu	His		
				325					330					335			
aac	att	cag	tct	gac	att	ctg	gaa	ctg	gaa	aac	cgc	gcc	gtt	gct	ggg	1056	
Asn	Ile	Gln	Ser	Asp	Ile	Leu	Glu	Leu	Glu	Asn	Arg	Ala	Val	Ala	Gly		
			340					345					350				
gtg	aac	atc	gaa	gag	ttt	tcc	cgt	agc	gat	aac	aaa	cgc	ccg	ctt	gat	1104	
Val	Asn	Ile	Glu	Glu	Phe	Ser	Arg	Ser	Asp	Asn	Lys	Arg	Pro	Leu	Asp		
		355					360					365					
cca	ctg	gat	agc	agt	atc	acc	ttc	cac	gtt	tgc	cat	agc	ccg	cag	cgt	1152	
Pro	Leu	Asp	Ser	Ser	Ile	Thr	Phe	His	Val	Cys	His	Ser	Pro	Gln	Arg		
		370				375					380						
gaa	gtt	gaa	gtt	tta	cac	gat	cgc	ctg	ctg	gcg	atg	ctg	gag	gaa	gac	1200	
Glu	Val	Glu	Val	Leu	His	Asp	Arg	Leu	Leu	Ala	Met	Leu	Glu	Glu	Asp		
		385			390					395					400		
ccg	aca	ctt	act	ccg	cgc	gac	atc	atc	gtg	atg	gtg	gct	gat	atc	gac	1248	
Pro	Thr	Leu	Thr	Pro	Arg	Asp	Ile	Ile	Val	Met	Val	Ala	Asp	Ile	Asp		
				405					410					415			
agc	tac	agt	ccg	ttt	att	cag	gct	gtg	ttt	ggg	agc	gca	cct	gcg	gat	1296	
Ser	Tyr	Ser	Pro	Phe	Ile	Gln	Ala	Val	Phe	Gly	Ser	Ala	Pro	Ala	Asp		
			420					425					430				
cgt	tac	cta	cct	tac	gcc	att	tcc	gac	cgt	cgt	gcg	ccg	cag	tca	cat	1344	
Arg	Tyr	Leu	Pro	Tyr	Ala	Ile	Ser	Asp	Arg	Arg	Ala	Arg	Gln	Ser	His		
		435					440					445					
ccg	gta	ctg	gaa	gcg	ttt	atc	agc	ctg	tta	tca	ctg	cct	gac	agt	cgt	1392	
Pro	Val	Leu	Glu	Ala	Phe	Ile	Ser	Leu	Leu	Ser	Leu	Pro	Asp	Ser	Arg		
		450				455					460						
ttt	gtg	tca	gag	gat	gtg	ctg	gcg	ttg	ctg	gat	gtg	ccg	gtg	ctg	gcg	1440	
Phe	Val	Ser	Glu	Asp	Val	Leu	Ala	Leu	Leu	Asp	Val	Pro	Val	Leu	Ala		
		465			470					475					480		
gcg	ccg	ttt	gac	atc	acc	gaa	gaa	ggg	ctg	cgt	tat	tta	cgc	cag	tgg	1488	
Ala	Arg	Phe	Asp	Ile	Thr	Glu	Glu	Gly	Leu	Arg	Tyr	Leu	Arg	Gln	Trp		
			485					490						495			
gtc	aac	gaa	tcc	ggc	att	cgt	tgg	ggc	ata	gat	gac	gac	aac	gtt	cgc	1536	
Val	Asn	Glu	Ser	Gly	Ile	Arg	Trp	Gly	Ile	Asp	Asp	Asp	Asn	Val	Arg		
			500					505					510				
gag	ctg	gaa	ctc	ccc	gcc	acc	gga	caa	cac	acc	tgg	cga	ttt	ggc	ctg	1584	

Glu	Leu	Glu	Leu	Pro	Ala	Thr	Gly	Gln	His	Thr	Trp	Arg	Phe	Gly	Leu		
		515					520					525					
acg	cgt	atg	ttg	ttg	ggc	tac	gcg	atg	gag	agc	gcg	cag	ggc	gag	tgg		1632
Thr	Arg	Met	Leu	Leu	Gly	Tyr	Ala	Met	Glu	Ser	Ala	Gln	Gly	Glu	Trp		
		530				535					540						
caa	tcg	gtt	cta	cct	tat	gat	gaa	tcg	agc	ggc	tta	att	gca	gaa	ctg		1680
Gln	Ser	Val	Leu	Pro	Tyr	Asp	Glu	Ser	Ser	Gly	Leu	Ile	Ala	Glu	Leu		
		545			550					555					560		
gtg	ggg	cat	ctg	gct	tca	ctg	cta	atg	cag	cta	aac	atc	tgg	cgt	cgc		1728
Val	Gly	His	Leu	Ala	Ser	Leu	Leu	Met	Gln	Leu	Asn	Ile	Trp	Arg	Arg		
				565					570					575			
ggg	ctg	gca	cag	gag	cgt	ccg	ctg	gaa	gag	tgg	ttg	ccg	gtt	tgt	cgc		1776
Gly	Leu	Ala	Gln	Glu	Arg	Pro	Leu	Glu	Glu	Trp	Leu	Pro	Val	Cys	Arg		
			580					585					590				
gat	atg	ctc	aac	gcc	ttc	ttc	ctg	ccg	gat	gcg	gaa	acc	gaa	gcg	gcg		1824
Asp	Met	Leu	Asn	Ala	Phe	Phe	Leu	Pro	Asp	Ala	Glu	Thr	Glu	Ala	Ala		
		595					600					605					
atg	acg	ctg	atc	gaa	caa	caa	tgg	cag	gcg	att	atc	gcc	gaa	ggc	tta		1872
Met	Thr	Leu	Ile	Glu	Gln	Gln	Trp	Gln	Ala	Ile	Ile	Ala	Glu	Gly	Leu		
		610				615					620						
ggc	gcg	cag	tat	ggc	gac	gcg	gtg	ccg	ctg	tca	cta	ttg	cgt	gat	gaa		1920
Gly	Ala	Gln	Tyr	Gly	Asp	Ala	Val	Pro	Leu	Ser	Leu	Leu	Arg	Asp	Glu		
				630					635						640		
ctg	gca	cag	cgt	ctg	gat	caa	gaa	cgt	atc	agc	cag	cgt	ttt	ctc	gcc		1968
Leu	Ala	Gln	Arg	Leu	Asp	Gln	Glu	Arg	Ile	Ser	Gln	Arg	Phe	Leu	Ala		
				645					650					655			
gga	ccg	gtt	aac	att	tgt	act	ctg	atg	cca	atg	cgt	tca	att	ccg	ttc		2016
Gly	Pro	Val	Asn	Ile	Cys	Thr	Leu	Met	Pro	Met	Arg	Ser	Ile	Pro	Phe		
			660					665					670				
aaa	gtg	gtt	tgc	ctg	ctg	gga	atg	aac	gac	ggc	gtt	tat	cca	cgt	cag		2064
Lys	Val	Val	Cys	Leu	Leu	Gly	Met	Asn	Asp	Gly	Val	Tyr	Pro	Arg	Gln		
		675					680					685					
ctt	gcg	cca	ttg	ggc	ttt	gac	ctg	atg	agc	cag	aaa	ccg	aag	cgt	ggc		2112
Leu	Ala	Pro	Leu	Gly	Phe	Asp	Leu	Met	Ser	Gln	Lys	Pro	Lys	Arg	Gly		
		690				695					700						
gac	cgt	agc	cgt	cgc	gat	gac	gac	cgc	tat	ctg	ttc	ctg	gaa	gcg	tta		2160
Asp	Arg	Ser	Arg	Arg	Asp	Asp	Asp	Arg	Tyr	Leu	Phe	Leu	Glu	Ala	Leu		
				710					715						720		
att	tcc	gcg	cag	caa	aaa	ctc	tat	atc	agc	tat	atc	ggc	cgt	tcc	att		2208
Ile	Ser	Ala	Gln	Gln	Lys	Leu	Tyr	Ile	Ser	Tyr	Ile	Gly	Arg	Ser	Ile		
				725					730					735			
cag	gat	aac	agt	gag	cgt	ttc	ccg	tcg	gta	ctg	gtg	cag	gaa	ctg	atc		2256
Gln	Asp	Asn	Ser	Glu	Arg	Phe	Pro	Ser	Val	Leu	Val	Gln	Glu	Leu	Ile		
			740					745					750				
gac	tac	atc	ggg	caa	agt	cat	tat	cta	ccg	ggc	gat	gaa	gcg	ctc	aac		2304

Asp	Tyr	Ile	Gly	Gln	Ser	His	Tyr	Leu	Pro	Gly	Asp	Glu	Ala	Leu	Asn	
		755					760					765				
tgt	gat	gaa	agc	gag	gca	agg	gta	aaa	gcg	cat	ctt	act	tgc	ctc	cat	2352
Cys	Asp	Glu	Ser	Glu	Ala	Arg	Val	Lys	Ala	His	Leu	Thr	Cys	Leu	His	
	770					775					780					
acc	cgg	atg	ccg	ttt	gat	cca	caa	aac	tac	cag	cca	ggc	gaa	cga	caa	2400
Thr	Arg	Met	Pro	Phe	Asp	Pro	Gln	Asn	Tyr	Gln	Pro	Gly	Glu	Arg	Gln	
785					790					795					800	
agc	tat	gct	cgt	gaa	tgg	cta	cct	gcg	gcc	agc	cag	gct	ggt	aaa	gca	2448
Ser	Tyr	Ala	Arg	Glu	Trp	Leu	Pro	Ala	Ala	Ser	Gln	Ala	Gly	Lys	Ala	
				805					810					815		
cat	tct	gaa	ttt	gtt	cag	ccg	ctg	ccg	ttt	acc	tta	ccg	gaa	acc	gtg	2496
His	Ser	Glu	Phe	Val	Gln	Pro	Leu	Pro	Phe	Thr	Leu	Pro	Glu	Thr	Val	
			820					825					830			
ccg	ctg	gaa	acg	cta	caa	cga	ttc	tgg	gca	cat	ccg	gtg	cgg	gca	ttt	2544
Pro	Leu	Glu	Thr	Leu	Gln	Arg	Phe	Trp	Ala	His	Pro	Val	Arg	Ala	Phe	
		835					840					845				
ttc	cag	atg	cgt	ttg	cag	gtg	aac	ttc	cgt	act	gaa	gac	agc	gaa	atc	2592
Phe	Gln	Met	Arg	Leu	Gln	Val	Asn	Phe	Arg	Thr	Glu	Asp	Ser	Glu	Ile	
		850				855					860					
ccc	gac	acc	gag	cca	ttt	att	ctg	gaa	gga	ctt	agc	cgt	tat	caa	atc	2640
Pro	Asp	Thr	Glu	Pro	Phe	Ile	Leu	Glu	Gly	Leu	Ser	Arg	Tyr	Gln	Ile	
865					870					875					880	
aat	cag	cag	tta	ttg	aat	gca	ctg	gtt	gag	cag	gat	gat	gcc	gaa	cgc	2688
Asn	Gln	Gln	Leu	Leu	Asn	Ala	Leu	Val	Glu	Gln	Asp	Asp	Ala	Glu	Arg	
				885					890					895		
ttg	ttc	cgc	cgc	ttc	cga	gcg	gca	ggg	gat	tta	ccg	tat	ggc	gct	ttt	2736
Leu	Phe	Arg	Arg	Phe	Arg	Ala	Ala	Gly	Asp	Leu	Pro	Tyr	Gly	Ala	Phe	
			900					905					910			
ggt	gaa	att	ttc	tgg	gaa	aca	cag	tgc	cag	gag	atg	cag	cag	ctt	gcc	2784
Gly	Glu	Ile	Phe	Trp	Glu	Thr	Gln	Cys	Gln	Glu	Met	Gln	Gln	Leu	Ala	
		915					920					925				
gac	aga	gtc	att	gcc	tgt	cgc	cag	ccg	ggg	cag	agt	atg	gaa	att	gat	2832
Asp	Arg	Val	Ile	Ala	Cys	Arg	Gln	Pro	Gly	Gln	Ser	Met	Glu	Ile	Asp	
		930				935					940					
ctc	gcc	tgc	aac	ggt	gtg	cag	ata	act	ggc	tgg	ttg	ccg	cag	gtg	cag	2880
Leu	Ala	Cys	Asn	Gly	Val	Gln	Ile	Thr	Gly	Trp	Leu	Pro	Gln	Val	Gln	
945					950					955					960	
ccg	gat	ggc	ctg	ttg	cgc	tgg	cgt	ccc	tct	tta	tta	agt	gtg	gcc	cag	2928
Pro	Asp	Gly	Leu	Leu	Arg	Trp	Arg	Pro	Ser	Leu	Leu	Ser	Val	Ala	Gln	
				965					970					975		
gga	atg	caa	ctt	tgg	ctg	gaa	cac	ctt	gtc	tac	tgt	gcc	agc	ggt	ggt	2976
Gly	Met	Gln	Leu	Trp	Leu	Glu	His	Leu	Val	Tyr	Cys	Ala	Ser	Gly	Gly	
			980					985					990			
aat	ggt	gaa	agt	cgc	ctt	ttt	cta	cgc	aaa	gac	ggc	gag	tgg	cgt	ttt	3024

Asn Gly Glu Ser Arg Leu Phe Leu Arg Lys Asp Gly Glu Trp Arg Phe	
995 1000 1005	
ccg ccg ctt gca gcc gaa cag gct ttg cat tac ctc tca caa ctg att	3072
Pro Pro Leu Ala Ala Glu Gln Ala Leu His Tyr Leu Ser Gln Leu Ile	
1010 1015 1020	
gag ggg tat cgt gaa gga atg tcc gcg cca ttg ctg gtg tta cct gaa	3120
Glu Gly Tyr Arg Glu Gly Met Ser Ala Pro Leu Leu Val Leu Pro Glu	
1025 1030 1035 1040	
agt ggc ggc gcg tgg cta aaa acc tgt tat gac gcg caa aac gat gcc	3168
Ser Gly Gly Ala Trp Leu Lys Thr Cys Tyr Asp Ala Gln Asn Asp Ala	
1045 1050 1055	
atg ctg gat gac gat tcc acg ttg caa aaa gcc cgt acg aaa ttc ctt	3216
Met Leu Asp Asp Asp Ser Thr Leu Gln Lys Ala Arg Thr Lys Phe Leu	
1060 1065 1070	
cag gct tac gaa ggc aac atg atg gtg cgt ggc gaa ggt gat gat atc	3264
Gln Ala Tyr Glu Gly Asn Met Met Val Arg Gly Glu Gly Asp Asp Ile	
1075 1080 1085	
tgg tat caa agg ctc tgg cgg caa tta aca cca gag aca atg gag gcc	3312
Trp Tyr Gln Arg Leu Trp Arg Gln Leu Thr Pro Glu Thr Met Glu Ala	
1090 1095 1100	
atc gtt gaa cag tcg caa cgt ttc ctg tta ccg ctg ttt cgc ttt aat	3360
Ile Val Glu Gln Ser Gln Arg Phe Leu Leu Pro Leu Phe Arg Phe Asn	
1105 1110 1115 1120	
cag tca tga	3369
Gln Ser *	

<210> 281
 <211> 324
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(324)

<400> 281	
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Met Ser Ala Ser Leu Lys Asn Gln Gln Gly Phe Ser Leu Pro Glu Val	
1 5 10 15	
atg ttg gcg atg gtg ttg atg gtg atg att gtc act gcg tta tcg ggt	96
Met Leu Ala Met Val Leu Met Val Met Ile Val Thr Ala Leu Ser Gly	
20 25 30	
ttc cag cga aca tta atg aac agt ctt gcc agc aga aac cag tac caa	144
Phe Gln Arg Thr Leu Met Asn Ser Leu Ala Ser Arg Asn Gln Tyr Gln	
35 40 45	
cag ctc tgg cgg cat ggc tgg cag caa acg caa ctg cgc gcg att tcg	192
Gln Leu Trp Arg His Gly Trp Gln Gln Thr Gln Leu Arg Ala Ile Ser	

50	55	60	
cca cct gcc aac tgg cag gtc aac cga atg cag aca tcg cag gcg gga			240
Pro Pro Ala Asn Trp Gln Val Asn Arg Met Gln Thr Ser Gln Ala Gly			
65	70	75	80
tgt gtc agc atc agc gtt acg cta gtt tca ccc ggg ggc aga gaa ggc			288
Cys Val Ser Ile Ser Val Thr Leu Val Ser Pro Gly Gly Arg Glu Gly			
	85	90	95
gag atg acc cgc ctg cat tgc ccg aat cgt cag tag			324
Glu Met Thr Arg Leu His Cys Pro Asn Arg Gln *			
	100	105	

<210> 282

<211> 366

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(366)

<400> 282

atg ctg ctg gtt ttg ggt agt ttg cta tta caa gga atg agc caa cag	48
Met Leu Leu Val Leu Gly Ser Leu Leu Leu Gln Gly Met Ser Gln Gln	
1	5
	10
	15

gat cgc agt ttt gcc tct cgc gtg agc atg gaa agt cag tca ttg cgc	96
Asp Arg Ser Phe Ala Ser Arg Val Ser Met Glu Ser Gln Ser Leu Arg	
	20
	25
	30

cgc cag gcc atc gtt cag tcg gcg ctg gcg tgg gga aaa atg cac tgc	144
Arg Gln Ala Ile Val Gln Ser Ala Leu Ala Trp Gly Lys Met His Cys	
	35
	40
	45

tgg cag acg cag cca gca gtt cag tgc tcg cag tac gct gaa acc gat	192
Trp Gln Thr Gln Pro Ala Val Gln Cys Ser Gln Tyr Ala Glu Thr Asp	
	50
	55
	60

gcc cag gtt tgt ttg cgt tta ctg gca gat aat gaa gcc tta ttg att	240
Ala Gln Val Cys Leu Arg Leu Leu Ala Asp Asn Glu Ala Leu Leu Ile	
65	70
	75
	80

gcc ggt tat gaa ggc gtt tcg ttg tgg cga aca ggc gaa gtc att gat	288
Ala Gly Tyr Glu Gly Val Ser Leu Trp Arg Thr Gly Glu Val Ile Asp	
	85
	90
	95

gga aac att gtt ttt tcg cca cgc ggc tgg agc gat ttt tgt ccg ctg	336
Gly Asn Ile Val Phe Ser Pro Arg Gly Trp Ser Asp Phe Cys Pro Leu	
	100
	105
	110

aaa gag agg gcg tta tgt cag ctt ccc tga	366
Lys Glu Arg Ala Leu Cys Gln Leu Pro *	
	115
	120

<210> 283

<211> 564

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(564)

<400> 283

atg cct gta aaa gag caa ggt ttt tct ctg ctg gaa gtg ttg att gct	48
Met Pro Val Lys Glu Gln Gly Phe Ser Leu Leu Glu Val Leu Ile Ala	
1 5 10 15	

atg gcg atc agt agc gta ttg ttg ctg ggg gcg gca cgc ttt ctg cct	96
Met Ala Ile Ser Ser Val Leu Leu Gly Ala Ala Arg Phe Leu Pro	
20 25 30	

gcg tta cag cgt gaa agt tta acg agc acc cgt aag ctg gcg ctg gaa	144
Ala Leu Gln Arg Glu Ser Leu Thr Ser Thr Arg Lys Leu Ala Leu Glu	
35 40 45	

gat gaa atc tgg ctg cgg gta ttt acc gtc gcg aag cat ctc cag agg	192
Asp Glu Ile Trp Leu Arg Val Phe Thr Val Ala Lys His Leu Gln Arg	
50 55 60	

gcg ggt tat tgt cat ggc atc tgt acc ggc gaa ggg ctg gaa att gtc	240
Ala Gly Tyr Cys His Gly Ile Cys Thr Gly Glu Gly Leu Glu Ile Val	
65 70 75 80	

gga cag ggt gac tgt gtc att gtg cag tgg gat gcg aac agt aac ggt	288
Gly Gln Gly Asp Cys Val Ile Val Gln Trp Asp Ala Asn Ser Asn Gly	
85 90 95	

atc tgg gat cgc gaa ccg gta aaa gag tcc gac cag att gga ttt cgt	336
Ile Trp Asp Arg Glu Pro Val Lys Glu Ser Asp Gln Ile Gly Phe Arg	
100 105 110	

ctg aag gag cat gtg ctg gaa acg cta cgc ggt gcg aca tcc tgt gaa	384
Leu Lys Glu His Val Leu Glu Thr Leu Arg Gly Ala Thr Ser Cys Glu	
115 120 125	

ggt aag ggc tgg gat aaa gtc act aat ccg gat gcc atc att atc gac	432
Gly Lys Gly Trp Asp Lys Val Thr Asn Pro Asp Ala Ile Ile Ile Asp	
130 135 140	

act ttt cag gtc gta cgt cag gat gtc agc ggc ttc tcg ccg gtg ttg	480
Thr Phe Gln Val Val Arg Gln Asp Val Ser Gly Phe Ser Pro Val Leu	
145 150 155 160	

acg gtt aat atg cgt gct gcc agt aag tct gaa ccg caa acc gtg gtg	528
Thr Val Asn Met Arg Ala Ala Ser Lys Ser Glu Pro Gln Thr Val Val	
165 170 175	

aat gcc agc tat agc gtg aca gga ttc aac ctg tga	564
Asn Ala Ser Tyr Ser Val Thr Gly Phe Asn Leu *	
180 185	

<210> 284

<211> 471

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(471)

<400> 284

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Met	Lys	Thr	Gln	Arg	Gly	Tyr	Thr	Leu	Ile	Glu	Thr	Leu	Val	Ala	Met	
1				5					10					15		

ctg	att	ttg	gtc	atg	cta	agc	gca	agt	gga	ctc	tat	ggc	tgg	caa	tac	96
Leu	Ile	Leu	Val	Met	Leu	Ser	Ala	Ser	Gly	Leu	Tyr	Gly	Trp	Gln	Tyr	
		20						25					30			

tgg	cag	cag	tcg	caa	cgg	cta	tgg	caa	acc	gcc	agc	cag	gcg	cgg	gac	144
Trp	Gln	Gln	Ser	Gln	Arg	Leu	Trp	Gln	Thr	Ala	Ser	Gln	Ala	Arg	Asp	
		35					40					45				

tat	ttg	ctc	tat	tta	cgt	gaa	gat	gcc	aac	tgg	cat	aac	cgc	gac	cac	192
Tyr	Leu	Leu	Tyr	Leu	Arg	Glu	Asp	Ala	Asn	Trp	His	Asn	Arg	Asp	His	
	50					55					60					

agt	atc	agc	gtt	atc	agg	gag	ggg	acg	tta	tgg	tgc	ctt	gtg	agt	tcc	240
Ser	Ile	Ser	Val	Ile	Arg	Glu	Gly	Thr	Leu	Trp	Cys	Leu	Val	Ser	Ser	
65					70					75					80	

gct	gct	ggg	gcc	aat	acc	tgt	cat	ggc	agt	tca	cca	ttg	gtc	ttt	gtg	288
Ala	Ala	Gly	Ala	Asn	Thr	Cys	His	Gly	Ser	Ser	Pro	Leu	Val	Phe	Val	
				85					90					95		

cca	cgc	tgg	ccc	gaa	gtc	gaa	atg	agc	gac	ctg	aca	cct	tcg	ctt	gct	336
Pro	Arg	Trp	Pro	Glu	Val	Glu	Met	Ser	Asp	Leu	Thr	Pro	Ser	Leu	Ala	
			100					105					110			

ttc	ttt	ggc	ctg	cgc	aat	acc	gca	tgg	gcc	ggg	cat	att	cgc	ttc	aaa	384
Phe	Phe	Gly	Leu	Arg	Asn	Thr	Ala	Trp	Ala	Gly	His	Ile	Arg	Phe	Lys	
		115					120					125				

aac	tca	acg	ggc	gag	tgg	tgg	ctg	gtg	gtt	tcg	ccg	tgg	gga	aga	ctc	432
Asn	Ser	Thr	Gly	Glu	Trp	Trp	Leu	Val	Val	Ser	Pro	Trp	Gly	Arg	Leu	
	130					135					140					

cgg	ctt	tgt	cag	caa	gga	gaa	aca	gaa	gga	tgc	ctg	taa				471
Arg	Leu	Cys	Gln	Gln	Gly	Glu	Thr	Glu	Gly	Cys	Leu	*				
145					150					155						

<210> 285

<211> 2136

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(2136)

<400> 285

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Met	Ser	Thr	Ile	Val	Ile	Phe	Leu	Ala	Ala	Leu	Leu	Ala	Cys	Ser	Leu	

1	5	10	15	
ctt gcg gga tgg ctg ata aaa gtg cga tcc aga cgg cgt cag ctg ccc				96
Leu Ala Gly Trp Leu Ile Lys Val Arg Ser Arg Arg Arg Gln Leu Pro				
20		25	30	
tgg acc aac gcc ttc gcg gat gcg caa acg cgt aaa ctc aca cct gaa				144
Trp Thr Asn Ala Phe Ala Asp Ala Gln Thr Arg Lys Leu Thr Pro Glu				
35		40	45	
gaa cgt agc gcc gtt gaa aat tat ctt gag agc ctg acg cag gta tta				192
Glu Arg Ser Ala Val Glu Asn Tyr Leu Glu Ser Leu Thr Gln Val Leu				
50		55	60	
cag gtg cct ggc cca acg gga gcc agc gcg gca ccg atc tct ctg gcg				240
Gln Val Pro Gly Pro Thr Gly Ala Ser Ala Ala Pro Ile Ser Leu Ala				
65		70	75	80
ctg aat gcc gaa agc aac aac gtc atg atg ctg aca cac gct atc acg				288
Leu Asn Ala Glu Ser Asn Asn Val Met Met Leu Thr His Ala Ile Thr				
85		90	95	
cgt tac ggc atc tct acc gac gat ccg aat aaa tgg cgt tac tac ctc				336
Arg Tyr Gly Ile Ser Thr Asp Asp Pro Asn Lys Trp Arg Tyr Tyr Leu				
100		105	110	
gat tcg gta gaa gtc cac ctg ccc cct ttc tgg gaa cag tac atc aac				384
Asp Ser Val Glu Val His Leu Pro Pro Phe Trp Glu Gln Tyr Ile Asn				
115		120	125	
gat gag aat acc gtt gaa ctg att cat acc gat tcg ctg ccg ctg gtt				432
Asp Glu Asn Thr Val Glu Leu Ile His Thr Asp Ser Leu Pro Leu Val				
130		135	140	
att tca ctc aac ggt cat acg ctg cag gag tac atg cag gaa act cgc				480
Ile Ser Leu Asn Gly His Thr Leu Gln Glu Tyr Met Gln Glu Thr Arg				
145		150	155	160
agc tat gcc ttg caa cct gtt ccg tca acg cag gcg tcg att cgc ggg				528
Ser Tyr Ala Leu Gln Pro Val Pro Ser Thr Gln Ala Ser Ile Arg Gly				
165		170	175	
gaa gag agt gag caa atc gag cta ctc aat att cgc aaa gaa acg cat				576
Glu Glu Ser Glu Gln Ile Glu Leu Leu Asn Ile Arg Lys Glu Thr His				
180		185	190	
gaa gaa tat gcg ctg agt cgt ccg cgc ggg ctg cgt gaa gcg ttg ctg				624
Glu Glu Tyr Ala Leu Ser Arg Pro Arg Gly Leu Arg Glu Ala Leu Leu				
195		200	205	
atc gtc gcc tcc ttc ctg atg ttc ttt ttc tgc ctg att acc ccg gat				672
Ile Val Ala Ser Phe Leu Met Phe Phe Phe Cys Leu Ile Thr Pro Asp				
210		215	220	
gta ttt gtt ccg tgg ctg gca ggc ggc gcg tta ctg ctg ctg ggc gca				720
Val Phe Val Pro Trp Leu Ala Gly Gly Ala Leu Leu Leu Leu Gly Ala				
225		230	235	240
ggt ctg tgg ggg cta ttc gcg ccc ccg gca aaa tcc tcc ctg ccg gaa				768
Gly Leu Trp Gly Leu Phe Ala Pro Pro Ala Lys Ser Ser Leu Arg Glu				

245										250										255												
att	cat	tgt	ctg	cgc	ggg	aca	ccc	cgt	cgt	tgg	gga	ttg	ttt	ggc	gaa																	816
Ile	His	Cys	Leu	Arg	Gly	Thr	Pro	Arg	Arg	Trp	Gly	Leu	Phe	Gly	Glu																	
			260					265					270																			
aac	gat	cag	gaa	cag	atc	aac	aat	att	tca	ctc	ggg	att	atc	gac	ctg																	864
Asn	Asp	Gln	Glu	Gln	Ile	Asn	Asn	Ile	Ser	Leu	Gly	Ile	Ile	Asp	Leu																	
			275				280					285																				
gtc	tat	ccc	gca	cac	tgg	cag	cca	tac	att	gct	cag	gat	ctc	ggg	caa																	912
Val	Tyr	Pro	Ala	His	Trp	Gln	Pro	Tyr	Ile	Ala	Gln	Asp	Leu	Gly	Gln																	
			290			295					300																					
caa	acc	gat	atc	gat	atc	tat	ctc	gac	cgc	cat	gta	gtg	cgt	cag	gga																	960
Gln	Thr	Asp	Ile	Asp	Ile	Tyr	Leu	Asp	Arg	His	Val	Val	Arg	Gln	Gly																	
			305			310				315					320																	
cga	tat	ctt	tcg	ctg	cat	gat	gaa	gta	aaa	aac	ttt	ccg	tta	cag	cac																	1008
Arg	Tyr	Leu	Ser	Leu	His	Asp	Glu	Val	Lys	Asn	Phe	Pro	Leu	Gln	His																	
				325				330						335																		
tgg	ctg	cgc	agt	acg	att	atc	gct	gcg	ggc	tcg	ctg	ctg	gtg	ctg	ttt																	1056
Trp	Leu	Arg	Ser	Thr	Ile	Ile	Ala	Ala	Gly	Ser	Leu	Leu	Val	Leu	Phe																	
			340					345					350																			
atg	ctg	tta	ttc	tgg	atc	ccg	ctg	gat	atg	ccg	ctg	aaa	ttc	act	ctc																	1104
Met	Leu	Leu	Phe	Trp	Ile	Pro	Leu	Asp	Met	Pro	Leu	Lys	Phe	Thr	Leu																	
			355				360					365																				
tca	tgg	atg	aaa	ggc	gcg	cag	acc	att	gaa	gcc	acc	agc	gta	aaa	caa																	1152
Ser	Trp	Met	Lys	Gly	Ala	Gln	Thr	Ile	Glu	Ala	Thr	Ser	Val	Lys	Gln																	
			370			375					380																					
ctg	gct	gac	gct	ggc	gtg	cgg	gta	ggc	gat	aca	ttg	cgt	att	agc	ggg																	1200
Leu	Ala	Asp	Ala	Gly	Val	Arg	Val	Gly	Asp	Thr	Leu	Arg	Ile	Ser	Gly																	
			385			390				395					400																	
acg	gga	atg	tgt	aat	att	cga	act	tcc	gga	acc	tgg	agc	gcg	aaa	acc																	1248
Thr	Gly	Met	Cys	Asn	Ile	Arg	Thr	Ser	Gly	Thr	Trp	Ser	Ala	Lys	Thr																	
				405				410						415																		
aat	tca	cct	ttt	tta	ccg	ttt	gac	tgc	tcg	cag	atc	atc	tgg	aac	gac																	1296
Asn	Ser	Pro	Phe	Leu	Pro	Phe	Asp	Cys	Ser	Gln	Ile	Ile	Trp	Asn	Asp																	
			420					425					430																			
gcc	cgc	tca	ttg	cca	tta	cca	gaa	tct	gaa	ctg	gtc	aac	aaa	gcg	acg																	1344
Ala	Arg	Ser	Leu	Pro	Leu	Pro	Glu	Ser	Glu	Leu	Val	Asn	Lys	Ala	Thr																	
			435				440					445																				
gca	ttg	act	gaa	gca	gtt	aat	cgc	cag	ctg	cac	cct	aaa	ccg	gaa	gat																	1392
Ala	Leu	Thr	Glu	Ala	Val	Asn	Arg	Gln	Leu	His	Pro	Lys	Pro	Glu	Asp																	
			450			455					460																					
gaa	tct	cgc	gtc	agt	gcc	tca	tta	cgt	tca	gca	att	caa	aaa	tcc	ggc																	1440
Glu	Ser	Arg	Val	Ser	Ala	Ser	Leu	Arg	Ser	Ala	Ile	Gln	Lys	Ser	Gly																	
			465			470				475					480																	
atg	gta	ttg	ctt	gat	gat	ttt	ggc	gac	att	gta	ctg	aag	aca	gcg	gat																	1488
Met	Val	Leu	Leu	Asp	Asp	Phe	Gly	Asp	Ile	Val	Leu	Lys	Thr	Ala	Asp																	

485	490	495	
tta tgt tct gcc aaa gat gac tgt gtg cga ctg aaa aat gcg ctg gtc Leu Cys Ser Ala Lys Asp Asp Cys Val Arg Leu Lys Asn Ala Leu Val 500 505 510			1536
aat ctc ggc aac agt aaa gac tgg gac gcg ctg gta aaa cgc gcc aac Asn Leu Gly Asn Ser Lys Asp Trp Asp Ala Leu Val Lys Arg Ala Asn 515 520 525			1584
gcc ggg aag ctc gat ggc gtg aat gtg tta tta cgc ccg gtg agt gcg Ala Gly Lys Leu Asp Gly Val Asn Val Leu Leu Arg Pro Val Ser Ala 530 535 540			1632
gaa tcg ctg gat aac ctg gtg gca acc tcc acc gcg ccg ttt atc acg Glu Ser Leu Asp Asn Leu Val Ala Thr Ser Thr Ala Pro Phe Ile Thr 545 550 555 560			1680
cat gaa acg gcg cga gcg gca caa tca cta aac agt ccg gcc ccc ggc His Glu Thr Ala Arg Ala Ala Gln Ser Leu Asn Ser Pro Ala Pro Gly 565 570 575			1728
gga ttc ctg att gtc agc gac gaa ggc agc gat ttt gtt gat cag ccc Gly Phe Leu Ile Val Ser Asp Glu Gly Ser Asp Phe Val Asp Gln Pro 580 585 590			1776
tgg cct tcg gca tca ctt tac gac tac ccg ccg caa gaa cag tgg aac Trp Pro Ser Ala Ser Leu Tyr Asp Tyr Pro Pro Gln Glu Gln Trp Asn 595 600 605			1824
gct ttc cag aaa ctg gca caa atg ctg atg cat acg ccg ttt aac gcc Ala Phe Gln Lys Leu Ala Gln Met Leu Met His Thr Pro Phe Asn Ala 610 615 620			1872
gag ggt atc gtc aca aaa atc ttc act gac gcc aat ggt acg cag cat Glu Gly Ile Val Thr Lys Ile Phe Thr Asp Ala Asn Gly Thr Gln His 625 630 635 640			1920
att ggc ctt cat ccg atc ccg gat cgt tcc ggc ctg tgg cgc tat ctc Ile Gly Leu His Pro Ile Pro Asp Arg Ser Gly Leu Trp Arg Tyr Leu 645 650 655			1968
agc acc aca ttg ctg cta ctg acg atg ctg ggt agc gcc att tac aat Ser Thr Thr Leu Leu Leu Leu Thr Met Leu Gly Ser Ala Ile Tyr Asn 660 665 670			2016
ggc gta cag gcc tgg cgt cgt tac cag cgt cat cgc act cgc atg atg Gly Val Gln Ala Trp Arg Arg Tyr Gln Arg His Arg Thr Arg Met Met 675 680 685			2064
gag att cag gcc tat tat gaa agc tgc ctg aac ccg caa ctg atc acc Glu Ile Gln Ala Tyr Tyr Glu Ser Cys Leu Asn Pro Gln Leu Ile Thr 690 695 700			2112
cct tca gaa agc ctt atc gaa taa Pro Ser Glu Ser Leu Ile Glu *			2136
705 710			

<210> 286

<211> 714

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(714)

<400> 286

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Met	Leu	Pro	Cys	Arg	Ala	Asn	Cys	Phe	Thr	Leu	Glu	Ile	Ser	Leu	Met	
1				5					10					15		

cat	atc	aac	att	gcc	tgg	cag	gac	gta	gat	acc	gtt	ctg	ctg	gat	atg	96
His	Ile	Asn	Ile	Ala	Trp	Gln	Asp	Val	Asp	Thr	Val	Leu	Leu	Asp	Met	
			20				25						30			

gac	ggc	acg	ttg	ctc	gac	ctc	gcc	ttc	gat	aac	tat	ttc	tgg	caa	aag	144
Asp	Gly	Thr	Leu	Leu	Asp	Leu	Ala	Phe	Asp	Asn	Tyr	Phe	Trp	Gln	Lys	
		35					40					45				

ctg	gtg	cct	gaa	aca	tgg	ggc	gcg	aaa	aac	ggg	gtt	acg	cca	cag	gaa	192
Leu	Val	Pro	Glu	Thr	Trp	Gly	Ala	Lys	Asn	Gly	Val	Thr	Pro	Gln	Glu	
	50					55					60					

gcg	atg	gaa	tat	atg	cgc	cag	caa	tat	cac	gac	gta	cag	cat	acg	cta	240
Ala	Met	Glu	Tyr	Met	Arg	Gln	Gln	Tyr	His	Asp	Val	Gln	His	Thr	Leu	
65					70					75				80		

aac	tgg	tac	tgt	ctt	gat	tac	tgg	agt	gag	caa	ctg	ggt	ctg	gat	atc	288
Asn	Trp	Tyr	Cys	Leu	Asp	Tyr	Trp	Ser	Glu	Gln	Leu	Gly	Leu	Asp	Ile	
			85						90					95		

tgt	gcg	atg	acc	acc	gag	atg	gga	ccg	cgt	gcc	gta	ctg	cgt	gaa	gat	336
Cys	Ala	Met	Thr	Thr	Glu	Met	Gly	Pro	Arg	Ala	Val	Leu	Arg	Glu	Asp	
			100					105					110			

acc	att	ccg	ttt	ctt	gag	gca	ctg	aaa	gcc	agc	ggt	aag	cag	cga	att	384
Thr	Ile	Pro	Phe	Leu	Glu	Ala	Leu	Lys	Ala	Ser	Gly	Lys	Gln	Arg	Ile	
		115					120					125				

ttg	ctc	acc	aat	gcg	cat	ccg	cac	aac	ctg	gcg	gta	aaa	ctt	gag	cat	432
Leu	Leu	Thr	Asn	Ala	His	Pro	His	Asn	Leu	Ala	Val	Lys	Leu	Glu	His	
	130					135					140					

acc	ggt	ctg	gac	gca	cac	ctt	gat	tta	tta	ctt	tcc	acc	cac	aca	ttt	480
Thr	Gly	Leu	Asp	Ala	His	Leu	Asp	Leu	Leu	Leu	Ser	Thr	His	Thr	Phe	
145				150						155					160	

ggt	tat	ccg	aaa	gag	gat	cag	cgg	tta	tgg	cat	gcg	gtg	gcc	gaa	gct	528
Gly	Tyr	Pro	Lys	Glu	Asp	Gln	Arg	Leu	Trp	His	Ala	Val	Ala	Glu	Ala	
			165						170					175		

acg	ggt	ctg	aaa	gct	gaa	aga	acg	ctg	ttt	att	gat	gac	agc	gaa	gcg	576
Thr	Gly	Leu	Lys	Ala	Glu	Arg	Thr	Leu	Phe	Ile	Asp	Asp	Ser	Glu	Ala	
			180					185					190			

att	ctc	gat	gct	gcc	gcg	caa	ttt	ggt	att	cgt	tac	tgc	ctc	ggc	gtg	624
Ile	Leu	Asp	Ala	Ala	Ala	Gln	Phe	Gly	Ile	Arg	Tyr	Cys	Leu	Gly	Val	
		195				200						205				

act aat cct gat tcc ggg att gcc gag aaa cag tat caa cgc cat ccg 672
 Thr Asn Pro Asp Ser Gly Ile Ala Glu Lys Gln Tyr Gln Arg His Pro
 210 215 220

tca ctg aat gac tac cgc cgc ctg atc ccc tcg cta atg tga 714
 Ser Leu Asn Asp Tyr Arg Arg Leu Ile Pro Ser Leu Met *
 225 230 235

<210> 287

<211> 402

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(402)

<400> 287

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 Met Lys Glu Lys Pro Ala Val Glu Val Arg Leu Asp Lys Trp Leu Trp
 1 5 10 15

gct gcc cgt ttt tat aaa acc cgc gcg ctg gcc cgt gaa atg att gaa 96
 Ala Ala Arg Phe Tyr Lys Thr Arg Ala Leu Ala Arg Glu Met Ile Glu
 20 25 30

ggc ggt aag gtg cat tac aac ggg cag cgc agc aag ccg agc aaa atc 144
 Gly Gly Lys Val His Tyr Asn Gly Gln Arg Ser Lys Pro Ser Lys Ile
 35 40 45

gtc gag ctg aat gcc acg ctc act ctg cgc cag gga aat gac gaa cgc 192
 Val Glu Leu Asn Ala Thr Leu Thr Leu Arg Gln Gly Asn Asp Glu Arg
 50 55 60

acg gtg att gta aag gcg att act gaa cag cgt cgc ccc gcc agc gag 240
 Thr Val Ile Val Lys Ala Ile Thr Glu Gln Arg Arg Pro Ala Ser Glu
 65 70 75 80

gca gcc ttg ctg tat gaa gag act gcg gaa agt gta gag aaa cgc gaa 288
 Ala Ala Leu Leu Tyr Glu Glu Thr Ala Glu Ser Val Glu Lys Arg Glu
 85 90 95

aaa atg gcg ctg gca cgt aaa ctt aat gcc tta acc atg ccg cac ccg 336
 Lys Met Ala Leu Ala Arg Lys Leu Asn Ala Leu Thr Met Pro His Pro
 100 105 110

gac cga cgc ccg gac aaa aaa gag cgc cgc gac ctg tta cga ttt aaa 384
 Asp Arg Arg Pro Asp Lys Lys Glu Arg Arg Asp Leu Leu Arg Phe Lys
 115 120 125

cac ggc gac agt gaa taa 402
 His Gly Asp Ser Glu *
 130

<210> 288

<211> 885

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(885)

<400> 288

atg	att	atg	ccg	caa	cat	gac	caa	tta	cat	cgc	tat	ctg	ttt	gaa	aac	48
Met	Ile	Met	Pro	Gln	His	Asp	Gln	Leu	His	Arg	Tyr	Leu	Phe	Glu	Asn	
1				5					10				15			

ttt	gcc	gtg	cgc	ggc	gaa	ctg	gta	acc	gtt	tcg	gaa	acc	ctg	caa	cag	96
Phe	Ala	Val	Arg	Gly	Glu	Leu	Val	Thr	Val	Ser	Glu	Thr	Leu	Gln	Gln	
			20					25					30			

atc	ctt	gag	aac	cac	gat	tat	ccg	cag	ccc	gtt	aaa	aac	gtg	ctg	gca	144
Ile	Leu	Glu	Asn	His	Asp	Tyr	Pro	Gln	Pro	Val	Lys	Asn	Val	Leu	Ala	
		35					40					45				

gaa	ctg	ctg	gtt	gcg	acc	agc	ctg	tta	acc	gct	acg	ctg	aag	ttt	gat	192
Glu	Leu	Leu	Val	Ala	Thr	Ser	Leu	Leu	Thr	Ala	Thr	Leu	Lys	Phe	Asp	
	50					55					60					

ggc	gat	atc	acc	gta	cag	ctg	cag	ggc	gac	ggc	ccg	atg	aat	ctg	gcg	240
Gly	Asp	Ile	Thr	Val	Gln	Leu	Gln	Gly	Asp	Gly	Pro	Met	Asn	Leu	Ala	
65					70				75					80		

gtt	att	aac	ggc	aac	aat	aac	cag	cag	atg	cgc	ggc	gtg	gcg	cgc	gtg	288
Val	Ile	Asn	Gly	Asn	Asn	Asn	Gln	Gln	Met	Arg	Gly	Val	Ala	Arg	Val	
			85					90						95		

cag	ggc	gaa	att	cca	gaa	aat	gcc	gac	ctg	aaa	acg	ctg	gtc	ggc	aat	336
Gln	Gly	Glu	Ile	Pro	Glu	Asn	Ala	Asp	Leu	Lys	Thr	Leu	Val	Gly	Asn	
			100					105					110			

ggc	tac	gtg	gtg	atc	acc	att	acc	ccg	agc	gaa	ggc	gaa	cgc	tat	cag	384
Gly	Tyr	Val	Val	Ile	Thr	Ile	Thr	Pro	Ser	Glu	Gly	Glu	Arg	Tyr	Gln	
		115					120					125				

ggc	gta	gtt	ggc	ctg	gaa	ggc	gat	acc	ctg	gcg	gcc	tgc	ctg	gaa	gat	432
Gly	Val	Val	Gly	Leu	Glu	Gly	Asp	Thr	Leu	Ala	Ala	Cys	Leu	Glu	Asp	
	130					135					140					

tac	ttt	atg	cgt	tct	gaa	cag	ctg	ccg	acg	cgc	ctg	ttt	att	cgc	acc	480
Tyr	Phe	Met	Arg	Ser	Glu	Gln	Leu	Pro	Thr	Arg	Leu	Phe	Ile	Arg	Thr	
145					150					155					160	

ggc	gac	gta	gac	ggc	aaa	ccg	gct	gca	ggc	ggc	atg	ttg	ttg	cag	gta	528
Gly	Asp	Val	Asp	Gly	Lys	Pro	Ala	Ala	Gly	Gly	Met	Leu	Leu	Gln	Val	
			165						170					175		

atg	cct	gcg	caa	aat	gcc	cag	cag	gac	gac	ttt	gac	cac	ctg	gcg	acg	576
Met	Pro	Ala	Gln	Asn	Ala	Gln	Gln	Asp	Asp	Phe	Asp	His	Leu	Ala	Thr	
			180					185					190			

cta	acc	gaa	acc	atc	aaa	acc	gaa	gaa	ctg	ctg	acc	tta	ccg	gca	aac	624
Leu	Thr	Glu	Thr	Ile	Lys	Thr	Glu	Glu	Leu	Leu	Thr	Leu	Pro	Ala	Asn	
		195					200					205				

gaa	gtg	ttg	tgg	cgt	ttg	tat	cac	gaa	gaa	gag	gtg	acg	gtt	tac	gat	672
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Glu Val Leu Trp Arg Leu Tyr His Glu Glu Glu Val Thr Val Tyr Asp	
210 215 220	
ccg cag gat gtg gag ttc aaa tgc acc tgc tcg cgt gaa cgt tgc gcc	720
Pro Gln Asp Val Glu Phe Lys Cys Thr Cys Ser Arg Glu Arg Cys Ala	
225 230 235 240	
gat gcg ctg aaa acg ctg cct gat gaa gaa gtt gat agc atc ctg gcg	768
Asp Ala Leu Lys Thr Leu Pro Asp Glu Glu Val Asp Ser Ile Leu Ala	
245 250 255	
gaa gat ggc gaa att gac atg cat tgt gat tac tgc ggt aac cac tat	816
Glu Asp Gly Glu Ile Asp Met His Cys Asp Tyr Cys Gly Asn His Tyr	
260 265 270	
ctg ttc aat gcg atg gat att gct gaa atc cgc aac aac gcg tct ccg	864
Leu Phe Asn Ala Met Asp Ile Ala Glu Ile Arg Asn Asn Ala Ser Pro	
275 280 285	
gca gat ccg caa gtt cat taa	885
Ala Asp Pro Gln Val His *	
290	
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<211> 363	
<212> DNA	
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<222> (1)...(363)	
<400> 289	
atg tta aag cta ttt gca aag tac acc tct att ggt gtg ctg aac acc	48
Met Leu Lys Leu Phe Ala Lys Tyr Thr Ser Ile Gly Val Leu Asn Thr	
1 5 10 15	
ctt ata cac tgg gtg gtt ttt ggt gtt tgt atc tat gtc gcg cat aca	96
Leu Ile His Trp Val Val Phe Gly Val Cys Ile Tyr Val Ala His Thr	
20 25 30	
aac caa gct ctt gca aac ttc gca ggt ttc gtt gtg gct gtg agc ttt	144
Asn Gln Ala Leu Ala Asn Phe Ala Gly Phe Val Val Ala Val Ser Phe	
35 40 45	
agc ttc ttc gcg aat gca aaa ttc aca ttc aag gca tcg act aca acg	192
Ser Phe Phe Ala Asn Ala Lys Phe Thr Phe Lys Ala Ser Thr Thr Thr	
50 55 60	
atg cgc tac atg cta tat gtt ggg ttc atg ggg aca ctg agt gct act	240
Met Arg Tyr Met Leu Tyr Val Gly Phe Met Gly Thr Leu Ser Ala Thr	
65 70 75 80	
gtt gga tgg gct gct gat aga tgc gca ctt ccc ccg atg ata act ctt	288
Val Gly Trp Ala Ala Asp Arg Cys Ala Leu Pro Pro Met Ile Thr Leu	
85 90 95	
gtc acc ttc tcc gcc atc agc ctg gtg tgc ggt ttc gtc tat tca aag	336
Val Thr Phe Ser Ala Ile Ser Leu Val Cys Gly Phe Val Tyr Ser Lys	

100	105	110	
ttc att gtc ttt agg gat gcg aaa tga			363
Phe Ile Val Phe Arg Asp Ala Lys *			
115	120		
<210> 290			
<211> 921			
<212> DNA			
<213> Escherichia coli			
<220>			
<221> CDS			
<222> (1)...(921)			
<400> 290			
atg aag ata tct ctt gta gtt cct gtc ttc aat gaa gaa gaa gcg ata			48
Met Lys Ile Ser Leu Val Val Pro Val Phe Asn Glu Glu Glu Ala Ile			
1	5	10	15
cca att ttt tat aaa acg gta cgt gaa ttc gaa gaa ttg aag tca tat			96
Pro Ile Phe Tyr Lys Thr Val Arg Glu Phe Glu Glu Leu Lys Ser Tyr			
	20	25	30
gaa gtg gaa atc gtt ttc ata aat gac ggc agc aaa gac gct acg gag			144
Glu Val Glu Ile Val Phe Ile Asn Asp Gly Ser Lys Asp Ala Thr Glu			
	35	40	45
tca atc att aat gct ctg gct gtt tca gat cct cta gtt gtt ccg ctg			192
Ser Ile Ile Asn Ala Leu Ala Val Ser Asp Pro Leu Val Val Pro Leu			
	50	55	60
tca ttt aca cgc aac ttt ggt aaa gaa cca gca ttg ttt gca ggg tta			240
Ser Phe Thr Arg Asn Phe Gly Lys Glu Pro Ala Leu Phe Ala Gly Leu			
65	70	75	80
gac cat gca acc ggg gat gcg ata atc cca att gat gtt gac ctg caa			288
Asp His Ala Thr Gly Asp Ala Ile Ile Pro Ile Asp Val Asp Leu Gln			
	85	90	95
gac ccg att gag gtt att cct cat ctt att gaa aaa tgg caa gca ggt			336
Asp Pro Ile Glu Val Ile Pro His Leu Ile Glu Lys Trp Gln Ala Gly			
	100	105	110
gct gat atg gtt ctt gct aaa aga tct gac cgc tca act gat gga cgc			384
Ala Asp Met Val Leu Ala Lys Arg Ser Asp Arg Ser Thr Asp Gly Arg			
	115	120	125
ctg aag cga aaa acg gct gag tgg ttc tat aag ctc cac aat aaa ata			432
Leu Lys Arg Lys Thr Ala Glu Trp Phe Tyr Lys Leu His Asn Lys Ile			
	130	135	140
agc aat cct aaa att gaa gag aat gtt ggt gat ttc agg ctg atg agc			480
Ser Asn Pro Lys Ile Glu Glu Asn Val Gly Asp Phe Arg Leu Met Ser			
145	150	155	160
cgt gat gtt gtc gaa aat att aaa ctt atg cca gaa cga aac ctt ttc			528
Arg Asp Val Val Glu Asn Ile Lys Leu Met Pro Glu Arg Asn Leu Phe			
	165	170	175

atg aaa ggt att ctg agc tgg gta gga gga aag aca gat att gtt gaa 576
 Met Lys Gly Ile Leu Ser Trp Val Gly Gly Lys Thr Asp Ile Val Glu
 180 185 190
 tac gtg cga gcg gaa aga att gct gga gat aca aaa ttt aat gga tgg 624
 Tyr Val Arg Ala Glu Arg Ile Ala Gly Asp Thr Lys Phe Asn Gly Trp
 195 200 205
 aaa ctt tgg aat tta gca ctt gag ggt att aca agc ttt tcc aca ttc 672
 Lys Leu Trp Asn Leu Ala Leu Glu Gly Ile Thr Ser Phe Ser Thr Phe
 210 215 220
 cct ctt cgc atc tgg aca tac ata ggg tta gtg gta gcc agt gta gca 720
 Pro Leu Arg Ile Trp Thr Tyr Ile Gly Leu Val Val Ala Ser Val Ala
 225 230 235 240
 ttt att tat ggg gcg tgg atg att tta gat act atc ata ttt gga aat 768
 Phe Ile Tyr Gly Ala Trp Met Ile Leu Asp Thr Ile Ile Phe Gly Asn
 245 250 255
 gct gtt agg gga tat cct tca cta ctt gtt tca ata ctg ttt tta ggt 816
 Ala Val Arg Gly Tyr Pro Ser Leu Leu Val Ser Ile Leu Phe Leu Gly
 260 265 270
 gga att cag atg att gga ata gga gta tta ggt gaa tat att gga cgc 864
 Gly Ile Gln Met Ile Gly Ile Gly Val Leu Gly Glu Tyr Ile Gly Arg
 275 280 285
 aca tac att gaa acc aaa aaa cgc ccg aaa tac atc atc aag aga gtc 912
 Thr Tyr Ile Glu Thr Lys Lys Arg Pro Lys Tyr Ile Ile Lys Arg Val
 290 295 300
 aaa aaa tga 921
 Lys Lys *
 305

<210> 291
 <211> 1332
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1332)

<400> 291
 atg aat aaa gca ata aaa gta tca ttg tat ata tct ttt gtt ttg att 48
 Met Asn Lys Ala Ile Lys Val Ser Leu Tyr Ile Ser Phe Val Leu Ile
 1 5 10 15
 att tgc gcc tta tct aaa aac ata atg atg tta aat aca tct gat ttc 96
 Ile Cys Ala Leu Ser Lys Asn Ile Met Met Leu Asn Thr Ser Asp Phe
 20 25 30
 gga aga gcc att aag cca tta att gaa gac ata cca gca ttt aca tat 144
 Gly Arg Ala Ile Lys Pro Leu Ile Glu Asp Ile Pro Ala Phe Thr Tyr
 35 40 45

gac tta cct tta ttg tat aaa ttg aaa ggt cat att gat tca att gat Asp Leu Pro Leu Leu Tyr Lys Leu Lys Gly His Ile Asp Ser Ile Asp 50 55 60	192
agc tat gag tat ata agt tca tat agt tat att ttg tat aca tac gtc Ser Tyr Glu Tyr Ile Ser Ser Tyr Ser Tyr Ile Leu Tyr Thr Tyr Val 65 70 75 80	240
ctg ttt att agc att ttt act gaa tat ctt gat gct agg gtg tta tcg Leu Phe Ile Ser Ile Phe Thr Glu Tyr Leu Asp Ala Arg Val Leu Ser 85 90 95	288
tta ttt cta aaa gta ata tat att tat tca tta tat gcg ata ttt act Leu Phe Leu Lys Val Ile Tyr Ile Tyr Ser Leu Tyr Ala Ile Phe Thr 100 105 110	336
tca tat ata aaa aca gaa agg tat gta act tta ttt aca ttc ttt att Ser Tyr Ile Lys Thr Glu Arg Tyr Val Thr Leu Phe Thr Phe Phe Ile 115 120 125	384
tta gct ttt ctt atg tgt tct tca tca aca ctg tca atg ttt gca tca Leu Ala Phe Leu Met Cys Ser Ser Ser Thr Leu Ser Met Phe Ala Ser 130 135 140	432
ttc tat caa gag caa ata gtt ata att ttc ctt cca ttt ttg gtg tat Phe Tyr Gln Glu Gln Ile Val Ile Ile Phe Leu Pro Phe Leu Val Tyr 145 150 155 160	480
tca tta aca tgc aaa aac aat aaa tct atg ctt ttg cta ttt ttt tcg Ser Leu Thr Cys Lys Asn Asn Lys Ser Met Leu Leu Leu Phe Phe Ser 165 170 175	528
ttg cta ata ata tct act gct aaa aat caa ttt ata tta acc cca cta Leu Leu Ile Ile Ser Thr Ala Lys Asn Gln Phe Ile Leu Thr Pro Leu 180 185 190	576
ata gtg tat tca tat tat att ttt ttt gat aga cac aaa cta att att Ile Val Tyr Ser Tyr Tyr Ile Phe Phe Asp Arg His Lys Leu Ile Ile 195 200 205	624
aaa tct gta ata tgc gtg gtg tgc ttg ctt gcg tca ata ttt gca ata Lys Ser Val Ile Cys Val Val Cys Leu Leu Ala Ser Ile Phe Ala Ile 210 215 220	672
tct tat tca aaa ggt gtt gtt gaa tta aat aag tac cat gca aca tac Ser Tyr Ser Lys Gly Val Val Glu Leu Asn Lys Tyr His Ala Thr Tyr 225 230 235 240	720
ttc ggt agt tat ctt tat atg aaa aac aac ggg tat aaa atg cca tcg Phe Gly Ser Tyr Leu Tyr Met Lys Asn Asn Gly Tyr Lys Met Pro Ser 245 250 255	768
tat gtt gat gat aag tgt gtt ggg tta gat gcc tgg ggt aat aaa ttc Tyr Val Asp Asp Lys Cys Val Gly Leu Asp Ala Trp Gly Asn Lys Phe 260 265 270	816
gac ata tca ttt ggc gca acc cca aca gaa gtt gga acg gaa tgt ttc Asp Ile Ser Phe Gly Ala Thr Pro Thr Glu Val Gly Thr Glu Cys Phe 275 280 285	864

gaa tct cat aaa gat gaa acg ttt tcg aat gca ctc ttt tta ttg gtt Glu Ser His Lys Asp Glu Thr Phe Ser Asn Ala Leu Phe Leu Leu Val 290 295 300	912
agc aaa cca agc acc atc ttc aaa ctt cca ttt gat gat ggt gtg atg Ser Lys Pro Ser Thr Ile Phe Lys Leu Pro Phe Asp Asp Gly Val Met 305 310 315 320	960
tct cag tat aaa gaa aat tat ttc cat gta tat aaa aaa cta cac gta Ser Gln Tyr Lys Glu Asn Tyr Phe His Val Tyr Lys Lys Leu His Val 325 330 335	1008
ata tat gga gaa tca aac ata cta acg act att act aac ata aaa gac Ile Tyr Gly Glu Ser Asn Ile Leu Thr Thr Ile Thr Asn Ile Lys Asp 340 345 350	1056
aat ata ttt aaa aac att aga ttt ata tca ttg tta tta ttt ttt att Asn Ile Phe Lys Asn Ile Arg Phe Ile Ser Leu Leu Leu Phe Phe Ile 355 360 365	1104
gct tct att ttt att aga aat aat aaa ata aag gca tct tta ttt gta Ala Ser Ile Phe Ile Arg Asn Asn Lys Ile Lys Ala Ser Leu Phe Val 370 375 380	1152
gta tct ctt ttt gga ata tct caa ttt tat gtg tca ttt ttc ggg gaa Val Ser Leu Phe Gly Ile Ser Gln Phe Tyr Val Ser Phe Phe Gly Glu 385 390 395 400	1200
gga tat aga gat tta agc aag cat tta ttt gga atg tat ttt tcg ttc Gly Tyr Arg Asp Leu Ser Lys His Leu Phe Gly Met Tyr Phe Ser Phe 405 410 415	1248
gac ctt tgc tta tac ata aca gtc gtt ttt tta att tat aaa ata att Asp Leu Cys Leu Tyr Ile Thr Val Phe Leu Ile Tyr Lys Ile Ile 420 425 430	1296
caa aga aat caa gac aat agc gat gta aag cac taa Gln Arg Asn Gln Asp Asn Ser Asp Val Lys His *	1332
435 440	

<210> 292

<211> 345

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(345)

<400> 292

ttg att ctc gat aga cac ata aca tcc agg ggt tat gtt tgt atg cgt Met Ile Leu Asp Arg His Ile Thr Ser Arg Gly Tyr Val Cys Met Arg 1 5 10 15	48
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ccc gcg act atc gcc cca tta acg cca tac gat aaa tgg gat ggt gag Pro Ala Thr Ile Ala Pro Leu Thr Pro Tyr Asp Lys Trp Asp Gly Glu 20 25 30	96
--	----

aaa tgg gtg acg gat acc gag gca cag cat agc gtc gca gta gat gca	144
---	-----

Lys	Trp	Val	Thr	Asp	Thr	Glu	Ala	Gln	His	Ser	Val	Ala	Val	Asp	Ala		
		35					40					45					
gca	gaa	gca	cag	cgc	cag	tcg	ctg	att	gat	act	gca	atg	gct	tcc	att	192	
Ala	Glu	Ala	Gln	Arg	Gln	Ser	Leu	Ile	Asp	Thr	Ala	Met	Ala	Ser	Ile		
	50					55					60						
agt	ctg	att	caa	ctg	aaa	tta	cag	gct	ggg	cgg	aag	ctg	atg	cag	gca	240	
Ser	Leu	Ile	Gln	Leu	Lys	Leu	Gln	Ala	Gly	Arg	Lys	Leu	Met	Gln	Ala		
65					70					75					80		
gag	acc	tcc	cga	ctt	aac	act	gtg	ctg	gat	tac	att	gac	gcg	gtg	acg	288	
Glu	Thr	Ser	Arg	Leu	Asn	Thr	Val	Leu	Asp	Tyr	Ile	Asp	Ala	Val	Thr		
			85						90					95			
gca	aca	gat	acc	agc	acc	gcg	ccg	gat	gtc	atc	tggt	cct	gaa	ctg	ccg	336	
Ala	Thr	Asp	Thr	Ser	Thr	Ala	Pro	Asp	Val	Ile	Trp	Pro	Glu	Leu	Pro		
			100					105					110				
gag	gag	tag														345	
Glu	Glu	*															
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<211> 447																	
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<222> (1)...(447)																	
 <400> 293																	
atg	aag	cca	cga	aat	att	aat	aat	agc	cta	cca	ctg	caa	cca	tta	gtt	48	
Met	Lys	Pro	Arg	Asn	Ile	Asn	Asn	Ser	Leu	Pro	Leu	Gln	Pro	Leu	Val		
1				5					10					15			
cct	gat	cag	gag	aac	aaa	aat	aag	aaa	aat	gaa	gag	aaa	tcc	gtt	aat	96	
Pro	Asp	Gln	Glu	Asn	Lys	Asn	Lys	Lys	Asn	Glu	Glu	Lys	Ser	Val	Asn		
			20					25					30				
cca	gtt	aaa	atc	aca	atg	ggg	tct	ggt	tta	aat	tat	att	gaa	caa	gaa	144	
Pro	Val	Lys	Ile	Thr	Met	Gly	Ser	Gly	Leu	Asn	Tyr	Ile	Glu	Gln	Glu		
		35					40					45					
tct	ctt	gga	gga	aaa	tat	cta	aca	cat	gat	ttg	tca	ata	aag	ata	gcg	192	
Ser	Leu	Gly	Gly	Lys	Tyr	Leu	Thr	His	Asp	Leu	Ser	Ile	Lys	Ile	Ala		
	50					55					60						
gat	att	tct	gaa	gag	ata	att	cag	caa	gca	ata	tta	tct	gct	atg	agc	240	
Asp	Ile	Ser	Glu	Glu	Ile	Ile	Gln	Gln	Ala	Ile	Leu	Ser	Ala	Met	Ser		
65					70				75					80			
ata	tat	aaa	ttt	tcg	ata	aca	gat	gat	tta	atg	agt	atg	gct	gta	aat	288	
Ile	Tyr	Lys	Phe	Ser	Ile	Thr	Asp	Asp	Leu	Met	Ser	Met	Ala	Val	Asn		
			85					90						95			
gaa	ctc	ata	aaa	ctg	acc	aaa	ata	gag	aat	aat	gta	gac	ctg	aat	aaa	336	
Glu	Leu	Ile	Lys	Leu	Thr	Lys	Ile	Glu	Asn	Asn	Val	Asp	Leu	Asn	Lys		

100	105	110	
ttc act act ata tgc aca gac gtt cta tcc ccc cgc gtc acc aga cat			384
Phe Thr Thr Ile Cys Thr Asp Val Leu Ser Pro Arg Val Thr Arg His			
115	120	125	
aat aaa gaa aaa aac aaa cga cat tct acc ctt ctc aaa aat ccc ctt			432
Asn Lys Glu Lys Asn Lys Arg His Ser Thr Leu Leu Lys Asn Pro Leu			
130	135	140	
ttt aat ttt cat tga			447
Phe Asn Phe His *			
145			
<210> 294			
<211> 504			
<212> DNA			
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<222> (1)...(504)			
<400> 294			
atg ccg ggc aac cgc ccg cat tat ggg cgt tgg cct caa cac gat ttt			48
Met Pro Gly Asn Arg Pro His Tyr Gly Arg Trp Pro Gln His Asp Phe			
1	5	10	15
ccg cca ttt aaa aaa ctc agg ccg cag tcg gta acc tcg cgc ata cag			96
Pro Pro Phe Lys Lys Leu Arg Pro Gln Ser Val Thr Ser Arg Ile Gln			
20	25	30	
ccg ggc agt gac gtc atc gtc tgc gcg gaa atg gac gaa cag tgg gga			144
Pro Gly Ser Asp Val Ile Val Cys Ala Glu Met Asp Glu Gln Trp Gly			
35	40	45	
tac gtc ggg gct aaa tcg cgc cag cgc tgg ctg ttt tac gcg tat gac			192
Tyr Val Gly Ala Lys Ser Arg Gln Arg Trp Leu Phe Tyr Ala Tyr Asp			
50	55	60	
agg ctc cgg aag acg gtt gtt gcg cac gta ttc ggt gaa cgc act atg			240
Arg Leu Arg Lys Thr Val Val Ala His Val Phe Gly Glu Arg Thr Met			
65	70	75	80
gcg acg ctg ggg cgt ctt atg agc ctg ctg tca ccc ttt gac gtg gtg			288
Ala Thr Leu Gly Arg Leu Met Ser Leu Leu Ser Pro Phe Asp Val Val			
85	90	95	
ata tgg atg acg gat ggc tgg ccg ctg tat gaa tcc cgc ctg aag gga			336
Ile Trp Met Thr Asp Gly Trp Pro Leu Tyr Glu Ser Arg Leu Lys Gly			
100	105	110	
aag ctg cac gta atc agc aag cga tat acg cag cga att gag cgg cat			384
Lys Leu His Val Ile Ser Lys Arg Tyr Thr Gln Arg Ile Glu Arg His			
115	120	125	
aac ctg aat ctg agg cag cac ctg gca cgg ctg gga cgg aag tcg ctg			432
Asn Leu Asn Leu Arg Gln His Leu Ala Arg Leu Gly Arg Lys Ser Leu			
130	135	140	

```

tcg ttc tca aaa tcg gtg gag cag cat gac aaa gtc atc ggg cat tat      480
Ser Phe Ser Lys Ser Val Glu Gln His Asp Lys Val Ile Gly His Tyr
145                      150                      155                      160

```

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ctg aac ata aaa cac tat caa taa      504
Leu Asn Ile Lys His Tyr Gln  *
                      165

```

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<210> 295
<211> 276
<212> DNA
<213> Escherichia coli

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<220>
<221> CDS
<222> (1)...(276)

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<400> 295
gtg gct tct gtt tct atc agc tgt ccc tcc tgt tca gct act gac ggg      48
Met Ala Ser Val Ser Ile Ser Cys Pro Ser Cys Ser Ala Thr Asp Gly
1                      5                      10                      15

```

```

gtg gtg cgt aac ggc aaa agc act gcc gga cat cag cgc tat ctc tgc      96
Val Val Arg Asn Gly Lys Ser Thr Ala Gly His Gln Arg Tyr Leu Cys
                20                      25                      30

```

```

tct cac tgc cgt aaa aca tgg caa ctg cag ttc act tac acc gct tct      144
Ser His Cys Arg Lys Thr Trp Gln Leu Gln Phe Thr Tyr Thr Ala Ser
                35                      40                      45

```

```

caa ccc ggt acg cac cag aaa atc att gat atg gcc atg aat ggc gtt      192
Gln Pro Gly Thr His Gln Lys Ile Ile Asp Met Ala Met Asn Gly Val
                50                      55                      60

```

```

gga tgc cgg gca acc gcc cgc att atg gcc gtt ggc ctc aac acg att      240
Gly Cys Arg Ala Thr Ala Arg Ile Met Gly Val Gly Leu Asn Thr Ile
        65                      70                      75                      80

```

```

ttc cgc cat tta aaa aac tca ggc cgc agt cgg taa      276
Phe Arg His Leu Lys Asn Ser Gly Arg Ser Arg  *
                85                      90

```

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<210> 296
<211> 4134
<212> DNA
<213> Escherichia coli

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<220>
<221> CDS
<222> (1)...(4134)

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<400> 296
atg agc gga aaa ccg gca gcg cgt cag ggc gac atg acg cag tat ggc      48
Met Ser Gly Lys Pro Ala Ala Arg Gln Gly Asp Met Thr Gln Tyr Gly
1                      5                      10                      15

```

```

ggg agc att gtt cag ggt tca gcc ggg gtg cgc att ggt gcc ccc acc      96

```


Gly	Ser	Ile	Val	Gln	Gly	Ser	Ala	Gly	Val	Arg	Ile	Gly	Ala	Pro	Thr		
			20					25					30				
ggc	gtg	gcc	tgt	tcg	gtg	tgc	ccc	ggc	gga	gtg	acg	tcc	ggc	cat	ccg	144	
Gly	Val	Ala	Cys	Ser	Val	Cys	Pro	Gly	Gly	Val	Thr	Ser	Gly	His	Pro		
		35					40					45					
gtc	aat	ccc	ctg	ctc	ggc	gca	aag	gtc	ctt	ccc	ggc	gaa	acc	gac	atc	192	
Val	Asn	Pro	Leu	Leu	Gly	Ala	Lys	Val	Leu	Pro	Gly	Glu	Thr	Asp	Ile		
	50					55					60						
gcc	ctg	ccc	ggc	ccg	ctg	ccg	ttc	atc	ctc	tcc	cgc	acc	tac	agc	agt	240	
Ala	Leu	Pro	Gly	Pro	Leu	Pro	Phe	Ile	Leu	Ser	Arg	Thr	Tyr	Ser	Ser		
	65				70					75					80		
tac	cgg	aca	aaa	acg	ccc	gcg	ccg	gtg	ggg	agc	ctc	ggc	ccc	ggc	tgg	288	
Tyr	Arg	Thr	Lys	Thr	Pro	Ala	Pro	Val	Gly	Ser	Leu	Gly	Pro	Gly	Trp		
			85					90						95			
aaa	atg	cct	gcg	gat	atc	cgc	tta	cag	ctg	cgc	gat	aac	aca	ctg	ata	336	
Lys	Met	Pro	Ala	Asp	Ile	Arg	Leu	Gln	Leu	Arg	Asp	Asn	Thr	Leu	Ile		
			100					105					110				
ctc	agt	gat	aac	ggc	ggc	aga	agc	ctg	tat	ttt	gag	cac	ctg	ttt	ccc	384	
Leu	Ser	Asp	Asn	Gly	Gly	Arg	Ser	Leu	Tyr	Phe	Glu	His	Leu	Phe	Pro		
		115					120					125					
ggc	gag	gac	ggc	tac	agc	cgc	agc	gag	tca	ctg	tgg	ctg	gtg	cgc	ggc	432	
Gly	Glu	Asp	Gly	Tyr	Ser	Arg	Ser	Glu	Ser	Leu	Trp	Leu	Val	Arg	Gly		
	130					135					140						
ggc	gtg	gcg	aaa	ctg	gat	gaa	ggc	cac	cgg	ctg	gcc	gca	ctc	tgg	cag	480	
Gly	Val	Ala	Lys	Leu	Asp	Glu	Gly	His	Arg	Leu	Ala	Ala	Leu	Trp	Gln		
	145				150					155					160		
gcg	ctg	ccg	gaa	gaa	ctc	cgc	tta	agt	ccg	cat	cgt	tat	ctg	gcg	aca	528	
Ala	Leu	Pro	Glu	Glu	Leu	Arg	Leu	Ser	Pro	His	Arg	Tyr	Leu	Ala	Thr		
			165					170					175				
aac	agt	ccg	cag	ggg	ccg	tgg	tgg	ctg	ctc	ggc	tgg	tgt	gag	cgg	gtg	576	
Asn	Ser	Pro	Gln	Gly	Pro	Trp	Trp	Leu	Leu	Gly	Trp	Cys	Glu	Arg	Val		
			180					185					190				
ccg	gaa	gcg	gat	gag	gtg	ctg	cct	gcg	ccg	ctg	ccg	ccg	tac	cgg	gta	624	
Pro	Glu	Ala	Asp	Glu	Val	Leu	Pro	Ala	Pro	Leu	Pro	Pro	Tyr	Arg	Val		
		195					200					205					
ctg	acc	ggg	ctg	gtg	gac	cgc	ttc	ggg	cgc	aca	cag	acg	ttc	cac	cgc	672	
Leu	Thr	Gly	Leu	Val	Asp	Arg	Phe	Gly	Arg	Thr	Gln	Thr	Phe	His	Arg		
	210					215					220						
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Glu	Ala	Ala	Gly	Glu	Phe	Ser	Gly	Glu	Ile	Thr	Gly	Val	Thr	Asp	Gly		
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Ala	Trp	Arg	His	Phe	Arg	Leu	Val	Leu	Thr	Thr	Gln	Ala	Gln	Arg	Ala		
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Glu	Glu	Ala	Arg	Gln	Gln	Ala	Ile	Ser	Gly	Gly	Thr	Glu	Pro	Ser	Ala	
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Phe	Pro	Asp	Thr	Leu	Pro	Gly	Tyr	Thr	Glu	Tyr	Gly	Arg	Asp	Asn	Gly	
			275				280					285				
atc	cgt	ctg	tct	gcc	gtg	tgg	ctg	acg	cac	gac	ccg	gaa	tac	ccg	gag	912
Ile	Arg	Leu	Ser	Ala	Val		Leu	Thr	His	Asp	Pro	Glu	Tyr	Pro	Glu	
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Thr	Tyr	Asp	Asp	Lys	Tyr	Arg	Gly	Arg	Met	Val	Ala	His	Arg	His	Thr	
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Gly	Arg	Pro	Glu	Ile	Arg	Tyr	Arg	Tyr	Asp	Ser	Asp	Gly	Arg	Val	Thr	
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Thr	Gln	Gly	Glu	Ala	Gly	Leu	Lys	Arg	Val	Val	Lys	Lys	Glu	His	Ala	
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Asp	Gly	Ser	Val	Thr	Gln	Ser	Gln	Phe	Asp	Ala	Val	Gly	Arg	Leu	Arg	
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Pro	His	Ser	Asp	Leu	Pro	Cys	Ala	Thr	Glu	Asp	Ala	Thr	Gly	Ser	Arg	
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Cys	Ser	Gly	Tyr	Val	Thr	Arg	Tyr	Asp	His	Asp	Arg	Phe	Gly	Gln	Met	
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Ile	Pro	Asp	Ser	Leu	Pro	Ala	Val	Glu	Trp	Leu	Thr	Tyr	Gly	Ser	Gly	
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Arg	Asp	Arg	Leu	His	Arg	Glu	Thr	Leu	Arg	Ser	Phe	Gly	Arg	Tyr	Glu	
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Pro	Glu	Leu	His	Pro	Asp	Ser	Thr	Leu	Ser	Met	Trp	Pro	Asp	Asn	Arg	
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Asp	Glu	Arg	Thr	His	Arg	Tyr	His	Tyr	Asp	Ser	Gln	His	Arg	Leu	Val	
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Tyr Asn Gln Cys Lys Lys Leu Asn Asp Asp Glu Leu Phe Arg Leu Leu	

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Gln Met Lys Asn Gln Met Asp Pro Val Tyr Thr Pro Ala Arg Lys Ile			
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85	90	95	
ccg ggg cag cag tat gat gag gag tcc ggc ctg tat tac aac cgc cac			336
Pro Gly Gln Gln Tyr Asp Glu Glu Ser Gly Leu Tyr Tyr Asn Arg His			
100	105	110	
cgc tat tat gac ccg ctg cag ggg cgg tat atc act cag gat ccg att			384
Arg Tyr Tyr Asp Pro Leu Gln Gly Arg Tyr Ile Thr Gln Asp Pro Ile			
115	120	125	
ggg ctg aag ggg gga tgg aat ttt tat cag tat ccg ttg aat ccg gtc			432
Gly Leu Lys Gly Gly Trp Asn Phe Tyr Gln Tyr Pro Leu Asn Pro Val			
130	135	140	
ata aat gta gat ccg caa ggt ttg gtt gat ata aat tta tac ccc gaa			480
Ile Asn Val Asp Pro Gln Gly Leu Val Asp Ile Asn Leu Tyr Pro Glu			
145	150	155	160
agt gat ctt atc cat tct gta gct gat gag att aat atc cca ggc gtt			528
Ser Asp Leu Ile His Ser Val Ala Asp Glu Ile Asn Ile Pro Gly Val			
165	170	175	

ttc aca atc ggg ggg cat ggt acc ccc aca tct att gaa tcc gca acg 576
 Phe Thr Ile Gly Gly His Gly Thr Pro Thr Ser Ile Glu Ser Ala Thr
 180 185 190
 cgc agt atc atg aca gct aaa gat cta gca tat cta att aaa ttt gat 624
 Arg Ser Ile Met Thr Ala Lys Asp Leu Ala Tyr Leu Ile Lys Phe Asp
 195 200 205
 ggg aat tat aaa gat ggg atg aca gtt tgg tta ttt tct tgt aat aca 672
 Gly Asn Tyr Lys Asp Gly Met Thr Val Trp Leu Phe Ser Cys Asn Thr
 210 215 220
 ggt aaa gga caa aat tca ttt gct agc taa 702
 Gly Lys Gly Gln Asn Ser Phe Ala Ser *
 225 230

<210> 299
 <211> 320
 <212> PRT
 <213> Escherichia coli

<400> 299
 Met Met Ile Lys Thr Arg Phe Ser Arg Trp Leu Thr Phe Phe Thr Phe
 1 5 10 15
 Ala Ala Ala Val Ala Leu Ala Leu Pro Ala Lys Ala Asn Thr Trp Pro
 20 25 30
 Leu Pro Pro Ala Gly Ser Arg Leu Val Gly Glu Asn Lys Phe His Val
 35 40 45
 Val Glu Asn Asp Gly Gly Ser Leu Glu Ala Ile Ala Lys Lys Tyr Asn
 50 55 60
 Val Gly Phe Leu Ala Leu Gln Ala Asn Pro Gly Val Asp Pro Tyr
 65 70 75 80
 Val Pro Arg Ala Gly Ser Val Leu Thr Ile Pro Leu Gln Thr Leu Leu
 85 90 95
 Pro Asp Ala Pro Arg Glu Gly Ile Val Ile Asn Ile Ala Glu Leu Arg
 100 105 110
 Leu Tyr Tyr Tyr Pro Pro Gly Lys Asn Ser Val Thr Val Tyr Pro Ile
 115 120 125
 Gly Ile Gly Gln Leu Gly Gly Asp Thr Leu Thr Pro Thr Met Val Thr
 130 135 140
 Thr Val Ser Asp Lys Arg Ala Asn Pro Thr Trp Thr Pro Thr Ala Asn
 145 150 155 160
 Ile Arg Ala Arg Tyr Lys Ala Gln Gly Ile Glu Leu Pro Ala Val Val
 165 170 175
 Pro Ala Gly Leu Asp Asn Pro Met Gly His His Ala Ile Arg Leu Ala
 180 185 190
 Ala Tyr Gly Gly Val Tyr Leu Leu His Gly Thr Asn Ala Asp Phe Gly
 195 200 205
 Ile Gly Met Arg Val Ser Ser Gly Cys Ile Arg Leu Arg Asp Asp Asp
 210 215 220
 Ile Lys Thr Leu Phe Ser Gln Val Thr Pro Gly Thr Lys Val Asn Ile
 225 230 235 240
 Ile Asn Thr Pro Ile Lys Val Ser Ala Glu Pro Asn Gly Ala Arg Leu
 245 250 255
 Val Glu Val His Gln Pro Leu Ser Glu Lys Ile Asp Asp Asp Pro Gln
 260 265 270
 Leu Leu Pro Ile Thr Leu Asn Ser Ala Met Gln Ser Phe Lys Asp Ala
 275 280 285

Ala	Gln	Thr	Asp	Ala	Glu	Val	Met	Gln	His	Val	Met	Asp	Val	Arg	Ser
290						295					300				
Gly	Met	Pro	Val	Asp	Val	Arg	Arg	His	Gln	Val	Ser	Pro	Gln	Thr	Leu
305					310					315					320

<210> 300

<211> 728

<212> PRT

<213> Escherichia coli

<400> 300

Met	Ile	Thr	Arg	Ile	Pro	Arg	Ser	Ser	Phe	Ser	Ala	Asn	Ile	Asn	Asn
1				5					10					15	
Thr	Ala	Gln	Thr	Asn	Glu	His	Gln	Thr	Leu	Ser	Glu	Leu	Phe	Tyr	Lys
			20					25					30		
Glu	Leu	Glu	Asp	Lys	Phe	Ser	Gly	Lys	Glu	Leu	Ala	Thr	Pro	Leu	Leu
		35					40					45			
Lys	Ser	Phe	Ser	Glu	Asn	Cys	Arg	Gln	Asn	Gly	Arg	His	Ile	Phe	Ser
	50					55					60				
Asn	Lys	Asp	Phe	Val	Ile	Lys	Phe	Ser	Thr	Ser	Val	Leu	Gln	Ala	Asp
65					70					75					80
Lys	Lys	Glu	Ile	Thr	Ile	Ile	Asn	Lys	Asn	Glu	Asn	Thr	Thr	Leu	Thr
			85						90					95	
Gln	Thr	Ile	Ala	Pro	Ile	Phe	Glu	Lys	Tyr	Leu	Met	Glu	Ile	Leu	Pro
			100						105					110	
Gln	Arg	Ser	Asp	Thr	Leu	Asp	Lys	Gln	Glu	Leu	Asn	Leu	Lys	Ser	Asp
			115				120						125		
Arg	Lys	Glu	Lys	Glu	Phe	Pro	Arg	Ile	Lys	Leu	Asn	Gly	Gln	Cys	Tyr
	130					135						140			
Phe	Pro	Gly	Arg	Pro	Gln	Asn	Arg	Ile	Val	Cys	Arg	His	Ile	Ala	Ala
145					150					155					160
Gln	Tyr	Ile	Asn	Asp	Ile	Tyr	Gln	Asn	Val	Asp	Tyr	Lys	Pro	His	Gln
			165						170					175	
Asp	Asp	Tyr	Ser	Ser	Ala	Glu	Lys	Phe	Leu	Thr	His	Phe	Asn	Lys	Lys
			180					185					190		
Cys	Lys	Asn	Gln	Thr	Leu	Ala	Leu	Val	Ser	Ser	Arg	Pro	Glu	Gly	Arg
		195					200						205		
Cys	Val	Ala	Ala	Cys	Gly	Asp	Phe	Gly	Leu	Val	Met	Lys	Ala	Tyr	Phe
	210					215					220				
Asp	Lys	Met	Glu	Ser	Asn	Gly	Ile	Ser	Val	Met	Ala	Ala	Ile	Leu	Leu
225					230					235					240
Val	Asp	Asn	His	Ala	Leu	Thr	Val	Arg	Leu	Arg	Ile	Lys	Asn	Thr	Thr
			245						250					255	
Glu	Gly	Cys	Thr	His	Tyr	Val	Val	Ser	Val	Tyr	Asp	Pro	Asn	Val	Thr
			260					265						270	
Asn	Asp	Lys	Ile	Arg	Ile	Met	Ser	Glu	Ser	Lys	Glu	Asn	Ile	Lys	His
		275					280						285		
Tyr	Ser	Leu	Met	Asp	Phe	Met	Asn	Val	Asp	Tyr	Ser	Leu	Leu	Lys	Trp
	290					295					300				
Ser	Asn	Asp	His	Val	Ile	Asn	Gln	Ser	Val	Ala	Ile	Ile	Pro	Ala	Leu
305					310					315					320
Pro	Lys	Glu	Gln	Leu	Leu	Met	Leu	Lys	Gly	Ser	Val	Asp	Glu	Ile	Thr
			325						330					335	
Pro	Pro	Leu	Ser	Pro	Ala	Thr	Met	Asn	Leu	Leu	Met	Ala	Ile	Gly	Gln
			340					345						350	
Asn	His	Gln	Leu	Thr	Gln	Leu	Met	Ile	Gln	Leu	Gln	Lys	Met	Pro	Glu
		355					360					365			
Leu	His	Arg	Thr	Glu	Met	Leu	Thr	Ala	Tyr	Asn	Ser	Ile	Asn	Leu	Pro
	370					375					380				
Gly	Leu	Tyr	Leu	Ala	Ile	Asn	Tyr	Gly	Asn	Ala	Asp	Ile	Val	Glu	Thr

```

385          390          395          400
Ile Phe Asn Ser Leu Ser Glu Thr Gly Tyr Glu Gly Leu Leu Ser Lys
          405          410          415
Lys Asn Leu Met His Ile Leu Glu Ala Lys Asp Lys Asn Gly Phe Ser
          420          425          430
Gly Leu Phe Leu Ala Ile Ser Arg Lys Asp Lys Asn Val Val Thr Ser
          435          440          445
Ile Leu Asn Ala Leu Pro Lys Leu Ala Ala Thr His His Leu Asp Asn
          450          455          460
Glu Gln Val Tyr Lys Phe Leu Ser Ala Lys Asn Arg Thr Ser Ser His
465          470          475          480
Val Leu Tyr His Val Met Ala Asn Gly Asp Ala Asp Met Leu Lys Ile
          485          490          495
Val Leu Asn Ala Leu Pro Leu Leu Ile Arg Thr Cys His Leu Thr Lys
          500          505          510
Glu Gln Val Leu Asp Leu Leu Lys Ala Lys Asp Phe Tyr Gly Cys Pro
          515          520          525
Gly Leu Tyr Leu Ala Met Gln Asn Gly His Ser Asp Ile Val Lys Val
          530          535          540
Ile Leu Glu Ala Leu Pro Ser Leu Ala Gln Glu Ile Asn Ile Ser Ala
545          550          555          560
Ser Asp Ile Val Asp Leu Leu Thr Ala Lys Ser Leu Ala Arg Asp Thr
          565          570          575
Gly Leu Phe Met Ala Met Gln Arg Gly His Met Asn Val Ile Asn Thr
          580          585          590
Ile Phe Asn Ala Leu Pro Thr Leu Phe Asn Thr Phe Lys Phe Asp Lys
          595          600          605
Lys Asn Met Lys Pro Leu Leu Ala Asn Asn Ser Asn Glu Tyr Pro
          610          615          620
Gly Leu Phe Ser Ala Ile Gln His Lys Gln Gln Asn Val Val Glu Thr
625          630          635          640
Val Tyr Leu Ala Leu Ser Asp His Ala Arg Leu Phe Gly Phe Thr Ala
          645          650          655
Glu Asp Ile Met Asp Phe Trp Gln His Lys Ala Pro Gln Lys Tyr Ser
          660          665          670
Ala Phe Glu Leu Ala Phe Glu Phe Gly His Arg Val Ile Ala Glu Leu
          675          680          685
Ile Leu Asn Thr Leu Asn Lys Met Ala Glu Ser Phe Gly Phe Thr Asp
          690          695          700
Asn Pro Arg Tyr Ile Ala Glu Lys Asn Tyr Met Glu Ala Leu Leu Lys
705          710          715          720
Lys Ala Ser Pro His Thr Val Arg
          725

```

<210> 301

<211> 84

<212> PRT

<213> Escherichia coli

<400> 301

```

Met Thr Asp Lys Ile Arg Thr Leu Gln Gly Arg Val Val Ser Asp Lys
 1          5          10          15
Met Glu Lys Ser Ile Val Val Ala Ile Glu Arg Phe Val Lys His Pro
          20          25          30
Ile Tyr Gly Lys Phe Ile Lys Arg Thr Thr Lys Leu His Val His Asp
          35          40          45
Glu Asn Asn Glu Cys Gly Ile Gly Asp Val Val Glu Ile Arg Glu Cys
          50          55          60
Arg Pro Leu Ser Lys Thr Lys Ser Trp Thr Leu Val Arg Val Val Glu
65          70          75          80

```

Lys Ala Val Leu

<210> 302

<211> 63

<212> PRT

<213> Escherichia coli

<400> 302

```
Met Lys Ala Lys Glu Leu Arg Glu Lys Ser Val Glu Glu Leu Asn Thr
 1           5           10           15
Glu Leu Leu Asn Leu Leu Arg Glu Gln Phe Asn Leu Arg Met Gln Ala
          20           25           30
Ala Ser Gly Gln Leu Gln Gln Ser His Leu Leu Lys Gln Val Arg Arg
          35           40           45
Asp Val Ala Arg Val Lys Thr Leu Leu Asn Glu Lys Ala Gly Ala
 50           55           60
```

<210> 303

<211> 136

<212> PRT

<213> Escherichia coli

<400> 303

```
Met Leu Gln Pro Lys Arg Thr Lys Phe Arg Lys Met His Lys Gly Arg
 1           5           10           15
Asn Arg Gly Leu Ala Gln Gly Thr Asp Val Ser Phe Gly Ser Phe Gly
          20           25           30
Leu Lys Ala Val Gly Arg Gly Arg Leu Thr Ala Arg Gln Ile Glu Ala
          35           40           45
Ala Arg Arg Ala Met Thr Arg Ala Val Lys Arg Gln Gly Lys Ile Trp
          50           55           60
Ile Arg Val Phe Pro Asp Lys Pro Ile Thr Glu Lys Pro Leu Ala Val
 65           70           75           80
Arg Met Gly Lys Gly Lys Gly Asn Val Glu Tyr Trp Val Ala Leu Ile
          85           90           95
Gln Pro Gly Lys Val Leu Tyr Glu Met Asp Gly Val Pro Glu Glu Leu
          100          105          110
Ala Arg Glu Ala Phe Lys Leu Ala Ala Lys Leu Pro Ile Lys Thr
          115          120          125
Thr Phe Val Thr Lys Thr Val Met
          130          135
```

<210> 304

<211> 233

<212> PRT

<213> Escherichia coli

<400> 304

```
Met Gly Gln Lys Val His Pro Asn Gly Ile Arg Leu Gly Ile Val Lys
 1           5           10           15
Pro Trp Asn Ser Thr Trp Phe Ala Asn Thr Lys Glu Phe Ala Asp Asn
          20           25           30
Leu Asp Ser Asp Phe Lys Val Arg Gln Tyr Leu Thr Lys Glu Leu Ala
          35           40           45
Lys Ala Ser Val Ser Arg Ile Val Ile Glu Arg Pro Ala Lys Ser Ile
          50           55           60
Arg Val Thr Ile His Thr Ala Arg Pro Gly Ile Val Ile Gly Lys Lys
          65           70           75           80
Gly Glu Asp Val Glu Lys Leu Arg Lys Val Val Ala Asp Ile Ala Gly
```

										85					90					95				
Val	Pro	Ala	Gln	Ile	Asn	Ile	Ala	Glu	Val	Arg	Lys	Pro	Glu	Leu	Asp									
100									105					110										
Ala	Lys	Leu	Val	Ala	Asp	Ser	Ile	Thr	Ser	Gln	Leu	Glu	Arg	Arg	Val									
115									120					125										
Met	Phe	Arg	Arg	Ala	Met	Lys	Arg	Ala	Val	Gln	Asn	Ala	Met	Arg	Leu									
130									135					140										
Gly	Ala	Lys	Gly	Ile	Lys	Val	Glu	Val	Ser	Gly	Arg	Leu	Gly	Gly	Ala									
145									150					155										
Glu	Ile	Ala	Arg	Thr	Glu	Trp	Tyr	Arg	Glu	Gly	Arg	Val	Pro	Leu	His									
165									170					175										
Thr	Leu	Arg	Ala	Asp	Ile	Asp	Tyr	Asn	Thr	Ser	Glu	Ala	His	Thr	Thr									
180									185					190										
Tyr	Gly	Val	Ile	Gly	Val	Lys	Val	Trp	Ile	Phe	Lys	Gly	Glu	Ile	Leu									
195									200					205										
Gly	Gly	Met	Ala	Ala	Val	Glu	Gln	Pro	Glu	Lys	Pro	Ala	Ala	Gln	Pro									
210									215					220										
Lys	Lys	Gln	Gln	Arg	Lys	Gly	Arg	Lys																
225									230															

```
<210> 305
<211> 110
<212> PRT
<213> Escherichia coli
```

<400> 305															
Met	Glu	Thr	Ile	Ala	Lys	His	Arg	His	Ala	Arg	Ser	Ser	Ala	Gln	Lys
1				5					10					15	
Val	Arg	Leu	Val	Ala	Asp	Leu	Ile	Arg	Gly	Lys	Lys	Val	Ser	Gln	Ala
			20					25					30		
Leu	Asp	Ile	Leu	Thr	Tyr	Thr	Asn	Lys	Lys	Ala	Ala	Val	Leu	Val	Lys
			35				40						45		
Lys	Val	Leu	Glu	Ser	Ala	Ile	Ala	Asn	Ala	Glu	His	Asn	Asp	Gly	Ala
			50				55					60			
Asp	Ile	Asp	Asp	Leu	Lys	Val	Thr	Lys	Ile	Phe	Val	Asp	Glu	Gly	Pro
65					70					75					80
Ser	Met	Lys	Arg	Ile	Met	Pro	Arg	Ala	Lys	Gly	Arg	Ala	Asp	Arg	Ile
				85					90					95	
Leu	Lys	Arg	Thr	Ser	His	Ile	Thr	Val	Val	Val	Ser	Asp	Arg		
			100					105					110		

```
<210> 306
<211> 92
<212> PRT
<213> Escherichia coli
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<400> 306															
Met	Pro	Arg	Ser	Leu	Lys	Lys	Gly	Pro	Phe	Ile	Asp	Leu	His	Leu	Leu
1				5					10					15	
Lys	Lys	Val	Glu	Lys	Ala	Val	Glu	Ser	Gly	Asp	Lys	Lys	Pro	Leu	Arg
			20					25					30		
Thr	Trp	Ser	Arg	Arg	Ser	Thr	Ile	Phe	Pro	Asn	Met	Ile	Gly	Leu	Thr
		35					40					45			
Ile	Ala	Val	His	Asn	Gly	Arg	Gln	His	Val	Pro	Val	Phe	Val	Thr	Asp
	50					55					60				
Glu	Met	Val	Gly	His	Lys	Leu	Gly	Glu	Phe	Ala	Pro	Thr	Arg	Thr	Tyr
65					70					75					80
Arg	Gly	His	Ala	Ala	Asp	Lys	Lys	Ala	Lys	Lys	Lys				
				85					90						

<210> 307
 <211> 273
 <212> PRT
 <213> Escherichia coli

<400> 307

```

Met Ala Val Val Lys Cys Lys Pro Thr Ser Pro Gly Arg Arg His Val
 1          5          10          15
Val Lys Val Val Asn Pro Glu Leu His Lys Gly Lys Pro Phe Ala Pro
          20          25          30
Leu Leu Glu Lys Asn Ser Lys Ser Gly Gly Arg Asn Asn Asn Gly Arg
          35          40          45
Ile Thr Thr Arg His Ile Gly Gly Gly His Lys Gln Ala Tyr Arg Ile
          50          55          60
Val Asp Phe Lys Arg Asn Lys Asp Gly Ile Pro Ala Val Val Glu Arg
65          70          75          80
Leu Glu Tyr Asp Pro Asn Arg Ser Ala Asn Ile Ala Leu Val Leu Tyr
          85          90          95
Lys Asp Gly Glu Arg Arg Tyr Ile Leu Ala Pro Lys Gly Leu Lys Ala
          100          105          110
Gly Asp Gln Ile Gln Ser Gly Val Asp Ala Ala Ile Lys Pro Gly Asn
          115          120          125
Thr Leu Pro Met Arg Asn Ile Pro Val Gly Ser Thr Val His Asn Val
          130          135          140
Glu Met Lys Pro Gly Lys Gly Gly Gln Leu Ala Arg Ser Ala Gly Thr
145          150          155          160
Tyr Val Gln Ile Val Ala Arg Asp Gly Ala Tyr Val Thr Leu Arg Leu
          165          170          175
Arg Ser Gly Glu Met Arg Lys Val Glu Ala Asp Cys Arg Ala Thr Leu
          180          185          190
Gly Glu Val Gly Asn Ala Glu His Met Leu Arg Val Leu Gly Lys Ala
          195          200          205
Gly Ala Ala Arg Trp Arg Gly Val Arg Pro Thr Val Arg Gly Thr Ala
          210          215          220
Met Asn Pro Val Asp His Pro His Gly Gly Gly Glu Gly Arg Asn Phe
225          230          235          240
Gly Lys His Pro Val Thr Pro Trp Gly Val Gln Thr Lys Gly Lys Lys
          245          250          255
Thr Arg Ser Asn Lys Arg Thr Asp Lys Phe Ile Val Arg Arg Arg Ser
          260          265          270
Lys

```

<210> 308
 <211> 100
 <212> PRT
 <213> Escherichia coli

<400> 308

```

Met Ile Arg Glu Glu Arg Leu Leu Lys Val Leu Arg Ala Pro His Val
 1          5          10          15
Ser Glu Lys Ala Ser Thr Ala Met Glu Lys Ser Asn Thr Ile Val Leu
          20          25          30
Lys Val Ala Lys Asp Ala Thr Lys Ala Glu Ile Lys Ala Ala Val Gln
          35          40          45
Lys Leu Phe Glu Val Glu Val Glu Val Val Asn Thr Leu Val Val Lys
          50          55          60
Gly Lys Val Lys Arg His Gly Gln Arg Ile Gly Arg Arg Ser Asp Trp
65          70          75          80
Lys Lys Ala Tyr Val Thr Leu Lys Glu Gly Gln Asn Leu Asp Phe Val

```

85 90 95

Gly Gly Ala Glu
100

<210> 309
<211> 201
<212> PRT
<213> Escherichia coli

<400> 309
Met Glu Leu Val Leu Lys Asp Ala Gln Ser Ala Leu Thr Val Ser Glu
1 5 10 15
Thr Thr Phe Gly Arg Asp Phe Asn Glu Ala Leu Val His Gln Val Val
20 25 30
Val Ala Tyr Ala Ala Gly Ala Arg Gln Gly Thr Arg Ala Gln Lys Thr
35 40 45
Arg Ala Glu Val Thr Gly Ser Gly Lys Lys Pro Trp Arg Gln Lys Gly
50 55 60
Thr Gly Arg Ala Arg Ser Gly Ser Ile Lys Ser Pro Ile Trp Arg Ser
65 70 75 80
Gly Gly Val Thr Phe Ala Ala Arg Pro Gln Asp His Ser Gln Lys Val
85 90 95
Asn Lys Lys Met Tyr Arg Gly Ala Leu Lys Ser Ile Leu Ser Glu Leu
100 105 110
Val Arg Gln Asp Arg Leu Ile Val Val Glu Lys Phe Ser Val Glu Ala
115 120 125
Pro Lys Thr Lys Leu Leu Ala Gln Lys Leu Lys Asp Met Ala Leu Glu
130 135 140
Asp Val Leu Ile Ile Thr Gly Glu Leu Asp Glu Asn Leu Phe Leu Ala
145 150 155 160
Ala Arg Asn Leu His Lys Val Asp Val Arg Asp Ala Thr Gly Ile Asp
165 170 175
Pro Val Ser Leu Ile Ala Phe Asp Lys Val Val Met Thr Ala Asp Ala
180 185 190
Val Lys Gln Val Glu Glu Met Leu Ala
195 200

<210> 310
<211> 209
<212> PRT
<213> Escherichia coli

<400> 310
Met Ile Gly Leu Val Gly Lys Lys Val Gly Met Thr Arg Ile Phe Thr
1 5 10 15
Glu Asp Gly Val Ser Ile Pro Val Thr Val Ile Glu Val Glu Ala Asn
20 25 30
Arg Val Thr Gln Val Lys Asp Leu Ala Asn Asp Gly Tyr Arg Ala Ile
35 40 45
Gln Val Thr Thr Gly Ala Lys Lys Ala Asn Arg Val Thr Lys Pro Glu
50 55 60
Ala Gly His Phe Ala Lys Ala Gly Val Glu Ala Gly Arg Gly Leu Trp
65 70 75 80
Glu Phe Arg Leu Ala Glu Gly Glu Glu Phe Thr Val Gly Gln Ser Ile
85 90 95
Ser Val Glu Leu Phe Ala Asp Val Lys Lys Val Asp Val Thr Gly Thr
100 105 110
Ser Lys Gly Lys Gly Phe Ala Gly Thr Val Lys Arg Trp Asn Phe Arg
115 120 125
Thr Gln Asp Ala Thr His Gly Asn Ser Leu Ser His Arg Val Pro Gly

130		135		140
Ser Ile Gly Gln Asn Gln Thr Pro Gly Lys Val Phe Lys Gly Lys Lys				
145		150		155
Met Ala Gly Gln Met Gly Asn Glu Arg Val Thr Val Gln Ser Leu Asp				160
	165		170	175
Val Val Arg Val Asp Ala Glu Arg Asn Leu Leu Leu Val Lys Gly Ala				
	180		185	190
Val Pro Gly Ala Thr Gly Ser Asp Leu Ile Val Lys Pro Ala Val Lys				
	195	200		205
Ala				

<210> 311
 <211> 103
 <212> PRT
 <213> Escherichia coli

<400> 311

Met Gln Asn Gln Arg Ile Arg Ile Arg Leu Lys Ala Phe Asp His Arg	
1	5
Leu Ile Asp Gln Ala Thr Ala Glu Ile Val Glu Thr Ala Lys Arg Thr	10
	20
Gly Ala Gln Val Arg Gly Pro Ile Pro Leu Pro Thr Arg Lys Glu Arg	25
	30
Phe Thr Val Leu Ile Ser Pro His Val Asn Lys Asp Ala Arg Asp Gln	35
	40
Tyr Glu Ile Arg Thr His Leu Arg Leu Val Asp Ile Val Glu Pro Thr	45
65	50
Glu Lys Thr Val Asp Ala Leu Met Arg Leu Asp Leu Ala Ala Gly Val	55
	60
Asp Val Gln Ile Ser Leu Gly	65
	70
	75
	80
	85
	90
	95
	100

<210> 312
 <211> 1569
 <212> PRT
 <213> Escherichia coli

<400> 312

Met Asn Thr Ile His Leu Arg Cys Leu Phe Arg Met Asn Pro Leu Val	
1	5
Trp Cys Leu Trp Ala Asp Val Ala Ala Lys Leu Arg Ser Leu Lys Arg	10
	20
Tyr Ser Val Phe Thr Phe Gln Arg Met Lys Phe Met Asn Arg Thr Ser	25
	30
Pro Tyr Tyr Cys Arg Arg Ser Val Leu Ser Leu Leu Ile Ser Ala Leu	35
	40
Ile Tyr Ala Pro Pro Gly Met Ala Ala Phe Thr Asn Val Ile Gly	45
65	50
Val Val Asn Asp Glu Thr Val Asp Gly Asn Gln Lys Val Asp Glu Arg	55
	60
Gly Thr Thr Asn Asn Thr His Ile Ile Asn His Gly Gln Gln Asn Val	65
	70
	75
	80
	85
	90
	95
	100
	105
	110
	115
	120
	125
Asp Ile Gly Ser His Asn Asn Phe Val Gly Gln Ala Asn Asn Thr Thr	130
	135
Ile Asn Gly Gly Arg Gln Ser Ile His Asp Gly Gly Ile Ser Thr Gly	140
145	145
	150
	155
	160
Thr Thr Ile Glu Ser Gly Asn Gln Asp Val Tyr Lys Gly Gly Ile Ser	165

Asn	Gly	Thr	Thr	165	Ile	Lys	Gly	Gly	Ala	170	Ser	Arg	Val	Glu	Gly	Gly	Ser	175
			180						185									190
Ala	Asn	Gly	Ile	Leu	Ile	Asp	Gly	Gly	Ser	Gln	Ile	Val	Lys	Val	Gln			
		195						200						205				
Gly	His	Ala	Asp	Gly	Thr	Thr	Ile	Asn	Lys	Ser	Gly	Ser	Gln	Asp	Val			
	210						215					220						
Val	Gln	Gly	Ser	Leu	Ala	Thr	Asn	Thr	Thr	Ile	Asn	Gly	Gly	Arg	Gln			
	225				230					235					240			
Tyr	Val	Glu	Gln	Ser	Thr	Val	Glu	Thr	Thr	Thr	Ile	Lys	Asn	Gly	Gly			
				245					250					255				
Glu	Gln	Arg	Val	Tyr	Glu	Ser	Arg	Ala	Leu	Asp	Thr	Thr	Ile	Glu	Gly			
		260						265					270					
Gly	Thr	Gln	Ser	Leu	Asn	Ser	Lys	Ser	Thr	Ala	Lys	Asn	Thr	His	Ile			
		275					280						285					
Tyr	Ser	Gly	Gly	Thr	Gln	Ile	Val	Asp	Asn	Thr	Ser	Thr	Ser	Asp	Val			
	290					295					300							
Ile	Glu	Val	Tyr	Ser	Gly	Gly	Val	Leu	Asp	Val	Arg	Gly	Gly	Thr	Ala			
	305				310				315						320			
Thr	Asn	Val	Thr	Gln	His	Asp	Gly	Ala	Ile	Leu	Lys	Thr	Asn	Thr	Asn			
				325					330					335				
Gly	Thr	Thr	Val	Ser	Gly	Thr	Asn	Ser	Glu	Gly	Ala	Phe	Ser	Ile	His			
		340					345						350					
Asn	His	Val	Ala	Asp	Asn	Val	Leu	Leu	Glu	Asn	Gly	Gly	His	Leu	Asp			
		355				360					365							
Ile	Asn	Ala	Tyr	Gly	Ser	Ala	Asn	Lys	Thr	Ile	Ile	Lys	Asp	Lys	Gly			
	370					375					380							
Thr	Met	Ser	Val	Leu	Thr	Asn	Ala	Lys	Ala	Asp	Ala	Thr	Arg	Ile	Asp			
	385				390				395					400				
Asn	Gly	Gly	Val	Met	Asp	Val	Ala	Gly	Asn	Ala	Thr	Asn	Thr	Ile	Ile			
			405						410					415				
Asn	Gly	Gly	Thr	Gln	Asn	Ile	Asn	Asn	Tyr	Gly	Ile	Ala	Thr	Gly	Thr			
		420					425						430					
Asn	Ile	Asn	Ser	Gly	Thr	Gln	Asn	Ile	Lys	Ser	Gly	Gly	Lys	Ala	Asp			
		435					440					445						
Thr	Thr	Ile	Ile	Ser	Ser	Gly	Ser	Arg	Gln	Val	Val	Glu	Lys	Asp	Gly			
	450					455					460							
Thr	Ala	Ile	Gly	Ser	Asn	Ile	Ser	Ala	Gly	Gly	Ser	Leu	Ile	Val	Tyr			
	465				470				475					480				
Thr	Gly	Gly	Ile	Ala	His	Gly	Val	Asn	Gln	Glu	Thr	Gly	Ser	Ala	Leu			
			485						490					495				
Val	Ala	Asn	Thr	Gly	Ala	Gly	Thr	Asp	Ile	Glu	Gly	Tyr	Asn	Lys	Leu			
		500					505						510					
Ser	His	Phe	Thr	Ile	Thr	Gly	Gly	Glu	Ala	Asn	Tyr	Val	Val	Leu	Glu			
		515				520						525						
Asn	Thr	Gly	Glu	Leu	Thr	Val	Val	Ala	Lys	Thr	Ser	Ala	Lys	Asn	Thr			
	530					535					540							
Thr	Ile	Asp	Thr	Gly	Gly	Lys	Leu	Ile	Val	Gln	Lys	Glu	Ala	Lys	Thr			
	545				550				555					560				
Asp	Ser	Thr	Arg	Leu	Asn	Asn	Gly	Gly	Val	Leu	Glu	Val	Gln	Asp	Gly			
			565				570							575				
Gly	Glu	Ala	Lys	His	Val	Glu	Gln	Gln	Ser	Gly	Gly	Ala	Leu	Ile	Ala			
		580					585					590						
Ser	Thr	Thr	Ser	Gly	Thr	Leu	Ile	Glu	Gly	Thr	Asn	Ser	Tyr	Gly	Asp			
		595				600						605						
Ala	Phe	Tyr	Ile	Arg	Asn	Ser	Glu	Ala	Lys	Asn	Val	Val	Leu	Glu	Asn			
	610					615					620							
Ala	Gly	Ser	Leu	Thr	Val	Val	Thr	Gly	Ser	Arg	Ala	Val	Asp	Thr	Ile			
	625				630				635					640				
Ile	Asn	Ala	Asn	Gly	Lys	Met	Asp	Val	Tyr	Gly	Lys	Asp	Val	Gly	Thr			

-296-

<210> 313
<211> 38

<212> PRT

<213> Escherichia coli

<400> 313

Met Lys Val Arg Ala Ser Val Lys Lys Leu Cys Arg Asn Cys Lys Ile
 1 5 10 15
 Val Lys Arg Asp Gly Val Ile Arg Val Ile Cys Ser Ala Glu Pro Lys
 20 25 30
 His Lys Gln Arg Gln Gly
 35

<210> 314

<211> 443

<212> PRT

<213> Escherichia coli

<400> 314

Met Ala Lys Gln Pro Gly Leu Asp Phe Gln Ser Ala Lys Gly Gly Leu
 1 5 10 15
 Gly Glu Leu Lys Arg Arg Leu Leu Phe Val Ile Gly Ala Leu Ile Val
 20 25 30
 Phe Arg Ile Gly Ser Phe Ile Pro Ile Pro Gly Ile Asp Ala Ala Val
 35 40 45
 Leu Ala Lys Leu Leu Glu Gln Gln Arg Gly Thr Ile Ile Glu Met Phe
 50 55 60
 Asn Met Phe Ser Gly Gly Ala Leu Ser Arg Ala Ser Ile Phe Ala Leu
 65 70 75 80
 Gly Ile Met Pro Tyr Ile Ser Ala Ser Ile Ile Ile Gln Leu Leu Thr
 85 90 95
 Val Val His Pro Thr Leu Ala Glu Ile Lys Lys Glu Gly Glu Ser Gly
 100 105 110
 Arg Arg Lys Ile Ser Gln Tyr Thr Arg Tyr Gly Thr Leu Val Leu Ala
 115 120 125
 Ile Phe Gln Ser Ile Gly Ile Ala Thr Gly Leu Pro Asn Met Pro Gly
 130 135 140
 Met Gln Gly Leu Val Ile Asn Pro Gly Phe Ala Phe Tyr Phe Thr Ala
 145 150 155 160
 Val Val Ser Leu Val Thr Gly Thr Met Phe Leu Met Trp Leu Gly Glu
 165 170 175
 Gln Ile Thr Glu Arg Gly Ile Gly Asn Gly Ile Ser Ile Ile Ile Phe
 180 185 190
 Ala Gly Ile Val Ala Gly Leu Pro Pro Ala Ile Ala His Thr Ile Glu
 195 200 205
 Gln Ala Arg Gln Gly Asp Leu His Phe Leu Val Leu Leu Val Ala
 210 215 220
 Val Leu Val Phe Ala Val Thr Phe Phe Val Val Phe Val Glu Arg Gly
 225 230 235 240
 Gln Arg Arg Ile Val Val Asn Tyr Ala Lys Arg Gln Gln Gly Arg Arg
 245 250 255
 Val Tyr Ala Ala Gln Ser Thr His Leu Pro Leu Lys Val Asn Met Ala
 260 265 270
 Gly Val Ile Pro Ala Ile Phe Ala Ser Ser Ile Ile Leu Phe Pro Ala
 275 280 285
 Thr Ile Ala Ser Trp Phe Gly Gly Gly Thr Gly Trp Asn Trp Leu Thr
 290 295 300
 Thr Ile Ser Leu Tyr Leu Gln Pro Gly Gln Pro Leu Tyr Val Leu Leu
 305 310 315 320
 Tyr Ala Ser Ala Ile Ile Phe Phe Cys Phe Phe Tyr Thr Ala Leu Val
 325 330 335
 Phe Asn Pro Arg Glu Thr Ala Asp Asn Leu Lys Lys Ser Gly Ala Phe

			340					345					350				
Val	Pro	Gly	Ile	Arg	Pro	Gly	Glu	Gln	Thr	Ala	Lys	Tyr	Ile	Asp	Lys		
		355					360					365					
Val	Met	Thr	Arg	Leu	Thr	Leu	Val	Gly	Ala	Leu	Tyr	Ile	Thr	Phe	Ile		
		370				375					380						
Cys	Leu	Ile	Pro	Glu	Phe	Met	Arg	Asp	Ala	Met	Lys	Val	Pro	Phe	Tyr		
385					390					395					400		
Phe	Gly	Gly	Thr	Ser	Leu	Leu	Ile	Val	Val	Val	Val	Ile	Met	Asp	Phe		
			405					410						415			
Met	Ala	Gln	Val	Gln	Thr	Leu	Met	Met	Ser	Ser	Gln	Tyr	Glu	Ser	Ala		
		420					425						430				
Leu	Lys	Lys	Ala	Asn	Leu	Lys	Gly	Tyr	Gly	Arg							
		435					440										

<210> 315
 <211> 144
 <212> PRT
 <213> Escherichia coli

<400> 315

Met	Arg	Leu	Asn	Thr	Leu	Ser	Pro	Ala	Glu	Gly	Ser	Lys	Lys	Ala	Gly		
1			5						10					15			
Lys	Arg	Leu	Gly	Arg	Gly	Ile	Gly	Ser	Gly	Leu	Gly	Lys	Thr	Gly	Gly		
		20					25						30				
Arg	Gly	His	Lys	Gly	Gln	Lys	Ser	Arg	Ser	Gly	Gly	Gly	Val	Arg	Arg		
		35				40						45					
Gly	Phe	Glu	Gly	Gly	Gln	Met	Pro	Leu	Tyr	Arg	Arg	Leu	Pro	Lys	Phe		
	50				55					60							
Gly	Phe	Thr	Ser	Arg	Lys	Ala	Ala	Ile	Thr	Ala	Glu	Ile	Arg	Leu	Ser		
65				70					75					80			
Asp	Leu	Ala	Lys	Val	Glu	Gly	Gly	Val	Val	Asp	Leu	Asn	Thr	Leu	Lys		
			85					90					95				
Ala	Ala	Asn	Ile	Ile	Gly	Ile	Gln	Ile	Glu	Phe	Ala	Lys	Val	Ile	Leu		
		100					105						110				
Ala	Gly	Glu	Val	Thr	Thr	Pro	Val	Thr	Val	Arg	Gly	Leu	Arg	Val	Thr		
		115				120						125					
Lys	Gly	Ala	Arg	Ala	Ala	Ile	Glu	Ala	Ala	Gly	Gly	Lys	Ile	Glu	Glu		
		130				135					140						

<210> 316
 <211> 59
 <212> PRT
 <213> Escherichia coli

<400> 316

Met	Ala	Lys	Thr	Ile	Lys	Ile	Thr	Gln	Thr	Arg	Ser	Ala	Ile	Gly	Arg		
1			5						10					15			
Leu	Pro	Lys	His	Lys	Ala	Thr	Leu	Leu	Gly	Leu	Gly	Leu	Arg	Arg	Ile		
		20					25						30				
Gly	His	Thr	Val	Glu	Arg	Glu	Asp	Thr	Pro	Ala	Ile	Arg	Gly	Met	Ile		
		35				40						45					
Asn	Ala	Val	Ser	Phe	Met	Val	Lys	Val	Glu	Glu							
		50				55											

<210> 317
 <211> 167
 <212> PRT
 <213> Escherichia coli

<400> 317

```

Met Ala His Ile Glu Lys Gln Ala Gly Glu Leu Gln Glu Lys Leu Ile
 1      5      10      15
Ala Val Asn Arg Val Ser Lys Thr Val Lys Gly Gly Arg Ile Phe Ser
      20      25      30
Phe Thr Ala Leu Thr Val Val Gly Asp Gly Asn Gly Arg Val Gly Phe
      35      40      45
Gly Tyr Gly Lys Ala Arg Glu Val Pro Ala Ala Ile Gln Lys Ala Met
 50      55      60
Glu Lys Ala Arg Arg Asn Met Ile Asn Val Ala Leu Asn Asn Gly Thr
65      70      75      80
Leu Gln His Pro Val Lys Gly Val His Thr Gly Ser Arg Val Phe Met
      85      90      95
Gln Pro Ala Ser Glu Gly Thr Gly Ile Ile Ala Gly Gly Ala Met Arg
      100      105      110
Ala Val Leu Glu Val Ala Gly Val His Asn Val Leu Ala Lys Ala Tyr
      115      120      125
Gly Ser Thr Asn Pro Ile Asn Val Val Arg Ala Thr Ile Asp Gly Leu
130      135      140
Glu Asn Met Asn Ser Pro Glu Met Val Ala Ala Lys Arg Gly Lys Ser
145      150      155      160
Val Glu Glu Ile Leu Gly Lys
      165

```

<210> 318

<211> 117

<212> PRT

<213> Escherichia coli

<400> 318

```

Met Asp Lys Lys Ser Ala Arg Ile Arg Arg Ala Thr Arg Ala Arg Arg
 1      5      10      15
Lys Leu Gln Glu Leu Gly Ala Thr Arg Leu Val Val His Arg Thr Pro
      20      25      30
Arg His Ile Tyr Ala Gln Val Ile Ala Pro Asn Gly Ser Glu Val Leu
      35      40      45
Val Ala Ala Ser Thr Val Glu Lys Ala Ile Ala Glu Gln Leu Lys Tyr
 50      55      60
Thr Gly Asn Lys Asp Ala Ala Ala Ala Val Gly Lys Ala Val Ala Glu
65      70      75      80
Arg Ala Leu Glu Lys Gly Ile Lys Asp Val Ser Phe Asp Arg Ser Gly
      85      90      95
Phe Gln Tyr His Gly Arg Val Gln Ala Leu Ala Asp Ala Ala Arg Glu
      100      105      110
Ala Gly Leu Gln Phe
      115

```

<210> 319

<211> 177

<212> PRT

<213> Escherichia coli

<400> 319

```

Met Ser Arg Val Ala Lys Ala Pro Val Val Val Pro Ala Gly Val Asp
 1      5      10      15
Val Lys Ile Asn Gly Gln Val Ile Thr Ile Lys Gly Lys Asn Gly Glu
      20      25      30
Leu Thr Arg Thr Leu Asn Asp Ala Val Glu Val Lys His Ala Asp Asn
      35      40      45
Thr Leu Thr Phe Gly Pro Arg Asp Gly Tyr Ala Asp Gly Trp Ala Gln
 50      55      60

```

Ala Gly Thr Ala Arg Ala Leu Leu Asn Ser Met Val Ile Gly Val Thr
 65 70 75 80
 Glu Gly Phe Thr Lys Lys Leu Gln Leu Val Gly Val Gly Tyr Arg Ala
 85 90 95
 Ala Val Lys Gly Asn Val Ile Asn Leu Ser Leu Gly Phe Ser His Pro
 100 105 110
 Val Asp His Gln Leu Pro Ala Gly Ile Thr Ala Glu Cys Pro Thr Gln
 115 120 125
 Thr Glu Ile Val Leu Lys Gly Ala Asp Lys Gln Val Ile Gly Gln Val
 130 135 140
 Ala Ala Asp Leu Arg Ala Tyr Arg Arg Pro Glu Pro Tyr Lys Gly Lys
 145 150 155 160
 Gly Val Arg Tyr Ala Asp Glu Val Val Arg Thr Lys Glu Ala Lys Lys
 165 170 175

Lys

<210> 320

<211> 130

<212> PRT

<213> Escherichia coli

<400> 320

Met Ser Met Gln Asp Pro Ile Ala Asp Met Leu Thr Arg Ile Arg Asn
 1 5 10 15
 Gly Gln Ala Ala Asn Lys Ala Ala Val Thr Met Pro Ser Ser Lys Leu
 20 25 30
 Lys Val Ala Ile Ala Asn Val Leu Lys Glu Glu Gly Phe Ile Glu Asp
 35 40 45
 Phe Lys Val Glu Gly Asp Thr Lys Pro Glu Leu Glu Leu Thr Leu Lys
 50 55 60
 Tyr Phe Gln Gly Lys Ala Val Val Glu Ser Ile Gln Arg Val Ser Arg
 65 70 75 80
 Pro Gly Leu Arg Ile Tyr Lys Arg Lys Asp Glu Leu Pro Lys Val Met
 85 90 95
 Ala Gly Leu Gly Ile Ala Val Val Ser Thr Ser Lys Gly Val Met Thr
 100 105 110
 Asp Arg Ala Ala Arg Gln Ala Gly Leu Gly Gly Glu Ile Ile Cys Tyr
 115 120 125
 Val Ala
 130

<210> 321

<211> 101

<212> PRT

<213> Escherichia coli

<400> 321

Met Ala Lys Gln Ser Met Lys Ala Arg Glu Val Lys Arg Val Ala Leu
 1 5 10 15
 Ala Asp Lys Tyr Phe Ala Lys Arg Ala Glu Leu Lys Ala Ile Ile Ser
 20 25 30
 Asp Val Asn Ala Ser Asp Glu Asp Arg Trp Asn Ala Val Leu Lys Leu
 35 40 45
 Gln Thr Leu Pro Arg Asp Ser Ser Pro Ser Arg Gln Arg Asn Arg Cys
 50 55 60
 Arg Gln Thr Gly Arg Pro His Gly Phe Leu Arg Lys Phe Gly Leu Ser
 65 70 75 80
 Arg Ile Lys Val Arg Glu Ala Ala Met Arg Gly Glu Ile Pro Gly Leu
 85 90 95

Lys Lys Ala Ser Trp
100

<210> 322

<211> 179

<212> PRT

<213> Escherichia coli

<400> 322

Met	Ala	Lys	Leu	His	Asp	Tyr	Tyr	Lys	Asp	Glu	Val	Val	Lys	Lys	Leu
1				5					10					15	
Met	Thr	Glu	Phe	Asn	Tyr	Asn	Ser	Val	Met	Gln	Val	Pro	Arg	Val	Glu
			20				25						30		
Lys	Ile	Thr	Leu	Asn	Met	Gly	Val	Gly	Glu	Ala	Ile	Ala	Asp	Lys	Lys
		35					40						45		
Leu	Leu	Asp	Asn	Ala	Ala	Ala	Asp	Leu	Ala	Ala	Ile	Ser	Gly	Gln	Lys
	50					55					60				
Pro	Leu	Ile	Thr	Lys	Ala	Arg	Lys	Ser	Val	Ala	Gly	Phe	Lys	Ile	Arg
65					70				75						80
Gln	Gly	Tyr	Pro	Ile	Gly	Cys	Lys	Val	Thr	Leu	Arg	Gly	Glu	Arg	Met
				85					90					95	
Trp	Glu	Phe	Phe	Glu	Arg	Leu	Ile	Thr	Ile	Ala	Val	Pro	Arg	Ile	Arg
			100					105					110		
Asp	Phe	Arg	Gly	Leu	Ser	Ala	Lys	Ser	Phe	Asp	Gly	Arg	Gly	Asn	Tyr
		115					120					125			
Ser	Met	Gly	Val	Arg	Glu	Gln	Ile	Ile	Phe	Pro	Glu	Ile	Asp	Tyr	Asp
	130					135					140				
Lys	Val	Asp	Arg	Val	Arg	Gly	Leu	Asp	Ile	Thr	Ile	Thr	Thr	Thr	Ala
145					150					155					160
Lys	Ser	Asp	Glu	Glu	Gly	Arg	Ala	Leu	Leu	Ala	Ala	Phe	Asp	Phe	Pro
			165					170						175	

Phe Arg Lys

<210> 323

<211> 104

<212> PRT

<213> Escherichia coli

<400> 323

Met	Ala	Ala	Lys	Ile	Arg	Arg	Asp	Asp	Glu	Val	Ile	Val	Leu	Thr	Gly
1				5					10					15	
Lys	Asp	Lys	Gly	Lys	Arg	Gly	Lys	Val	Lys	Asn	Val	Leu	Ser	Ser	Gly
			20				25						30		
Lys	Val	Ile	Val	Glu	Gly	Ile	Asn	Leu	Val	Lys	Lys	His	Gln	Lys	Pro
		35					40						45		
Val	Pro	Ala	Leu	Asn	Gln	Pro	Gly	Gly	Ile	Val	Glu	Lys	Glu	Ala	Ala
	50					55					60				
Ile	Gln	Val	Ser	Asn	Val	Ala	Ile	Phe	Asn	Ala	Ala	Thr	Gly	Lys	Ala
65					70				75						80
Asp	Arg	Val	Gly	Phe	Arg	Phe	Glu	Asp	Gly	Lys	Lys	Val	Arg	Phe	Phe
				85					90					95	

Lys Ser Asn Ser Glu Thr Ile Lys
100

<210> 324

<211> 123

<212> PRT

<213> Escherichia coli

<400> 324

```

Met Ile Gln Glu Gln Thr Met Leu Asn Val Ala Asp Asn Ser Gly Ala
 1           5           10           15
Arg Arg Val Met Cys Ile Lys Val Leu Gly Gly Ser His Arg Arg Tyr
          20           25           30
Ala Gly Val Gly Asp Ile Ile Lys Ile Thr Ile Lys Glu Ala Ile Pro
          35           40           45
Arg Gly Lys Val Lys Lys Gly Asp Val Leu Lys Ala Val Val Val Arg
          50           55           60
Thr Lys Lys Gly Val Arg Arg Pro Asp Gly Ser Val Ile Arg Phe Asp
65           70           75           80
Gly Asn Ala Cys Val Leu Leu Asn Asn Asn Ser Glu Gln Pro Ile Gly
          85           90           95
Thr Arg Ile Phe Gly Pro Val Thr Arg Glu Leu Arg Ser Glu Lys Phe
          100          105          110
Met Lys Ile Ile Ser Leu Ala Pro Glu Val Leu
          115          120

```

<210> 325

<211> 396

<212> PRT

<213> Escherichia coli

<400> 325

```

Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
 1           5           10           15
Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
          20           25           30
Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
          35           40           45
Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
          50           55           60
His Pro Asp Lys Leu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
65           70           75           80
Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
          85           90           95
Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
          100          105          110
Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
          115          120          125
Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
          130          135          140
Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
145          150          155          160
Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
          165          170          175
Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
          180          185          190
Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
          195          200          205
Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu
          210          215          220
Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu
225          230          235          240
Ala Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp
          245          250          255
Ala Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val
          260          265          270
Leu Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu
          275          280          285

```

Ser Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu
 290 295 300
 Phe Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn
 305 310 315 320
 Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu
 325 330 335
 Leu Ala Lys Asp Pro Arg Ile Ala Ala Thr Met Glu Asn Ala Gln Lys
 340 345 350
 Gly Glu Ile Met Pro Asn Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala
 355 360 365
 Val Arg Thr Ala Val Ile Asn Ala Ala Ser Gly Arg Gln Thr Val Asp
 370 375 380
 Glu Ala Leu Lys Asp Ala Gln Thr Arg Ile Thr Lys
 385 390 395

<210> 326

<211> 514

<212> PRT

<213> Escherichia coli

<400> 326

Met Asp Val Ile Lys Lys Lys His Trp Trp Gln Ser Asp Ala Leu Lys
 1 5 10 15
 Trp Ser Val Leu Gly Leu Leu Gly Leu Leu Val Gly Tyr Leu Val Val
 20 25 30
 Leu Met Tyr Ala Gln Gly Glu Tyr Leu Phe Ala Ile Thr Thr Leu Ile
 35 40 45
 Leu Ser Ser Ala Gly Leu Tyr Ile Phe Ala Asn Arg Lys Ala Tyr Ala
 50 55 60
 Trp Arg Tyr Val Tyr Pro Gly Met Ala Gly Met Gly Leu Phe Val Leu
 65 70 75 80
 Phe Pro Leu Val Cys Thr Ile Ala Ile Ala Phe Thr Asn Tyr Ser Ser
 85 90 95
 Thr Asn Gln Leu Thr Phe Glu Arg Ala Gln Glu Val Leu Leu Asp Arg
 100 105 110
 Ser Trp Gln Ala Gly Lys Thr Tyr Asn Phe Gly Leu Tyr Pro Ala Gly
 115 120 125
 Asp Glu Trp Gln Leu Ala Leu Ser Asp Gly Glu Thr Gly Lys Asn Tyr
 130 135 140
 Leu Ser Asp Ala Phe Lys Phe Gly Gly Glu Gln Lys Leu Gln Leu Lys
 145 150 155 160
 Glu Thr Thr Ala Gln Pro Glu Gly Glu Arg Ala Asn Leu Arg Val Ile
 165 170 175
 Thr Gln Asn Arg Gln Ala Leu Ser Asp Ile Thr Ala Ile Leu Pro Asp
 180 185 190
 Gly Asn Lys Val Met Met Ser Ser Leu Arg Gln Phe Ser Gly Thr Gln
 195 200 205
 Pro Leu Tyr Thr Leu Asp Gly Asp Gly Thr Leu Thr Asn Asn Gln Ser
 210 215 220
 Gly Val Lys Tyr Arg Pro Asn Asn Gln Ile Gly Phe Tyr Gln Ser Ile
 225 230 235 240
 Thr Ala Asp Gly Asn Trp Gly Asp Glu Lys Leu Ser Pro Gly Tyr Thr
 245 250 255
 Val Thr Thr Gly Trp Lys Asn Phe Thr Arg Val Phe Thr Asp Glu Gly
 260 265 270
 Ile Gln Lys Pro Phe Leu Ala Ile Phe Val Trp Thr Val Val Phe Ser
 275 280 285
 Leu Ile Thr Val Phe Leu Thr Val Ala Val Gly Met Val Leu Ala Cys
 290 295 300
 Leu Val Gln Trp Glu Ala Leu Arg Gly Lys Ala Val Tyr Arg Val Leu

```

305          310          315          320
Leu Ile Leu Pro Tyr Ala Val Pro Ser Phe Ile Ser Ile Leu Ile Phe
          325          330          335
Lys Gly Leu Phe Asn Gln Ser Phe Gly Glu Ile Asn Met Met Leu Ser
          340          345          350
Ala Leu Phe Gly Val Lys Pro Ala Trp Phe Ser Asp Pro Thr Thr Ala
          355          360          365
Arg Thr Met Leu Ile Ile Val Asn Thr Trp Leu Gly Tyr Pro Tyr Met
          370          375          380
Met Ile Leu Cys Met Gly Leu Leu Lys Ala Ile Pro Asp Asp Leu Tyr
          385          390          395          400
Glu Ala Ser Ala Met Asp Gly Ala Gly Pro Phe Gln Asn Phe Phe Lys
          405          410          415
Ile Thr Leu Pro Leu Leu Ile Lys Pro Leu Thr Pro Leu Met Ile Ala
          420          425          430
Ser Phe Ala Phe Asn Phe Asn Asn Phe Val Leu Ile Gln Leu Leu Thr
          435          440          445
Asn Gly Gly Pro Asp Arg Leu Gly Thr Thr Thr Pro Ala Gly Tyr Thr
          450          455          460
Asp Leu Leu Val Asn Tyr Thr Tyr Arg Ile Ala Phe Glu Gly Gly Gly
          465          470          475          480
Gly Gln Asp Phe Gly Leu Ala Ala Ala Ile Ala Thr Leu Ile Phe Leu
          485          490          495
Leu Val Gly Ala Leu Ala Ile Val Asn Leu Lys Ala Thr Arg Met Lys
          500          505          510
Phe Asp

```

<210> 327

<211> 296

<212> PRT

<213> Escherichia coli

<400> 327

```

Met Ala Met Val Gln Pro Lys Ser Gln Lys Ala Arg Leu Phe Ile Thr
1          5          10          15
His Leu Leu Leu Leu Leu Phe Ile Ala Ala Ile Met Phe Pro Leu Leu
          20          25          30
Met Val Val Ala Ile Ser Leu Arg Gln Gly Asn Phe Ala Thr Gly Ser
          35          40          45
Leu Ile Pro Glu Gln Ile Ser Trp Asp His Trp Lys Leu Ala Leu Gly
          50          55          60
Phe Ser Val Glu Gln Ala Asp Gly Arg Ile Thr Pro Pro Pro Phe Pro
          65          70          75          80
Val Leu Leu Trp Leu Trp Asn Ser Val Lys Val Ala Gly Ile Ser Ala
          85          90          95
Ile Gly Ile Val Ala Leu Ser Thr Thr Cys Ala Tyr Ala Phe Ala Arg
          100          105          110
Met Arg Phe Pro Gly Lys Ala Thr Leu Leu Lys Gly Met Leu Ile Phe
          115          120          125
Gln Met Phe Pro Ala Val Leu Ser Leu Val Ala Leu Tyr Ala Leu Phe
          130          135          140
Asp Arg Leu Gly Glu Tyr Ile Pro Phe Ile Gly Leu Asn Thr His Gly
          145          150          155          160
Gly Val Ile Phe Ala Tyr Leu Gly Gly Ile Ala Leu His Val Trp Thr
          165          170          175
Ile Lys Gly Tyr Phe Glu Thr Ile Asp Ser Ser Leu Glu Glu Ala Ala
          180          185          190
Ala Leu Asp Gly Ala Thr Pro Trp Gln Ala Phe Arg Leu Val Leu Leu
          195          200          205

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```

Pro Leu Ser Val Pro Ile Leu Ala Val Val Phe Ile Leu Ser Phe Ile
 210          215          220
Ala Ala Ile Thr Glu Val Pro Val Ala Ser Leu Leu Arg Asp Val
225          230          235          240
Asn Ser Tyr Thr Leu Ala Val Gly Met Gln Gln Tyr Leu Asn Pro Gln
          245          250          255
Asn Tyr Leu Trp Gly Asp Phe Ala Ala Ala Val Met Ser Ala Leu
          260          265          270
Pro Ile Thr Ile Val Phe Leu Leu Ala Gln Arg Trp Leu Val Asn Gly
          275          280          285
Leu Thr Ala Gly Gly Val Lys Gly
 290          295

```

<210> 328

<211> 673

<212> PRT

<213> Escherichia coli

<400> 328

```

Met Arg Leu Asn Pro Gly Gln Gln Gln Ala Val Glu Phe Val Thr Gly
 1          5          10          15
Pro Cys Leu Val Leu Ala Gly Ala Gly Ser Gly Lys Thr Arg Val Ile
          20          25          30
Thr Asn Lys Ile Ala His Leu Ile Arg Gly Cys Gly Tyr Gln Ala Arg
          35          40          45
His Ile Ala Ala Val Thr Phe Thr Asn Lys Ala Ala Arg Glu Met Lys
          50          55          60
Glu Arg Val Gly Gln Thr Leu Gly Arg Lys Glu Ala Arg Gly Leu Met
65          70          75          80
Ile Ser Thr Phe His Thr Leu Gly Leu Asp Ile Ile Lys Arg Glu Tyr
          85          90          95
Ala Ala Leu Gly Met Lys Ala Asn Phe Ser Leu Phe Asp Asp Thr Asp
          100          105          110
Gln Leu Ala Leu Leu Lys Glu Leu Thr Glu Gly Leu Ile Glu Asp Asp
          115          120          125
Lys Val Leu Leu Gln Gln Leu Ile Ser Thr Ile Ser Asn Trp Lys Asn
130          135          140
Asp Leu Lys Thr Pro Ser Gln Ala Ala Ala Ser Ala Ile Gly Glu Arg
145          150          155          160
Asp Arg Ile Phe Ala His Cys Tyr Gly Leu Tyr Asp Ala His Leu Lys
          165          170          175
Ala Cys Asn Val Leu Asp Phe Asp Asp Leu Ile Leu Leu Pro Thr Leu
          180          185          190
Leu Leu Gln Ala Asn Glu Glu Val Arg Lys Arg Trp Gln Asn Lys Ile
          195          200          205
Arg Tyr Leu Leu Val Asp Glu Tyr Gln Asp Thr Asn Thr Ser Gln Tyr
210          215          220
Glu Leu Val Lys Leu Leu Val Gly Ser Arg Ala Arg Phe Thr Val Val
225          230          235          240
Gly Asp Asp Asp Gln Ser Ile Tyr Ser Trp Arg Gly Ala Arg Pro Gln
          245          250          255
Asn Leu Val Leu Leu Ser Gln Asp Phe Pro Ala Leu Lys Val Ile Lys
          260          265          270
Leu Glu Gln Asn Tyr Arg Ser Ser Gly Arg Ile Leu Lys Ala Ala Asn
          275          280          285
Ile Leu Ile Ala Asn Asn Pro His Val Phe Glu Lys Arg Leu Phe Ser
290          295          300
Glu Leu Gly Tyr Gly Ala Glu Leu Lys Val Leu Ser Ala Asn Asn Glu
305          310          315          320
Glu His Glu Ala Glu Arg Val Thr Gly Glu Leu Ile Ala His His Phe

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          325          330          335
Val Asn Lys Thr Gln Tyr Lys Asp Tyr Ala Ile Leu Tyr Arg Gly Asn
          340          345          350
His Gln Ser Arg Val Phe Glu Lys Phe Leu Met Gln Asn Arg Ile Pro
          355          360          365
Tyr Lys Ile Ser Gly Gly Thr Ser Phe Phe Ser Arg Pro Glu Ile Lys
          370          375          380
Asp Leu Leu Ala Tyr Leu Arg Val Leu Thr Asn Pro Asp Asp Asp Ser
385          390          395          400
Ala Phe Leu Arg Ile Val Asn Thr Pro Lys Arg Glu Ile Gly Pro Ala
          405          410          415
Thr Leu Lys Lys Leu Gly Glu Trp Ala Met Thr Arg Asn Lys Ser Met
          420          425          430
Phe Thr Ala Ser Phe Asp Met Gly Leu Ser Gln Thr Leu Ser Gly Arg
          435          440          445
Gly Tyr Glu Ala Leu Thr Arg Phe Thr His Trp Leu Ala Glu Ile Gln
          450          455          460
Arg Leu Ala Glu Arg Glu Pro Ile Ala Ala Val Arg Asp Leu Ile His
465          470          475          480
Gly Met Asp Tyr Glu Ser Trp Leu Tyr Glu Thr Ser Pro Ser Pro Lys
          485          490          495
Ala Ala Glu Met Arg Met Lys Asn Val Asn Gln Leu Phe Ser Trp Met
          500          505          510
Thr Glu Met Leu Glu Gly Ser Glu Leu Asp Glu Pro Met Thr Leu Thr
          515          520          525
Gln Val Val Thr Arg Phe Thr Leu Arg Asp Met Met Glu Arg Gly Glu
          530          535          540
Ser Glu Glu Glu Leu Asp Gln Val Gln Leu Met Thr Leu His Ala Ser
545          550          555          560
Lys Gly Leu Glu Phe Pro Tyr Val Tyr Met Val Gly Met Glu Glu Gly
          565          570          575
Phe Leu Pro His Gln Ser Ser Ile Asp Glu Asp Asn Ile Asp Glu Glu
          580          585          590
Arg Arg Leu Ala Tyr Val Gly Ile Thr Arg Ala Gln Lys Glu Leu Thr
          595          600          605
Phe Thr Leu Cys Lys Glu Arg Arg Gln Tyr Gly Glu Leu Val Arg Pro
          610          615          620
Glu Pro Ser Arg Phe Leu Leu Glu Leu Pro Gln Asp Asp Leu Ile Trp
625          630          635          640
Glu Gln Glu Arg Lys Val Val Ser Ala Glu Glu Arg Met Gln Lys Gly
          645          650          655
Gln Ser His Leu Ala Asn Leu Lys Ala Met Met Ala Ala Lys Arg Gly
          660          665          670
Lys

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<210> 329

<211> 403

<212> PRT

<213> Escherichia coli

<400> 329

```

Met Met Val Thr Val Val Ser Asn Tyr Cys Gln Leu Ser Gln Thr Gln
 1          5          10          15
Leu Ser Gln Thr Phe Ala Glu Lys Phe Thr Val Thr Glu Glu Leu Leu
          20          25          30
Gln Ser Leu Lys Lys Thr Ala Leu Ser Gly Asp Glu Glu Ser Ile Glu
          35          40          45
Leu Leu His Asn Ile Ala Leu Gly Tyr Asp Lys Phe Gly Lys Glu Ala
50          55          60

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Glu Asp Ile Leu Tyr His Ile Val Arg Thr Pro Thr Asn Glu Thr Leu
 65 70 75 80
 Ser Ile Ile Arg Leu Ile Lys Asn Ala Cys Leu Lys Leu Tyr Asn Leu
 85 90 95
 Ala His Ile Ala Thr Asn Ser Pro Leu Lys Ser His Asp Ser Asp Asp
 100 105 110
 Leu Leu Phe Lys Lys Leu Phe Ser Pro Ser Lys Leu Met Thr Ile Ile
 115 120 125
 Gly Asp Glu Ile Pro Leu Ile Ser Glu Lys Gln Ser Leu Ser Lys Val
 130 135 140
 Leu Leu Asn Asp Glu Asn Asn Glu Leu Ser Asp Gly Thr Asn Phe Trp
 145 150 155 160
 Asp Lys Asn Arg Gln Leu Thr Thr Asp Glu Ile Ala Cys Tyr Leu Gln
 165 170 175
 Lys Ile Ala Ala Asn Ala Lys Asn Thr Gln Val Asn Tyr Pro Thr Gly
 180 185 190
 Leu Tyr Val Pro Tyr Ser Thr Arg Thr His Leu Glu Asp Ala Leu Asn
 195 200 205
 Glu Asn Ile Lys Ser Asp Pro Ser Trp Pro Asn Glu Val Gln Leu Phe
 210 215 220
 Pro Ile Asn Thr Gly Gly His Trp Ile Leu Val Ser Leu Gln Lys Ile
 225 230 235 240
 Val Asn Lys Lys Asn Asn Lys Leu Gln Ile Lys Cys Val Ile Phe Asn
 245 250 255
 Ser Leu Arg Ala Leu Gly Tyr Asp Lys Glu Asn Ser Leu Lys Arg Val
 260 265 270
 Ile Asn Ser Phe Asn Ser Glu Leu Met Gly Glu Met Ser Asn Asn Asn
 275 280 285
 Ile Lys Val His Leu Asn Glu Pro Glu Ile Ile Phe Leu His Ala Asp
 290 295 300
 Leu Gln Gln Tyr Leu Ser Gln Ser Cys Gly Ala Phe Val Cys Met Ala
 305 310 315 320
 Ala Gln Glu Val Ile Glu Gln Arg Glu Ser Asn Ser Asp Ser Ala Pro
 325 330 335
 Tyr Thr Leu Leu Lys Asn His Ala Asp Arg Phe Lys Lys Tyr Ser Ala
 340 345 350
 Glu Glu Gln Tyr Glu Ile Asp Phe Gln His Arg Leu Ala Asn Arg Asn
 355 360 365
 Cys Tyr Leu Asp Lys Tyr Gly Asp Ala Asn Ile Asn His Tyr Tyr Arg
 370 375 380
 Asn Leu Glu Ile Lys His Ser Gln Pro Lys Asn Arg Ala Ser Gly Lys
 385 390 395 400
 Arg Val Ser

<210> 330

<211> 296

<212> PRT

<213> Escherichia coli

<400> 330

Met Met Phe Lys Gln Tyr Leu Gln Val Thr Lys Pro Gly Ile Ile Phe
 1 5 10 15
 Gly Asn Leu Ile Ser Val Ile Gly Gly Phe Leu Leu Ala Ser Lys Gly
 20 25 30
 Ser Ile Asp Tyr Pro Leu Phe Ile Tyr Thr Leu Val Gly Val Ser Leu
 35 40 45
 Val Val Ala Ser Gly Cys Val Phe Asn Asn Tyr Ile Asp Arg Asp Ile
 50 55 60
 Asp Arg Lys Met Glu Arg Thr Lys Asn Arg Val Leu Val Lys Gly Leu

65					70					75					80
Ile	Ser	Pro	Ala	Val	Ser	Leu	Val	Tyr	Ala	Thr	Leu	Leu	Gly	Ile	Ala
				85					90					95	
Gly	Phe	Met	Leu	Leu	Trp	Phe	Gly	Ala	Asn	Pro	Leu	Ala	Cys	Trp	Leu
			100					105					110		
Gly	Val	Met	Gly	Phe	Val	Val	Tyr	Val	Gly	Val	Tyr	Ser	Leu	Tyr	Met
		115					120					125			
Lys	Arg	His	Ser	Val	Tyr	Gly	Thr	Leu	Ile	Gly	Ser	Leu	Ser	Gly	Ala
		130				135					140				
Ala	Pro	Pro	Val	Ile	Gly	Tyr	Cys	Ala	Val	Thr	Gly	Glu	Phe	Asp	Ser
145					150					155					160
Gly	Ala	Ala	Ile	Leu	Leu	Ala	Ile	Phe	Ser	Leu	Trp	Gln	Met	Pro	His
				165					170					175	
Ser	Tyr	Ala	Ile	Ala	Ile	Phe	Arg	Phe	Lys	Asp	Tyr	Gln	Ala	Ala	Asn
			180					185					190		
Ile	Pro	Val	Leu	Pro	Val	Val	Lys	Gly	Ile	Ser	Val	Ala	Lys	Asn	His
		195					200					205			
Ile	Thr	Leu	Tyr	Ile	Ile	Ala	Phe	Ala	Val	Ala	Thr	Leu	Met	Leu	Ser
		210				215					220				
Leu	Gly	Gly	Tyr	Ala	Gly	Tyr	Lys	Tyr	Leu	Val	Val	Ala	Ala	Ala	Val
225					230					235					240
Ser	Val	Trp	Trp	Leu	Gly	Met	Ala	Leu	Arg	Gly	Tyr	Lys	Val	Ala	Asp
				245					250					255	
Asp	Arg	Ile	Trp	Ala	Arg	Lys	Leu	Phe	Gly	Phe	Ser	Ile	Ile	Ala	Ile
			260					265					270		
Thr	Ala	Leu	Ser	Val	Met	Met	Ser	Val	Asp	Phe	Met	Val	Pro	Asp	Ser
		275					280					285			
His	Thr	Leu	Leu	Ala	Ala	Val	Trp								
		290				295									

<210> 331

<211> 315

<212> PRT

<213> Escherichia coli

<400> 331

Met	Arg	Leu	Arg	Lys	Tyr	Asn	Lys	Ser	Leu	Gly	Trp	Leu	Ser	Leu	Phe
1				5					10					15	
Ala	Gly	Thr	Val	Leu	Leu	Ser	Gly	Cys	Asn	Ser	Ala	Leu	Leu	Asp	Pro
			20					25					30		
Lys	Gly	Gln	Ile	Gly	Leu	Glu	Gln	Arg	Ser	Leu	Ile	Leu	Thr	Ala	Phe
		35					40					45			
Gly	Leu	Met	Leu	Ile	Val	Val	Ile	Pro	Ala	Ile	Leu	Met	Ala	Val	Gly
		50				55					60				
Phe	Ala	Trp	Lys	Tyr	Arg	Ala	Ser	Asn	Lys	Asp	Ala	Lys	Tyr	Ser	Pro
65					70				75						80
Asn	Trp	Ser	His	Ser	Asn	Lys	Val	Glu	Ala	Val	Val	Trp	Thr	Val	Pro
			85						90				95		
Ile	Leu	Ile	Ile	Ile	Phe	Leu	Ala	Val	Leu	Thr	Trp	Lys	Thr	Thr	His
			100					105					110		
Ala	Leu	Glu	Pro	Ser	Lys	Pro	Leu	Ala	His	Asp	Glu	Lys	Pro	Ile	Thr
			115				120					125			
Ile	Glu	Val	Val	Ser	Met	Asp	Trp	Lys	Trp	Phe	Phe	Ile	Tyr	Pro	Glu
		130				135					140				
Gln	Gly	Ile	Ala	Thr	Val	Asn	Glu	Ile	Ala	Phe	Pro	Ala	Asn	Thr	Pro
145					150					155					160
Val	Tyr	Phe	Lys	Val	Thr	Ser	Asn	Ser	Val	Met	Asn	Ser	Phe	Phe	Ile
				165					170					175	
Pro	Arg	Leu	Gly	Ser	Gln	Ile	Tyr	Ala	Met	Ala	Gly	Met	Gln	Thr	Arg
			180					185					190		

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Leu His Leu Ile Ala Asn Glu Pro Gly Thr Tyr Asp Gly Ile Ser Ala
    195                200                205
Ser Tyr Ser Gly Pro Gly Phe Ser Gly Met Lys Phe Lys Ala Ile Ala
    210                215                220
Thr Pro Asp Arg Ala Ala Phe Asp Gln Trp Val Ala Lys Ala Lys Gln
    225                230                235                240
Ser Pro Asn Thr Met Ser Asp Met Ala Ala Phe Glu Lys Leu Ala Ala
    245                250                255
Pro Ser Glu Tyr Asn Gln Val Glu Tyr Phe Ser Asn Val Lys Pro Asp
    260                265                270
Leu Phe Ala Asp Val Ile Asn Lys Phe Met Ala His Gly Lys Ser Met
    275                280                285
Asp Met Thr Gln Pro Glu Gly Glu His Ser Ala His Glu Gly Met Glu
    290                295                300
Gly Met Asp Met Ser His Ala Glu Ser Ala His
    305                310                315

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<210> 332

<211> 663

<212> PRT

<213> Escherichia coli

<400> 332

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Met Phe Gly Lys Leu Ser Leu Asp Ala Val Pro Phe His Glu Pro Ile
  1          5          10          15
Val Met Val Thr Ile Ala Gly Ile Ile Leu Gly Gly Leu Ala Leu Val
    20          25          30
Gly Leu Ile Thr Tyr Phe Gly Lys Trp Thr Tyr Leu Trp Lys Glu Trp
    35          40          45
Leu Thr Ser Val Asp His Lys Arg Leu Gly Ile Met Tyr Ile Ile Val
    50          55          60
Ala Ile Val Met Leu Leu Arg Gly Phe Ala Asp Ala Ile Met Met Arg
    65          70          75          80
Ser Gln Gln Ala Leu Ala Ser Ala Gly Glu Ala Gly Phe Leu Pro Pro
    85          90          95
His His Tyr Asp Gln Ile Phe Thr Ala His Gly Val Ile Met Ile Phe
    100         105         110
Phe Val Ala Met Pro Phe Val Ile Gly Leu Met Asn Leu Val Val Pro
    115         120         125
Leu Gln Ile Gly Ala Arg Asp Val Ala Phe Pro Phe Leu Asn Asn Leu
    130         135         140
Ser Phe Trp Phe Thr Val Val Gly Val Ile Leu Val Asn Val Ser Leu
    145         150         155         160
Gly Val Gly Glu Phe Ala Gln Thr Gly Trp Leu Ala Tyr Pro Pro Leu
    165         170         175
Ser Gly Ile Glu Tyr Ser Pro Gly Val Gly Val Asp Tyr Trp Ile Trp
    180         185         190
Ser Leu Gln Leu Ser Gly Ile Gly Thr Thr Leu Thr Gly Ile Asn Phe
    195         200         205
Phe Val Thr Ile Leu Lys Met Arg Ala Pro Gly Met Thr Met Phe Lys
    210         215         220
Met Pro Val Phe Thr Trp Ala Ser Leu Cys Ala Asn Val Leu Ile Ile
    225         230         235         240
Ala Ser Phe Pro Ile Leu Thr Val Thr Val Ala Leu Leu Thr Leu Asp
    245         250         255
Arg Tyr Leu Gly Thr His Phe Phe Thr Asn Asp Met Gly Gly Asn Met
    260         265         270
Met Met Tyr Ile Asn Leu Ile Trp Ala Trp Gly His Pro Glu Val Tyr
    275         280         285
Ile Leu Ile Leu Pro Val Phe Gly Val Phe Ser Glu Ile Ala Ala Thr

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290
 Phe Ser Arg Lys Arg Leu Phe Gly Tyr Thr Ser Leu Val Trp Ala Thr
 305 310 315 320
 Val Cys Ile Thr Val Leu Ser Phe Ile Val Trp Leu His His Phe Phe
 325 330 335
 Thr Met Gly Ala Gly Ala Asn Val Asn Ala Phe Phe Gly Ile Thr Thr
 340 345 350
 Met Ile Ile Ala Ile Pro Thr Gly Val Lys Ile Phe Asn Trp Leu Phe
 355 360 365
 Thr Met Tyr Gln Gly Arg Ile Val Phe His Ser Ala Met Leu Trp Thr
 370 375 380
 Ile Gly Phe Ile Val Thr Phe Ser Val Gly Gly Met Thr Gly Val Leu
 385 390 395 400
 Leu Ala Val Pro Gly Ala Asp Phe Val Leu His Asn Ser Leu Phe Leu
 405 410 415
 Ile Ala His Phe His Asn Val Ile Ile Gly Gly Val Val Phe Gly Cys
 420 425 430
 Phe Ala Gly Met Thr Tyr Trp Trp Pro Lys Ala Phe Gly Phe Lys Leu
 435 440 445
 Asn Glu Thr Trp Gly Lys Arg Ala Phe Trp Phe Trp Ile Ile Gly Phe
 450 455 460
 Phe Val Ala Phe Met Pro Leu Tyr Ala Leu Gly Phe Met Gly Met Thr
 465 470 475 480
 Arg Arg Leu Ser Gln Gln Ile Asp Pro Gln Phe His Thr Met Leu Met
 485 490 495
 Ile Ala Ala Ser Gly Ala Val Leu Ile Ala Leu Gly Ile Leu Cys Leu
 500 505 510
 Val Ile Gln Met Tyr Val Ser Ile Arg Asp Arg Asp Gln Asn Arg Asp
 515 520 525
 Leu Thr Gly Asp Pro Trp Gly Gly Arg Thr Leu Glu Trp Ala Thr Ser
 530 535 540
 Ser Pro Pro Pro Phe Tyr Asn Phe Ala Val Val Pro His Val His Glu
 545 550 555 560
 Arg Asp Ala Phe Trp Glu Met Lys Glu Lys Gly Glu Ala Tyr Lys Lys
 565 570 575
 Pro Asp His Tyr Glu Glu Ile His Met Pro Lys Asn Ser Gly Ala Gly
 580 585 590
 Ile Val Ile Ala Ala Phe Ser Thr Ile Phe Gly Phe Ala Met Ile Trp
 595 600 605
 His Ile Trp Trp Leu Ala Ile Val Gly Phe Ala Gly Met Ile Ile Thr
 610 615 620
 Trp Ile Val Lys Ser Phe Asp Glu Asp Val Asp Tyr Tyr Val Pro Val
 625 630 635 640
 Ala Glu Ile Glu Lys Leu Glu Asn Gln His Phe Asp Glu Ile Thr Lys
 645 650 655
 Ala Gly Leu Lys Asn Gly Asn
 660

<210> 333

<211> 204

<212> PRT

<213> Escherichia coli

<400> 333

Met Ala Thr Asp Thr Leu Thr His Ala Thr Ala His Ala His Glu His
 1 5 10 15
 Gly His His Asp Ala Gly Gly Thr Lys Ile Phe Gly Phe Trp Ile Tyr
 20 25 30
 Leu Met Ser Asp Cys Ile Leu Phe Ser Ile Leu Phe Ala Thr Tyr Ala
 35 40 45

Val Leu Val Asn Gly Thr Ala Gly Gly Pro Thr Gly Lys Asp Ile Phe
 50 55 60
 Glu Leu Pro Phe Val Leu Val Glu Thr Phe Leu Leu Phe Ser Ser
 65 70 75 80
 Ile Thr Tyr Gly Met Ala Ala Ile Ala Met Tyr Lys Asn Asn Lys Ser
 85 90 95
 Gln Val Ile Ser Trp Leu Ala Leu Thr Trp Leu Phe Gly Ala Gly Phe
 100 105 110
 Ile Gly Met Glu Ile Tyr Glu Phe His His Leu Ile Val Asn Gly Met
 115 120 125
 Gly Pro Asp Arg Ser Gly Phe Leu Ser Ala Phe Phe Ala Leu Val Gly
 130 135 140
 Thr His Gly Leu His Val Thr Ser Gly Leu Ile Trp Met Ala Val Leu
 145 150 155 160
 Met Val Gln Ile Ala Arg Arg Gly Leu Thr Ser Thr Asn Arg Thr Arg
 165 170 175
 Ile Met Cys Leu Ser Leu Phe Trp His Phe Leu Asp Val Val Trp Ile
 180 185 190
 Cys Val Phe Thr Val Val Tyr Leu Met Gly Ala Met
 195 200

<210> 334
 <211> 109
 <212> PRT
 <213> Escherichia coli

<400> 334
 Met Ser His Ser Thr Asp His Ser Gly Ala Ser His Gly Ser Val Lys
 1 5 10 15
 Thr Tyr Met Thr Gly Phe Ile Leu Ser Ile Ile Leu Thr Val Ile Pro
 20 25 30
 Phe Trp Met Val Met Thr Gly Ala Ala Ser Pro Ala Val Ile Leu Gly
 35 40 45
 Thr Ile Leu Ala Met Ala Val Val Gln Val Leu Val His Leu Val Cys
 50 55 60
 Phe Leu His Met Asn Thr Lys Ser Asp Glu Gly Trp Asn Met Thr Ala
 65 70 75 80
 Phe Val Phe Thr Val Leu Ile Ile Ala Ile Leu Val Val Gly Ser Ile
 85 90 95
 Trp Ile Met Trp Asn Leu Asn Tyr Asn Met Met Met His
 100 105

<210> 335
 <211> 587
 <212> PRT
 <213> Escherichia coli

<400> 335
 Met Gln Trp Gln Thr Lys Leu Pro Leu Ile Ala Ile Leu Arg Gly Ile
 1 5 10 15
 Thr Pro Asp Glu Ala Leu Ala His Val Gly Ala Val Ile Asp Ala Gly
 20 25 30
 Phe Asp Ala Val Glu Ile Pro Leu Asn Ser Pro Gln Trp Glu Gln Ser
 35 40 45
 Ile Pro Ala Ile Val Asp Ala Tyr Gly Asp Lys Ala Leu Ile Gly Ala
 50 55 60
 Gly Thr Val Leu Lys Pro Glu Gln Val Asp Ala Leu Ala Arg Met Gly
 65 70 75 80
 Cys Gln Leu Ile Val Thr Pro Asn Ile His Ser Glu Val Ile Arg Arg
 85 90 95

Ala	Val	Gly	Tyr	Gly	Met	Thr	Val	Cys	Pro	Gly	Cys	Ala	Thr	Ala	Thr	100	105	110
Glu	Ala	Phe	Thr	Ala	Leu	Glu	Ala	Gly	Ala	Ala	Gly	Ala	Glu	Asn	Ile	115	120	125
Ser	Val	Ile	Gly	Phe	Trp	Ser	Ala	Ile	His	Gln	Ser	Val	Lys	Ser	Gly	130	135	140
Ile	Ala	Ile	Gly	His	Arg	Ser	Leu	Cys	Arg	Trp	Arg	Arg	Asp	Ala	Glu	145	150	155
Asn	Leu	Ala	Gln	Trp	Ile	Asp	Ala	Gly	Cys	Ala	Gly	Ala	Gly	Leu	Gly	165	170	175
Ser	Asp	Leu	Tyr	Arg	Ala	Gly	Gln	Ser	Val	Glu	Arg	Thr	Ala	Gln	Gln	180	185	190
Ala	Ala	Ala	Phe	Val	Lys	Ala	Tyr	Arg	Glu	Ala	Gly	Ala	Met	Lys	Ile	195	200	205
Thr	Lys	Ile	Thr	Thr	Tyr	Arg	Leu	Pro	Pro	Arg	Trp	Met	Phe	Leu	Lys	210	215	220
Ile	Glu	Thr	Asp	Glu	Gly	Val	Val	Gly	Trp	Gly	Glu	Pro	Val	Ile	Glu	225	230	235
Gly	Arg	Ala	Arg	Thr	Val	Glu	Ala	Ala	Val	His	Glu	Leu	Gly	Asp	Tyr	245	250	255
Leu	Ile	Gly	Gln	Asp	Pro	Ser	Arg	Ile	Asn	Asp	Leu	Trp	Gln	Val	Met	260	265	270
Tyr	Arg	Ala	Gly	Phe	Tyr	Arg	Gly	Gly	Pro	Ile	Leu	Met	Ser	Ala	Ile	275	280	285
Ala	Gly	Ile	Asp	Gln	Ala	Leu	Trp	Asp	Ile	Lys	Gly	Lys	Val	Leu	Asn	290	295	300
Ala	Pro	Val	Trp	Gln	Leu	Met	Gly	Gly	Leu	Val	Arg	Asp	Lys	Ile	Lys	305	310	315
Ala	Tyr	Ser	Trp	Val	Gly	Gly	Asp	Arg	Pro	Ala	Asp	Val	Ile	Asp	Gly	325	330	335
Ile	Lys	Thr	Leu	Arg	Glu	Ile	Gly	Phe	Asp	Thr	Phe	Lys	Leu	Asn	Gly	340	345	350
Cys	Glu	Glu	Leu	Gly	Leu	Ile	Asp	Asn	Ser	Arg	Ala	Val	Asp	Ala	Ala	355	360	365
Val	Asn	Thr	Val	Ala	Gln	Ile	Arg	Glu	Ala	Phe	Gly	Asn	Gln	Ile	Glu	370	375	380
Phe	Gly	Leu	Asp	Phe	His	Gly	Arg	Val	Ser	Ala	Pro	Met	Ala	Lys	Val	385	390	395
Leu	Ile	Lys	Glu	Leu	Glu	Pro	Tyr	Arg	Pro	Leu	Phe	Ile	Glu	Glu	Pro	405	410	415
Val	Leu	Ala	Glu	Gln	Ala	Glu	Tyr	Tyr	Pro	Lys	Leu	Ala	Ala	Gln	Thr	420	425	430
His	Ile	Pro	Leu	Ala	Ala	Gly	Glu	Arg	Met	Phe	Ser	Arg	Phe	Asp	Phe	435	440	445
Lys	Arg	Val	Leu	Glu	Ala	Gly	Gly	Ile	Ser	Ile	Leu	Gln	Pro	Asp	Leu	450	455	460
Ser	His	Ala	Gly	Gly	Ile	Thr	Glu	Cys	Tyr	Lys	Ile	Ala	Gly	Met	Ala	465	470	475
Glu	Ala	Tyr	Asp	Val	Thr	Leu	Ala	Pro	His	Cys	Pro	Leu	Gly	Pro	Ile	485	490	495
Ala	Leu	Ala	Ala	Cys	Leu	His	Ile	Asp	Phe	Val	Ser	Tyr	Asn	Ala	Val	500	505	510
Leu	Gln	Glu	Gln	Ser	Met	Gly	Ile	His	Tyr	Asn	Lys	Gly	Ala	Glu	Leu	515	520	525
Leu	Asp	Phe	Val	Lys	Asn	Lys	Glu	Asp	Phe	Ser	Met	Val	Gly	Gly	Phe	530	535	540
Phe	Lys	Pro	Leu	Thr	Lys	Pro	Gly	Leu	Gly	Val	Glu	Ile	Asp	Glu	Ala	545	550	555
Lys	Val	Ile	Glu	Phe	Ser	Lys	Asn	Ala	Pro	Asp	Trp	Arg	Asn	Pro	Leu	565	570	575

Trp Arg His Glu Asp Asn Ser Val Ala Glu Trp
 580 585

<210> 336
 <211> 292
 <212> PRT
 <213> Escherichia coli

<400> 336
 Met Thr Ala Arg Tyr Ile Ala Ile Asp Trp Gly Ser Thr Asn Leu Arg
 1 5 10 15
 Ala Trp Leu Tyr Gln Gly Asp His Cys Leu Glu Ser Arg Gln Ser Glu
 20 25 30
 Ala Gly Val Thr Arg Leu Asn Gly Lys Ser Pro Ala Ala Val Leu Ala
 35 40 45
 Glu Val Thr Thr Asp Trp Arg Glu Glu Lys Thr Pro Val Val Met Ala
 50 55 60
 Gly Met Val Gly Ser Asn Val Gly Trp Lys Val Ala Pro Tyr Leu Ser
 65 70 75 80
 Val Pro Ala Cys Phe Ser Ser Ile Gly Glu Gln Leu Thr Ser Val Gly
 85 90 95
 Asp Asn Ile Trp Ile Ile Pro Gly Leu Cys Val Ser His Asp Asn
 100 105 110
 His Asn Val Met Arg Gly Glu Glu Thr Gln Leu Ile Gly Ala Arg Ala
 115 120 125
 Leu Ala Pro Ser Ser Leu Tyr Val Met Pro Gly Thr His Cys Lys Trp
 130 135 140
 Val Gln Ala Asp Ser Gln Gln Ile Asn Asp Phe Arg Thr Val Met Thr
 145 150 155 160
 Gly Glu Leu His His Leu Leu Leu Asn His Ser Leu Ile Gly Ala Gly
 165 170 175
 Leu Pro Pro Gln Glu Asn Ser Ala Asp Ala Phe Thr Ala Gly Leu Glu
 180 185 190
 Arg Gly Leu Asn Thr Pro Ala Ile Leu Pro Gln Leu Phe Glu Val Arg
 195 200 205
 Ala Ser His Val Leu Gly Thr Leu Pro Arg Glu Gln Val Ser Glu Phe
 210 215 220
 Leu Ser Gly Leu Leu Ile Gly Ala Glu Val Ala Ser Met Arg Asp Tyr
 225 230 235 240
 Val Ala His Gln His Ala Ile Thr Leu Val Ala Gly Thr Ser Leu Thr
 245 250 255
 Ala Arg Tyr Gln Gln Ala Phe Gln Ala Met Gly Cys Asp Val Thr Ala
 260 265 270
 Val Ala Gly Asp Thr Ala Phe Gln Ala Gly Ile Arg Ser Ile Ala His
 275 280 285
 Ala Val Ala Asn
 290

<210> 337
 <211> 128
 <212> PRT
 <213> Escherichia coli

<400> 337
 Met Thr Leu Asn Lys Thr Asp Arg Ile Val Ile Thr Leu Gly Lys Gln
 1 5 10 15
 Ile Val His Gly Lys Tyr Val Pro Gly Ser Pro Leu Pro Ala Glu Ala
 20 25 30
 Glu Leu Cys Glu Glu Phe Ala Thr Ser Arg Asn Ile Ile Arg Glu Val
 35 40 45

Phe Arg Ser Leu Met Ala Lys Arg Leu Ile Glu Met Lys Arg Tyr Arg
 50 55 60
 Gly Ala Phe Val Ala Pro Arg Asn Gln Trp Asn Tyr Leu Asp Thr Asp
 65 70 75 80
 Val Leu Gln Trp Val Leu Glu Asn Asp Tyr Asp Pro Arg Leu Ile Ser
 85 90 95
 Ala Met Ser Glu Val Arg Asn Leu Val Glu Pro Ala Ile Ala Arg Trp
 100 105 110
 Glu Gln Ser Ala Arg Leu Pro Ala Ile Trp Arg Arg Leu Asn Arg Arg
 115 120 125

<210> 338
 <211> 98
 <212> PRT
 <213> Escherichia coli

<400> 338
 Met Ile Ala Asn Asn Gln Asp Arg Glu Ala Phe Asn Glu Ala Asp Ile
 1 5 10 15
 Arg Tyr His Glu Ala Val Leu Gln Ser Val His Asn Pro Val Leu Gln
 20 25 30
 Gln Leu Ser Ile Ala Ile Ser Ser Leu Gln Arg Ala Val Phe Glu Arg
 35 40 45
 Thr Trp Met Gly Asp Glu Ala Asn Met Pro Gln Thr Leu Gln Glu His
 50 55 60
 Lys Ala Leu Phe Asp Ala Ile Arg His Gln Asp Gly Asp Ala Ala Glu
 65 70 75 80
 Gln Ala Ala Leu Thr Met Ile Ala Ser Ser Thr Arg Arg Leu Lys Glu
 85 90 95
 Ile Thr

<210> 339
 <211> 118
 <212> PRT
 <213> Escherichia coli

<400> 339
 Met Ala Arg Val Lys Arg Gly Val Ile Ala Arg Ala Arg His Lys Lys
 1 5 10 15
 Ile Leu Lys Gln Ala Lys Gly Tyr Tyr Gly Ala Arg Ser Arg Val Tyr
 20 25 30
 Arg Val Ala Phe Gln Ala Val Ile Lys Ala Gly Gln Tyr Ala Tyr Arg
 35 40 45
 Asp Arg Arg Gln Arg Lys Arg Gln Phe Arg Gln Leu Trp Ile Ala Arg
 50 55 60
 Ile Asn Ala Ala Ala Arg Gln Asn Gly Ile Ser Tyr Ser Lys Phe Ile
 65 70 75 80
 Asn Gly Leu Lys Lys Ala Ser Val Glu Ile Asp Arg Lys Ile Leu Ala
 85 90 95
 Asp Ile Ala Val Phe Asp Lys Val Ala Phe Thr Ala Leu Val Glu Lys
 100 105 110
 Ala Lys Ala Ala Leu Ala
 115

<210> 340
 <211> 65
 <212> PRT
 <213> Escherichia coli

<400> 340

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Met Pro Lys Ile Lys Thr Val Arg Gly Ala Ala Lys Arg Phe Lys Lys
 1           5           10           15
Thr Gly Lys Gly Gly Phe Lys His Lys His Ala Asn Leu Arg His Ile
           20           25           30
Leu Thr Lys Lys Ala Thr Lys Arg Lys Arg His Leu Arg Pro Lys Ala
           35           40           45
Met Val Ser Lys Gly Asp Leu Gly Leu Val Ile Ala Cys Leu Pro Tyr
 50           55           60
Ala
65

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<210> 341

<211> 180

<212> PRT

<213> Escherichia coli

<400> 341

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Met Lys Gly Gly Lys Arg Val Gln Thr Ala Arg Pro Asn Arg Ile Asn
 1           5           10           15
Gly Glu Ile Arg Ala Gln Glu Val Arg Leu Thr Gly Leu Glu Gly Glu
           20           25           30
Gln Leu Gly Ile Val Ser Leu Arg Glu Ala Leu Glu Lys Ala Glu Glu
           35           40           45
Ala Gly Val Asp Leu Val Glu Ile Ser Pro Asn Ala Glu Pro Pro Val
           50           55           60
Cys Arg Ile Met Asp Tyr Gly Lys Phe Leu Tyr Glu Lys Ser Lys Ser
65           70           75           80
Ser Lys Glu Gln Lys Lys Lys Gln Lys Val Ile Gln Val Lys Glu Ile
           85           90           95
Lys Phe Arg Pro Gly Thr Asp Glu Gly Asp Tyr Gln Val Lys Leu Arg
           100          105          110
Ser Leu Ile Arg Phe Leu Glu Glu Gly Asp Lys Ala Lys Ile Thr Leu
           115          120          125
Arg Phe Arg Gly Arg Glu Met Ala His Gln Gln Ile Gly Met Glu Val
           130          135          140
Leu Asn Arg Val Lys Asp Asp Leu Gln Glu Leu Ala Val Val Glu Ser
145           150           155           160
Phe Pro Thr Lys Ile Glu Gly Arg Gln Met Ile Met Val Leu Ala Pro
           165          170          175
Lys Lys Lys Gln
           180

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<210> 342

<211> 642

<212> PRT

<213> Escherichia coli

<400> 342

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Met Pro Val Ile Thr Leu Pro Asp Gly Ser Gln Arg His Tyr Asp His
 1           5           10           15
Ala Val Ser Pro Met Asp Val Ala Leu Asp Ile Gly Pro Gly Leu Ala
           20           25           30
Lys Ala Cys Ile Ala Gly Arg Val Asn Gly Glu Leu Val Asp Ala Cys
           35           40           45
Asp Leu Ile Glu Asn Asp Ala Gln Leu Ser Ile Ile Thr Ala Lys Asp
50           55           60
Glu Glu Gly Leu Glu Ile Ile Arg His Ser Cys Ala His Leu Leu Gly
65           70           75           80
His Ala Ile Lys Gln Leu Trp Pro His Thr Lys Met Ala Ile Gly Pro

```

				85					90					95		
Val	Ile	Asp	Asn	Gly	Phe	Tyr	Tyr	Asp	Val	Asp	Leu	Asp	Arg	Thr	Leu	
			100					105					110			
Thr	Gln	Glu	Asp	Val	Glu	Ala	Leu	Glu	Lys	Arg	Met	His	Glu	Leu	Ala	
		115					120					125				
Glu	Lys	Asn	Tyr	Asp	Val	Ile	Lys	Lys	Lys	Val	Ser	Trp	His	Glu	Ala	
	130					135					140					
Arg	Glu	Thr	Phe	Ala	Asn	Arg	Gly	Glu	Ser	Tyr	Lys	Val	Ser	Ile	Leu	
145				150						155					160	
Asp	Glu	Asn	Ile	Ala	His	Asp	Asp	Lys	Pro	Gly	Leu	Tyr	Phe	His	Glu	
			165						170					175		
Glu	Tyr	Val	Asp	Met	Cys	Arg	Gly	Pro	His	Val	Pro	Asn	Met	Arg	Phe	
			180					185					190			
Cys	His	His	Phe	Lys	Leu	Met	Lys	Thr	Ala	Gly	Ala	Tyr	Trp	Arg	Gly	
	195						200					205				
Asp	Ser	Asn	Asn	Lys	Met	Leu	Gln	Arg	Ile	Tyr	Gly	Thr	Ala	Trp	Ala	
	210				215						220					
Asp	Lys	Lys	Ala	Leu	Asn	Ala	Tyr	Leu	Gln	Arg	Leu	Glu	Glu	Ala	Ala	
225				230						235					240	
Lys	Arg	Asp	His	Arg	Lys	Ile	Gly	Lys	Gln	Leu	Asp	Leu	Tyr	His	Met	
			245						250					255		
Gln	Glu	Glu	Ala	Pro	Gly	Met	Val	Phe	Trp	His	Asn	Asp	Gly	Trp	Thr	
			260					265					270			
Ile	Phe	Arg	Glu	Leu	Glu	Val	Phe	Val	Arg	Ser	Lys	Leu	Lys	Glu	Tyr	
	275					280						285				
Gln	Tyr	Gln	Glu	Val	Lys	Gly	Pro	Phe	Met	Met	Asp	Arg	Val	Leu	Trp	
	290					295					300					
Glu	Lys	Thr	Gly	His	Trp	Asp	Asn	Tyr	Lys	Asp	Ala	Met	Phe	Thr	Thr	
305				310						315					320	
Ser	Ser	Glu	Asn	Arg	Glu	Tyr	Cys	Ile	Lys	Pro	Met	Asn	Cys	Pro	Gly	
			325						330					335		
His	Val	Gln	Ile	Phe	Asn	Gln	Gly	Leu	Lys	Ser	Tyr	Arg	Asp	Leu	Pro	
			340					345					350			
Leu	Arg	Met	Ala	Glu	Phe	Gly	Ser	Cys	His	Arg	Asn	Glu	Pro	Ser	Gly	
		355				360						365				
Ser	Leu	His	Gly	Leu	Met	Arg	Val	Arg	Gly	Phe	Thr	Gln	Asp	Asp	Ala	
	370					375					380					
His	Ile	Phe	Cys	Thr	Glu	Gln	Ile	Arg	Asp	Glu	Val	Asn	Gly	Cys		
385				390					395					400		
Ile	Arg	Leu	Val	Tyr	Asp	Met	Tyr	Ser	Thr	Phe	Gly	Phe	Glu	Lys	Ile	
			405						410					415		
Val	Val	Lys	Leu	Ser	Thr	Arg	Pro	Glu	Lys	Arg	Ile	Gly	Ser	Asp	Glu	
			420					425								

				565					570					575			
Lys	Ile	Gly	Phe	Lys	Ile	Arg	Glu	His	Thr	Leu	Arg	Arg	Val	Pro	Tyr		
			580					585					590				
Met	Leu	Val	Cys	Gly	Asp	Lys	Glu	Val	Glu	Ser	Gly	Lys	Val	Ala	Val		
		595					600					605					
Arg	Thr	Arg	Arg	Gly	Lys	Asp	Leu	Gly	Ser	Met	Asp	Val	Asn	Glu	Val		
	610					615					620						
Ile	Glu	Lys	Leu	Gln	Gln	Glu	Ile	Arg	Ser	Arg	Ser	Leu	Lys	Gln	Leu		
625				630						635					640		
Glu	Glu																

<210> 343

<211> 330

<212> PRT

<213> Escherichia coli

<400> 343

Met	Lys	Ile	Lys	Asn	Ile	Leu	Leu	Thr	Leu	Cys	Thr	Ser	Leu	Leu	Leu		
1				5					10					15			
Thr	Asn	Val	Ala	Ala	His	Ala	Lys	Glu	Val	Lys	Ile	Gly	Met	Ala	Ile		
		20						25					30				
Asp	Asp	Leu	Arg	Leu	Glu	Arg	Trp	Gln	Lys	Asp	Arg	Asp	Ile	Phe	Val		
		35					40					45					
Lys	Lys	Ala	Glu	Ser	Leu	Gly	Ala	Lys	Val	Phe	Val	Gln	Ser	Ala	Asn		
	50					55				60							
Gly	Asn	Glu	Glu	Thr	Gln	Met	Ser	Gln	Ile	Glu	Asn	Met	Ile	Asn	Arg		
65				70					75				80				
Gly	Val	Asp	Val	Leu	Val	Ile	Ile	Pro	Tyr	Asn	Gly	Gln	Val	Leu	Ser		
			85					90					95				
Asn	Val	Val	Lys	Glu	Ala	Lys	Gln	Glu	Gly	Ile	Lys	Val	Leu	Ala	Tyr		
		100						105					110				
Asp	Arg	Met	Ile	Asn	Asp	Ala	Asp	Ile	Asp	Phe	Tyr	Ile	Ser	Phe	Asp		
		115					120					125					
Asn	Glu	Lys	Val	Gly	Glu	Leu	Gln	Ala	Lys	Ala	Leu	Val	Asp	Ile	Val		
	130					135					140						
Pro	Gln	Gly	Asn	Tyr	Phe	Leu	Met	Gly	Gly	Ser	Pro	Val	Asp	Asn	Asn		
145				150						155				160			
Ala	Lys	Leu	Phe	Arg	Ala	Gly	Gln	Met	Lys	Val	Leu	Lys	Pro	Tyr	Val		
			165					170					175				
Asp	Ser	Gly	Lys	Ile	Lys	Val	Val	Gly	Asp	Gln	Trp	Val	Asp	Gly	Trp		
		180						185					190				
Leu	Pro	Glu	Asn	Ala	Leu	Lys	Ile	Met	Glu	Asn	Ala	Leu	Thr	Ala	Asn		
		195					200					205					
Asn	Asn	Lys	Ile	Asp	Ala	Val	Val	Ala	Ser	Asn	Asp	Ala	Thr	Ala	Gly		
	210					215					220						
Gly	Ala	Ile	Gln	Ala	Leu	Ser	Ala	Gln	Gly	Leu	Ser	Gly	Lys	Val	Ala		
225				230					235					240			
Ile	Ser	Gly	Gln	Asp	Ala	Asp	Leu	Ala	Gly	Ile	Lys	Arg	Ile	Ala	Ala		
			245					250					255				
Gly	Thr	Gln	Thr	Met	Thr	Val	Tyr	Lys	Pro	Ile	Thr	Leu	Leu	Ala	Asn		
		260						265					270				
Thr	Ala	Ala	Glu	Ile	Ala	Val	Glu	Leu	Gly	Asn	Gly	Gln	Glu	Pro	Lys		
		275					280					285					
Ala	Asp	Thr	Thr	Leu	Asn	Asn	Gly	Leu	Lys	Asp	Val	Pro	Ser	Arg	Leu		
	290					295					300						
Leu	Thr	Pro	Ile	Asp	Val	Asn	Lys	Asn	Asn	Ile	Lys	Asp	Thr	Val	Ile		
305				310						315					320		
Lys	Asp	Gly	Phe	His	Lys	Glu	Ser	Glu	Leu								
			325					330									

<210> 344
 <211> 55
 <212> PRT
 <213> Escherichia coli

<400> 344
 Met Asn Lys Phe Ile Lys Val Ala Leu Val Gly Ala Val Leu Ala Thr
 1 5 10 15
 Leu Thr Ala Cys Thr Gly His Ile Glu Asn Arg Asp Lys Asn Cys Ser
 20 25 30
 Tyr Asp Tyr Leu Leu His Pro Ala Ile Ser Ile Ser Lys Ile Ile Gly
 35 40 45
 Gly Cys Gly Pro Thr Ala Gln
 50 55

<210> 345
 <211> 462
 <212> PRT
 <213> Escherichia coli

<400> 345
 Met Thr Ala Asn Ser Pro Leu Gln Arg Ile Gly Gln Glu Lys Gly Ile
 1 5 10 15
 Ala Met Gly Ser Gln Glu Leu Gln Arg Lys Leu Gly Phe Trp Ala Val
 20 25 30
 Leu Ala Ile Ala Val Gly Thr Thr Val Gly Ser Gly Ile Phe Val Ser
 35 40 45
 Val Gly Glu Val Ala Lys Ala Ala Gly Thr Pro Trp Leu Thr Val Leu
 50 55 60
 Ala Phe Val Ile Gly Gly Leu Ile Val Ile Pro Gln Met Cys Val Tyr
 65 70 75 80
 Ala Glu Leu Ser Thr Ala Tyr Pro Glu Asn Gly Ala Asp Tyr Val Tyr
 85 90 95
 Leu Lys Asn Ala Gly Ser Arg Pro Leu Ala Phe Leu Ser Gly Trp Ala
 100 105 110
 Ser Phe Trp Ala Asn Asp Ala Pro Ser Leu Ser Ile Met Ala Leu Ala
 115 120 125
 Ile Val Ser Asn Leu Gly Phe Leu Thr Pro Ile Asp Pro Leu Leu Gly
 130 135 140
 Lys Phe Ile Ala Ala Gly Leu Ile Ile Ala Phe Met Leu Leu His Leu
 145 150 155 160
 Arg Ser Val Glu Gly Gly Ala Ala Phe Gln Thr Leu Ile Thr Ile Ala
 165 170 175
 Lys Ile Ile Pro Phe Thr Ile Val Ile Gly Leu Gly Ile Phe Trp Phe
 180 185 190
 Lys Ala Glu Asn Phe Ala Ala Pro Thr Thr Thr Ala Ile Gly Ala Thr
 195 200 205
 Gly Ser Phe Met Ala Leu Leu Ala Gly Ile Ser Ala Thr Ser Trp Ser
 210 215 220
 Tyr Thr Gly Met Ala Ser Ile Cys Tyr Met Thr Gly Glu Ile Lys Asn
 225 230 235 240
 Pro Gly Lys Thr Met Pro Arg Ala Leu Ile Gly Ser Cys Leu Leu Val
 245 250 255
 Leu Val Leu Tyr Thr Leu Leu Ala Leu Val Ile Ser Gly Leu Met Pro
 260 265 270
 Phe Asp Lys Leu Ala Asn Ser Glu Thr Pro Ile Ser Asp Ala Leu Thr
 275 280 285
 Trp Ile Pro Ala Leu Gly Ser Thr Ala Gly Ile Phe Val Ala Ile Thr
 290 295 300

Ala Met Ile Val Ile Leu Gly Ser Leu Ser Ser Cys Val Met Tyr Gln
 305 310 315 320
 Pro Arg Leu Glu Tyr Ala Met Ala Lys Asp Asn Leu Phe Phe Lys Cys
 325 330 335
 Phe Gly His Val His Pro Lys Tyr Asn Thr Pro Asp Val Ser Ile Ile
 340 345 350
 Leu Gln Gly Ala Leu Gly Ile Phe Phe Ile Phe Val Ser Asp Leu Thr
 355 360 365
 Ser Leu Leu Gly Tyr Phe Thr Leu Val Met Cys Phe Lys Asn Thr Leu
 370 375 380
 Thr Phe Gly Ser Ile Ile Trp Cys Arg Lys Arg Asp Asp Tyr Lys Pro
 385 390 395 400
 Leu Trp Arg Thr Pro Ala Phe Gly Leu Met Thr Thr Leu Ala Ile Ala
 405 410 415
 Ser Ser Leu Ile Leu Val Ala Ser Thr Phe Val Trp Ala Pro Ile Pro
 420 425 430
 Gly Leu Ile Cys Ala Val Ile Val Ile Ala Thr Gly Leu Pro Ala Tyr
 435 440 445
 Ala Phe Trp Ala Lys Arg Ser Arg Gln Leu Asn Ala Leu Ser
 450 455 460

<210> 346

<211> 347

<212> PRT

<213> Escherichia coli

<400> 346

Met Leu Ser Gly Glu Asn Lys Met Leu Asp Ile Asp Lys Ser Thr Val
 1 5 10 15
 Asp Phe Leu Val Thr Glu Asn Met Val Gln Glu Val Glu Lys Val Leu
 20 25 30
 Ser His Asp Val Pro Leu Val His Ala Ile Val Glu Glu Met Val Lys
 35 40 45
 Arg Asp Ile Asp Arg Ile Tyr Phe Val Ala Cys Gly Ser Pro Leu Asn
 50 55 60
 Ala Ala Gln Thr Ala Lys His Leu Ala Asp Arg Phe Ser Asp Leu Gln
 65 70 75 80
 Val Tyr Ala Ile Ser Gly Trp Glu Phe Cys Asp Asn Thr Pro Tyr Arg
 85 90 95
 Leu Asp Asp Arg Cys Ala Val Ile Gly Val Ser Asp Tyr Gly Lys Thr
 100 105 110
 Glu Glu Val Ile Lys Ala Leu Glu Gly Arg Ala Cys Gly Ala Leu
 115 120 125
 Thr Ala Ala Phe Thr Lys Arg Ala Asp Ser Pro Ile Thr Ser Ala Ala
 130 135 140
 Glu Phe Ser Ile Asp Tyr Gln Ala Asp Cys Ile Trp Glu Ile His Leu
 145 150 155 160
 Leu Leu Cys Tyr Ser Val Val Leu Glu Met Ile Thr Arg Leu Ala Pro
 165 170 175
 Asn Ala Glu Ile Gly Lys Ile Lys Asn Asp Leu Lys Gln Leu Pro Asn
 180 185 190
 Ala Leu Gly His Leu Val Arg Thr Trp Glu Glu Lys Gly Arg Gln Leu
 195 200 205
 Gly Glu Leu Ala Ser Gln Trp Pro Met Ile Tyr Thr Val Ala Ala Gly
 210 215 220
 Pro Leu Arg Pro Leu Gly Tyr Lys Glu Gly Ile Val Thr Leu Met Glu
 225 230 235 240
 Phe Thr Trp Thr His Gly Cys Val Ile Glu Ser Gly Glu Phe Arg His
 245 250 255
 Gly Pro Leu Glu Ile Val Glu Pro Gly Val Pro Phe Leu Phe Leu Leu

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<210> 347
<211> 149
<212> PRT
<213> Escherichia coli
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<210> 348
<211> 127
<212> PRT
<213> Escherichia coli
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-321-

115 120 125

<210> 349
 <211> 453
 <212> PRT
 <213> Escherichia coli

<400> 349

Met	Phe	Asp	Asn	Leu	Thr	Asp	Arg	Leu	Ser	Arg	Thr	Leu	Arg	Asn	Ile
1			5					10						15	
Ser	Gly	Arg	Gly	Arg	Leu	Thr	Glu	Asp	Asn	Val	Lys	Asp	Thr	Leu	Arg
		20					25					30			
Glu	Val	Arg	Met	Ala	Leu	Leu	Glu	Ala	Asp	Val	Ala	Leu	Pro	Val	Val
	35						40					45			
Arg	Glu	Phe	Ile	Asn	Arg	Val	Lys	Glu	Lys	Ala	Val	Gly	His	Glu	Val
	50				55						60				
Asn	Lys	Ser	Leu	Thr	Pro	Gly	Gln	Glu	Phe	Val	Lys	Ile	Val	Arg	Asn
65				70					75					80	
Glu	Leu	Val	Ala	Ala	Met	Gly	Glu	Glu	Asn	Gln	Thr	Leu	Asn	Leu	Ala
			85					90						95	
Ala	Gln	Pro	Pro	Ala	Val	Val	Leu	Met	Ala	Gly	Leu	Gln	Gly	Ala	Gly
		100						105					110		
Lys	Thr	Thr	Ser	Val	Gly	Lys	Leu	Gly	Lys	Phe	Leu	Arg	Glu	Lys	His
	115					120						125			
Lys	Lys	Lys	Val	Leu	Val	Val	Ser	Ala	Asp	Val	Tyr	Arg	Pro	Ala	Ala
	130					135					140				
Ile	Lys	Gln	Leu	Glu	Thr	Leu	Ala	Glu	Gln	Val	Gly	Val	Asp	Phe	Phe
145				150					155					160	
Pro	Ser	Asp	Val	Gly	Gln	Lys	Pro	Val	Asp	Ile	Val	Asn	Ala	Ala	Leu
			165					170						175	
Lys	Glu	Ala	Lys	Leu	Lys	Phe	Tyr	Asp	Val	Leu	Leu	Val	Asp	Thr	Ala
		180						185					190		
Gly	Arg	Leu	His	Val	Asp	Glu	Ala	Met	Met	Asp	Glu	Ile	Lys	Gln	Val
	195					200						205			
His	Ala	Ser	Ile	Asn	Pro	Val	Glu	Thr	Leu	Phe	Val	Val	Asp	Ala	Met
	210				215						220				
Thr	Gly	Gln	Asp	Ala	Ala	Asn	Thr	Ala	Lys	Ala	Phe	Asn	Glu	Ala	Leu
225				230					235					240	
Pro	Leu	Thr	Gly	Val	Val	Leu	Thr	Lys	Val	Asp	Gly	Asp	Ala	Arg	Gly
			245					250					255		
Gly	Ala	Ala	Leu	Ser	Ile	Arg	His	Ile	Thr	Gly	Lys	Pro	Ile	Lys	Phe
		260						265					270		
Leu	Gly	Val	Gly	Glu	Lys	Thr	Glu	Ala	Leu	Glu	Pro	Phe	His	Pro	Asp
	275					280						285			
Arg	Ile	Ala	Ser	Arg	Ile	Leu	Gly	Met	Gly	Asp	Val	Leu	Ser	Leu	Ile
	290				295					300					
Glu	Asp	Ile	Glu	Ser	Lys	Val	Asp	Arg	Ala	Gln	Ala	Glu	Lys	Leu	Ala
305					310				315					320	
Ser	Lys	Leu	Lys	Lys	Gly	Asp	Gly	Phe	Asp	Leu	Asn	Asp	Phe	Leu	Glu
			325					330						335	
Gln	Leu	Arg	Gln	Met	Lys	Asn	Met	Gly	Gly	Met	Ala	Ser	Leu	Met	Gly
		340						345					350		
Lys	Leu	Pro	Gly	Met	Gly	Gln	Ile	Pro	Asp	Asn	Val	Lys	Ser	Gln	Met
	355					360						365			
Asp	Asp	Lys	Val	Leu	Val	Arg	Met	Glu	Ala	Ile	Ile	Asn	Ser	Met	Thr
	370				375						380				
Met	Lys	Glu	Arg	Ala	Lys	Pro	Glu	Ile	Ile	Lys	Gly	Ser	Arg	Lys	Arg
385					390					395					400
Arg	Ile	Ala	Ala	Gly	Cys	Gly	Met	Gln	Val	Gln	Asp	Val	Asn	Arg	Leu
			405					410						415	

Leu Lys Gln Phe Asp Asp Met Gln Arg Met Met Lys Lys Met Lys Lys
 420 425 430
 Gly Gly Met Ala Lys Met Met Arg Ser Met Lys Gly Met Met Pro Pro
 435 440 445
 Gly Phe Pro Gly Arg
 450

<210> 350

<211> 577

<212> PRT

<213> Escherichia coli

<400> 350

Met Lys Gln Gln Ile Gln Leu Arg Arg Arg Glu Val Asp Glu Thr Ala
 1 5 10 15
 Asp Leu Pro Ala Glu Leu Pro Pro Leu Leu Arg Arg Leu Tyr Ala Ser
 20 25 30
 Arg Gly Val Arg Ser Ala Gln Glu Leu Glu Arg Ser Val Lys Gly Met
 35 40 45
 Leu Pro Trp Gln Gln Leu Ser Gly Val Glu Lys Ala Val Glu Ile Leu
 50 55 60
 Tyr Asn Ala Phe Arg Glu Gly Thr Arg Ile Ile Val Val Gly Asp Phe
 65 70 75 80
 Asp Ala Asp Gly Ala Thr Ser Thr Ala Leu Ser Val Leu Ala Met Arg
 85 90 95
 Ser Leu Gly Cys Ser Asn Ile Asp Tyr Leu Val Pro Asn Arg Phe Glu
 100 105 110
 Asp Gly Tyr Gly Leu Ser Pro Glu Val Val Asp Gln Ala His Ala Arg
 115 120 125
 Gly Ala Gln Leu Ile Val Thr Val Asp Asn Gly Ile Ser Ser His Ala
 130 135 140
 Gly Val Glu His Ala Arg Ser Leu Gly Ile Pro Val Ile Val Thr Asp
 145 150 155 160
 His His Leu Pro Gly Asp Thr Leu Pro Ala Ala Glu Ala Ile Ile Asn
 165 170 175
 Pro Asn Leu Arg Asp Cys Asn Phe Pro Ser Lys Ser Leu Ala Gly Val
 180 185 190
 Gly Val Ala Phe Tyr Leu Met Leu Ala Leu Arg Thr Phe Leu Arg Asp
 195 200 205
 Gln Gly Trp Phe Asp Glu Arg Asn Ile Ala Ile Pro Asn Leu Ala Glu
 210 215 220
 Leu Leu Asp Leu Val Ala Leu Gly Thr Val Ala Asp Val Val Pro Leu
 225 230 235 240
 Asp Ala Asn Asn Arg Ile Leu Thr Trp Gln Gly Met Ser Arg Ile Arg
 245 250 255
 Ala Gly Lys Cys Arg Pro Gly Ile Lys Ala Leu Leu Glu Val Ala Asn
 260 265 270
 Arg Asp Ala Gln Lys Leu Ala Ala Ser Asp Leu Gly Phe Ala Leu Gly
 275 280 285
 Pro Arg Leu Asn Ala Ala Gly Arg Leu Asp Asp Met Ser Val Gly Val
 290 295 300
 Ala Leu Leu Leu Cys Asp Asn Ile Gly Glu Ala Arg Val Leu Ala Asn
 305 310 315 320
 Glu Leu Asp Ala Leu Asn Gln Thr Arg Lys Glu Ile Glu Gln Gly Met
 325 330 335
 Gln Ile Glu Ala Leu Thr Leu Cys Glu Lys Leu Glu Arg Ser Arg Asp
 340 345 350
 Thr Leu Pro Gly Gly Leu Ala Met Tyr His Pro Glu Trp His Gln Gly
 355 360 365
 Val Val Gly Ile Leu Ala Ser Arg Ile Lys Glu Arg Phe His Arg Pro

370	375	380
Val Ile Ala Phe Ala Pro Ala Gly Asp Gly Thr Leu Lys Gly Ser Gly		
385	390	395
Arg Ser Ile Gln Gly Leu His Met Arg Asp Ala Leu Glu Arg Leu Asp		400
	405	410
Thr Leu Tyr Pro Gly Met Met Leu Lys Phe Gly Gly His Ala Met Ala		415
	420	425
Ala Gly Leu Ser Leu Glu Glu Asp Lys Phe Lys Leu Phe Gln Gln Arg		430
	435	440
Phe Gly Glu Leu Val Thr Glu Trp Leu Asp Pro Ser Leu Leu Gln Gly		445
	450	455
Glu Val Val Ser Asp Gly Pro Leu Ser Pro Ala Glu Met Thr Met Glu		460
465	470	475
Val Ala Gln Leu Leu Arg Asp Ala Gly Pro Trp Gly Gln Met Phe Pro		480
	485	490
Glu Pro Leu Phe Asp Gly His Phe Arg Leu Leu Gln Gln Arg Leu Val		495
	500	505
Gly Glu Arg His Leu Lys Val Met Val Glu Pro Val Gly Gly Gly Pro		510
	515	520
Leu Leu Asp Gly Ile Ala Phe Asn Val Asp Thr Ala Leu Trp Pro Asp		525
	530	535
Asn Gly Val Arg Glu Val Gln Leu Ala Tyr Lys Leu Asp Ile Asn Glu		540
545	550	555
Phe Arg Gly Asn Arg Ser Leu Gln Ile Ile Ile Asp Asn Ile Trp Pro		560
	565	570
		575

Ile

<210> 351

<211> 236

<212> PRT

<213> Escherichia coli

<400> 351

Met Lys Lys Gly Phe Met Leu Phe Thr Leu Leu Ala Ala Phe Ser Gly	
1	5
Phe Ala Gln Ala Asp Asp Ala Ala Ile Gln Gln Thr Leu Ala Lys Met	
	20
Gly Ile Lys Ser Ser Asp Ile Gln Pro Ala Pro Val Ala Gly Met Lys	
	35
Thr Val Leu Thr Asn Ser Gly Val Leu Tyr Ile Thr Asp Asp Gly Lys	
	50
His Ile Ile Gln Gly Pro Met Tyr Asp Val Ser Gly Thr Ala Pro Val	
65	70
Asn Val Thr Asn Lys Met Leu Leu Lys Gln Leu Asn Ala Leu Glu Lys	
	85
Glu Met Ile Val Tyr Lys Ala Pro Gln Glu Lys His Val Ile Thr Val	
	100
Phe Thr Asp Ile Thr Cys Gly Tyr Cys His Lys Leu His Glu Gln Met	
	115
Ala Asp Tyr Asn Ala Leu Gly Ile Thr Val Arg Tyr Leu Ala Phe Pro	
	130
Arg Gln Gly Leu Asp Ser Asp Ala Glu Lys Glu Met Lys Ala Ile Trp	
145	150
Cys Ala Lys Asp Lys Asn Lys Ala Phe Asp Asp Val Met Ala Gly Lys	
	165
Ser Val Ala Pro Ala Ser Cys Asp Val Asp Ile Ala Asp His Tyr Ala	
	180
Leu Gly Val Gln Leu Gly Val Ser Gly Thr Pro Ala Val Val Leu Ser	
	195
	200
	205

Asn Gly Thr Leu Val Pro Gly Tyr Gln Pro Pro Lys Glu Met Lys Glu
 210 215 220
 Phe Leu Asp Glu His Gln Lys Met Thr Ser Gly Lys
 225 230 235

<210> 352
 <211> 298
 <212> PRT
 <213> Escherichia coli

<400> 352
 Met Lys Gln Asp Leu Ala Arg Ile Glu Gln Phe Leu Asp Ala Leu Trp
 1 5 10 15
 Leu Glu Lys Asn Leu Ala Glu Asn Thr Leu Asn Ala Tyr Arg Arg Asp
 20 25 30
 Leu Ser Met Met Val Glu Trp Leu His His Arg Gly Leu Thr Leu Ala
 35 40 45
 Thr Ala Gln Ser Asp Asp Leu Gln Ala Leu Leu Ala Glu Arg Leu Glu
 50 55 60
 Gly Gly Tyr Lys Ala Thr Ser Ser Ala Arg Leu Ser Ala Val Arg
 65 70 75 80
 Arg Leu Phe Gln Tyr Leu Tyr Arg Glu Lys Phe Arg Glu Asp Asp Pro
 85 90 95
 Ser Ala His Leu Ala Ser Pro Lys Leu Pro Gln Arg Leu Pro Lys Asp
 100 105 110
 Leu Ser Glu Ala Gln Val Glu Arg Leu Leu Gln Ala Pro Leu Ile Asp
 115 120 125
 Gln Pro Leu Glu Leu Arg Asp Lys Ala Met Leu Glu Val Leu Tyr Ala
 130 135 140
 Thr Gly Leu Arg Val Ser Glu Leu Val Gly Leu Thr Met Ser Asp Ile
 145 150 155 160
 Ser Leu Arg Gln Gly Val Val Arg Val Ile Gly Lys Gly Asn Lys Glu
 165 170 175
 Arg Leu Val Pro Leu Gly Glu Glu Ala Val Tyr Trp Leu Glu Thr Tyr
 180 185 190
 Leu Glu His Gly Arg Pro Trp Leu Asn Gly Val Ser Ile Asp Val
 195 200 205
 Leu Phe Pro Ser Gln Arg Ala Gln Gln Met Thr Arg Gln Thr Phe Trp
 210 215 220
 His Arg Ile Lys His Tyr Ala Val Leu Ala Gly Ile Asp Ser Glu Lys
 225 230 235 240
 Leu Ser Pro His Val Leu Arg His Ala Phe Ala Thr His Leu Leu Asn
 245 250 255
 His Gly Ala Asp Leu Arg Val Val Gln Met Leu Leu Gly His Ser Asp
 260 265 270
 Leu Ser Thr Thr Gln Ile Tyr Thr His Val Ala Thr Glu Arg Leu Arg
 275 280 285
 Gln Leu His Gln Gln His His Pro Arg Ala
 290 295

<210> 353
 <211> 246
 <212> PRT
 <213> Escherichia coli

<400> 353
 Met Phe Phe Asn Thr Lys His Thr Thr Ala Leu Cys Phe Val Thr Cys
 1 5 10 15
 Met Ala Phe Ser Ser Ser Ser Ile Ala Asp Ile Val Ile Ser Gly Thr
 20 25 30

```

Arg Val Ile Tyr Lys Ser Asp Gln Lys Ser Val Asn Val Arg Leu Glu
    35          40          45
Asn Lys Gly Asn Asn Pro Leu Val Gln Ser Trp Leu Asp Thr Gly
    50          55          60
Asp Asp Asn Ala Glu Pro Gly Ser Ile Thr Val Pro Phe Thr Ala Thr
    65          70          75          80
Pro Pro Val Ser Arg Ile Asp Ala Lys Arg Gly Gln Thr Ile Lys Leu
    85          90          95
Met Tyr Thr Ala Ser Thr Ser Leu Pro Lys Asp Arg Glu Ser Val Phe
    100          105          110
Trp Phe Asn Val Leu Glu Val Pro Pro Lys Pro Asp Ala Glu Lys Val
    115          120          125
Ala Asn Gln Ser Leu Leu Gln Leu Ala Phe Arg Thr Arg Ile Lys Leu
    130          135          140
Phe Tyr Arg Pro Asp Gly Leu Lys Gly Asn Pro Ser Glu Ala Pro Leu
    145          150          155          160
Ala Leu Lys Trp Phe Trp Ser Gly Ser Glu Gly Lys Ala Ser Leu Arg
    165          170          175
Val Thr Asn Pro Thr Pro Tyr Tyr Val Ser Phe Ser Ser Gly Asp Leu
    180          185          190
Glu Ala Ser Gly Lys Arg Tyr Pro Ile Asp Val Lys Met Ile Ala Pro
    195          200          205
Phe Ser Asp Glu Val Met Lys Val Asn Gly Leu Asn Gly Lys Ala Asn
    210          215          220
Ser Ala Lys Val His Phe Tyr Ala Ile Asn Asp Phe Gly Gly Ala Ile
    225          230          235          240
Glu Gly Asn Ala Arg Leu
    245

```

<210> 354

<211> 865

<212> PRT

<213> Escherichia coli

<400> 354

```

Met Thr Ile Glu Tyr Thr Lys Asn Tyr His His Leu Thr Arg Ile Ala
    1          5          10          15
Thr Phe Cys Ala Leu Leu Tyr Cys Asn Thr Ala Phe Ser Ala Glu Leu
    20          25          30
Val Glu Tyr Asp His Thr Phe Leu Met Gly Gln Asn Ala Ser Asn Ile
    35          40          45
Asp Leu Ser Arg Tyr Ser Glu Gly Asn Pro Ala Ile Pro Gly Val Tyr
    50          55          60
Asp Val Ser Val Tyr Val Asn Asp Gln Pro Ile Ile Asn Gln Ser Ile
    65          70          75          80
Thr Phe Val Ala Ile Glu Gly Lys Lys Asn Ala Gln Ala Cys Ile Thr
    85          90          95
Leu Lys Asn Leu Leu Gln Phe His Ile Asn Ser Pro Asp Ile Asn Asn
    100          105          110
Glu Lys Ala Val Leu Leu Ala Arg Asp Glu Thr Leu Gly Asn Cys Leu
    115          120          125
Asn Leu Thr Glu Ile Ile Pro Gln Ala Ser Val Arg Tyr Asp Val Asn
    130          135          140
Asp Gln Arg Leu Asp Ile Asp Val Pro Gln Ala Trp Val Met Lys Asn
    145          150          155          160
Tyr Gln Asn Tyr Val Asp Pro Ser Leu Trp Glu Asn Gly Ile Asn Ala
    165          170          175
Ala Met Leu Ser Tyr Asn Leu Asn Gly Tyr His Ser Glu Thr Pro Gly
    180          185          190
Arg Lys Asn Glu Ser Ile Tyr Ala Ala Phe Asn Gly Gly Met Asn Leu

```


195					200					205					
Gly	Ala	Trp	Arg	Leu	Arg	Ala	Ser	Gly	Asn	Tyr	Asn	Trp	Met	Thr	Asp
210					215					220					
Ser	Gly	Ser	Asn	Tyr	Asp	Phe	Lys	Asn	Arg	Tyr	Val	Gln	Arg	Asp	Ile
225					230					235					240
Ala	Ser	Leu	Arg	Ser	Gln	Leu	Ile	Leu	Gly	Glu	Ser	Tyr	Thr	Thr	Gly
				245					250					255	
Glu	Thr	Phe	Asp	Ser	Val	Ser	Ile	Arg	Gly	Ile	Arg	Leu	Tyr	Ser	Asp
			260					265					270		
Ser	Arg	Met	Leu	Pro	Pro	Thr	Leu	Ala	Ser	Phe	Ala	Pro	Ile	Ile	His
			275				280					285			
Gly	Val	Ala	Asn	Thr	Asn	Ala	Lys	Val	Thr	Ile	Thr	Gln	Gly	Gly	Tyr
290					295					300					
Lys	Ile	Tyr	Glu	Thr	Thr	Val	Pro	Pro	Gly	Ala	Phe	Val	Ile	Asp	Asp
305					310					315					320
Leu	Ser	Pro	Ser	Gly	Tyr	Gly	Ser	Asp	Leu	Ile	Val	Thr	Ile	Glu	Glu
				325					330					335	
Ser	Asp	Gly	Ser	Lys	Arg	Thr	Phe	Ser	Gln	Pro	Phe	Ser	Ser	Val	Val
				340				345					350		
Gln	Met	Leu	Arg	Pro	Gly	Val	Gly	Arg	Trp	Asp	Ile	Ser	Gly	Gly	Gln
			355				360					365			
Val	Leu	Lys	Asp	Asp	Ile	Gln	Asp	Glu	Pro	Asn	Leu	Phe	Gln	Ala	Ser
					370		375				380				
Tyr	Tyr	Tyr	Gly	Leu	Asn	Asn	Tyr	Leu	Thr	Gly	Tyr	Thr	Gly	Ile	Gln
385					390					395					400
Ile	Thr	Asp	Asn	Asn	Tyr	Thr	Ala	Gly	Leu	Leu	Gly	Leu	Gly	Leu	Asn
				405					410					415	
Thr	Ser	Val	Gly	Ala	Phe	Ser	Phe	Asp	Val	Thr	His	Ser	Asn	Val	Arg
				420				425					430		
Ile	Pro	Asp	Asp	Lys	Thr	Tyr	Gln	Gly	Gln	Ser	Tyr	Arg	Val	Ser	Trp
				435			440					445			
Asn	Lys	Leu	Phe	Glu	Glu	Thr	Ser	Thr	Ser	Leu	Asn	Ile	Ala	Ala	Tyr
					450		455				460				
Arg	Tyr	Ser	Thr	Gln	Asn	Tyr	Leu	Gly	Leu	Asn	Asp	Ala	Leu	Thr	Leu
465					470					475					480
Ile	Asp	Glu	Val	Lys	His	Pro	Glu	Gln	Asp	Leu	Glu	Pro	Lys	Ser	Met
				485					490					495	
Arg	Asn	Tyr	Ser	Arg	Met	Lys	Asn	Gln	Val	Thr	Val	Ser	Ile	Asn	Gln
				500				505					510		
Pro	Leu	Lys	Phe	Glu	Lys	Lys	Asp	Tyr	Gly	Ser	Phe	Tyr	Leu	Ser	Gly
				515			520					525			
Ser	Trp	Ser	Asp	Tyr	Trp	Ala	Ser	Gly	Gln	Asn	Arg	Ser	Asn	Tyr	Ser
					530		535				540				
Ile	Gly	Tyr	Ser	Asn	Ser	Thr	Ser	Trp	Gly	Ser	Tyr	Ser	Val	Ser	Ala
545					550					555					560
Gln	Arg	Ser	Trp	Asn	Glu	Asp	Gly	Asp	Thr	Asp	Asp	Ser	Val	Tyr	Leu
				565					570					575	
Ser	Phe	Thr	Ile	Pro	Ile	Glu	Lys	Leu	Leu	Gly	Thr	Glu	Gln	Arg	Thr
				580				585					590		
Ser	Gly	Phe	Gln	Ser	Ile	Asp	Thr	Gln	Ile	Ser	Ser	Asp	Phe	Lys	Gly
				595			600					605			
Asn	Asn	Gln	Leu	Asn	Val	Ser	Ser	Ser	Gly	Tyr	Ser	Asp	Asn	Ala	Arg
					610		615				620				
Val	Ser	Tyr	Ser	Val	Asn	Thr	Gly	Tyr	Thr	Met	Asn	Lys	Ala	Ser	Lys
625					630					635					640
Asp	Leu	Ser	Tyr	Val	Gly	Gly	Tyr	Ala	Ser	Tyr	Glu	Ser	Pro	Trp	Gly
				645					650					655	
Thr	Leu	Ala	Gly	Ser	Ile	Ser	Ala	Asn	Ser	Asp	Asn	Ser	Arg	Gln	Val
				660				665					670		
Ser	Leu	Ser	Thr	Asp	Gly	Gly	Phe	Val	Leu	His	Ser	Gly	Gly	Leu	Thr

675	680	685
Phe Ser Asn Asp Ser Phe	Ser Asp Ser Asp Thr	Leu Ala Val Val Gln
690	695	700
Ala Pro Gly Ala Gln Gly	Ala Arg Ile Asn Tyr	Gly Asn Ser Thr Ile
705	710	715
Asp Arg Trp Gly Tyr Gly	Val Thr Ser Ala Leu	Ser Pro Tyr His Glu
725	730	735
Asn Arg Ile Ala Leu Asp	Ile Asn Asp Leu Glu	Asn Asp Val Glu Leu
740	745	750
Lys Ser Thr Ser Ala Val	Ala Val Pro Arg Gln	Gly Ser Val Val Phe
755	760	765
Ala Asp Phe Glu Thr Val	Gln Gly Gln Ser Ala	Ile Met Asn Ile Thr
770	775	780
Arg Ser Asp Gly Lys Asn	Ile Pro Phe Ala Ala	Asp Ile Tyr Asp Glu
785	790	795
Gln Gly Asn Val Ile Gly	Asn Val Gly Gln Gly	Gln Ala Phe Val
805	810	815
Arg Gly Ile Glu Gln Gln	Gly Asn Ile Ser Ile	Lys Trp Leu Glu Gln
820	825	830
Ser Lys Pro Val Ser Cys	Leu Ala His Tyr Gln	Gln Ser Pro Glu Ala
835	840	845
Glu Lys Ile Ala Gln Ser	Ile Ile Leu Asn Gly	Ile Arg Cys Gln Ile
850	855	860
Gln		
865		

<210> 355

<211> 661

<212> PRT

<213> Escherichia coli

<400> 355

Met Lys Thr Val Arg Glu Ser Thr Thr	Leu Tyr Asn Phe Leu Gly Ser
1	5 10 15
His Asn Pro Tyr Trp Arg Leu Thr Glu Ser Ser Asp Val Leu Arg Phe	
20	25 30
Ser Thr Thr Glu Thr Thr Glu Pro Asp Arg Thr Leu Gln Leu Ser Ala	
35	40 45
Glu Gln Ala Ala Arg Ile Arg Glu Met Thr Val Ile Thr Ser Ser Leu	
50	55 60
Met Met Ser Leu Thr Val Asp Glu Ser Asp Leu Ser Val His Leu Val	
65	70 75 80
Gly Arg Lys Ile Asn Lys Arg Glu Trp Ala Gly Asn Ala Ser Ala Trp	
85	90 95
His Asp Thr Pro Ala Val Ala Arg Asp Leu Ser His Gly Leu Ser Phe	
100	105 110
Ala Glu Gln Val Val Ser Glu Ala His Ser Ala Ile Val Ile Leu Asp	
115	120 125
Ser Arg Gly Asn Ile Gln Arg Phe Asn Arg Leu Cys Glu Asp Tyr Thr	
130	135 140
Gly Leu Lys Glu His Asp Val Ile Gly Gln Ser Val Phe Lys Leu Phe	
145	150 155 160
Met Ser Arg Arg Glu Ala Ala Ala Ser Arg Arg Asn Asn Arg Val Phe	
165	170 175
Phe Arg Ser Gly Asn Ala Tyr Glu Val Glu Leu Trp Ile Pro Thr Cys	
180	185 190
Lys Gly Gln Arg Leu Phe Leu Phe Arg Asn Lys Phe Val His Ser Gly	
195	200 205
Ser Gly Lys Asn Glu Ile Phe Leu Ile Cys Ser Gly Thr Asp Ile Thr	
210	215 220

Glu Glu Arg Arg Ala Gln Glu Arg Leu Arg Ile Leu Ala Asn Thr Asp
 225 230 235 240
 Ser Ile Thr Gly Leu Pro Asn Arg Asn Ala Met Gln Asp Leu Ile Asp
 245 250 255
 His Ala Ile Asn His Ala Asp Asn Asn Lys Val Gly Val Val Tyr Leu
 260 265 270
 Asp Leu Asp Asn Phe Lys Lys Val Asn Asp Ala Tyr Gly His Leu Phe
 275 280 285
 Gly Asp Gln Leu Leu Arg Asp Val Ser Leu Ala Ile Leu Ser Cys Leu
 290 295 300
 Glu His Asp Gln Val Leu Ala Arg Pro Gly Gly Asp Glu Phe Leu Val
 305 310 315 320
 Leu Ala Ser Asn Thr Ser Gln Ser Ala Leu Glu Ala Met Ala Ser Arg
 325 330 335
 Ile Leu Thr Arg Leu Arg Leu Pro Phe Arg Ile Gly Leu Ile Glu Val
 340 345 350
 Tyr Thr Ser Cys Ser Val Gly Ile Ala Leu Ser Pro Glu His Gly Ser
 355 360 365
 Asp Ser Thr Ala Ile Ile Arg His Ala Asp Thr Ala Met Tyr Thr Ala
 370 375 380
 Lys Glu Gly Gly Arg Gly Gln Phe Cys Val Phe Thr Pro Glu Met Asn
 385 390 395 400
 Gln Arg Val Phe Glu Tyr Leu Trp Leu Asp Thr Asn Leu Arg Lys Ala
 405 410 415
 Leu Glu Asn Asp Gln Leu Val Ile His Tyr Gln Pro Lys Ile Thr Trp
 420 425 430
 Arg Gly Glu Val Arg Ser Leu Glu Ala Leu Val Arg Trp Gln Ser Pro
 435 440 445
 Glu Arg Gly Leu Ile Pro Pro Leu Asp Phe Ile Ser Tyr Ala Glu Glu
 450 455 460
 Ser Gly Leu Ile Val Pro Leu Gly Arg Trp Val Ile Leu Asp Val Val
 465 470 475 480
 Arg Gln Val Ala Lys Trp Arg Asp Lys Gly Ile Asn Leu Arg Val Ala
 485 490 495
 Val Asn Ile Ser Ala Arg Gln Leu Ala Asp Gln Thr Ile Phe Thr Ala
 500 505 510
 Leu Lys Gln Val Leu Gln Glu Leu Asn Phe Glu Tyr Cys Pro Ile Asp
 515 520 525
 Val Glu Leu Thr Glu Ser Cys Leu Ile Glu Asn Asp Glu Leu Ala Leu
 530 535 540
 Ser Val Ile Gln Gln Phe Ser Gln Leu Gly Ala Gln Val His Leu Asp
 545 550 555 560
 Asp Phe Gly Thr Gly Tyr Ser Ser Leu Ser Gln Leu Ala Arg Phe Pro
 565 570 575
 Ile Asp Ala Ile Lys Leu Asp Gln Val Phe Val Arg Asp Ile His Lys
 580 585 590
 Gln Pro Val Ser Gln Ser Leu Val Arg Ala Ile Val Ala Val Ala Gln
 595 600 605
 Ala Leu Asn Leu Gln Val Ile Ala Glu Gly Val Glu Ser Ala Lys Glu
 610 615 620
 Asp Ala Phe Leu Thr Lys Asn Gly Ile Asn Glu Arg Gln Gly Phe Leu
 625 630 635 640
 Phe Ala Lys Pro Met Pro Ala Val Ala Phe Glu Arg Trp Tyr Lys Arg
 645 650 655
 Tyr Leu Lys Arg Ala
 660

<210> 356

<211> 230

<212> PRT

<213> Escherichia coli

<400> 356

```

Met Met Thr Lys Ile Lys Leu Leu Met Leu Ile Ile Phe Tyr Leu Ile
 1          5          10          15
Ile Ser Ala Ser Ala His Ala Ala Gly Gly Ile Ala Leu Gly Ala Thr
          20          25          30
Arg Ile Ile Tyr Pro Ala Asp Ala Lys Gln Thr Ala Val Trp Ile Arg
          35          40          45
Asn Ser His Thr Asn Glu Arg Phe Leu Val Asn Ser Trp Ile Glu Asn
50          55          60
Ser Ser Gly Val Lys Glu Lys Ser Phe Ile Ile Thr Pro Pro Leu Phe
65          70          75          80
Val Ser Glu Pro Lys Ser Glu Asn Thr Leu Arg Ile Ile Tyr Thr Gly
          85          90          95
Pro Pro Leu Ala Ala Asp Arg Glu Ser Leu Phe Trp Met Asn Val Lys
          100          105          110
Thr Ile Pro Ser Val Asp Lys Asn Ala Leu Asn Gly Arg Asn Val Leu
          115          120          125
Gln Leu Ala Ile Leu Ser Arg Met Lys Leu Phe Leu Arg Pro Ile Gln
130          135          140
Leu Gln Glu Leu Pro Ala Glu Ala Pro Asp Thr Leu Lys Phe Ser Arg
145          150          155          160
Ser Gly Asn Tyr Ile Asn Val His Asn Pro Ser Pro Phe Tyr Val Thr
          165          170          175
Leu Val Asn Leu Gln Val Gly Ser Gln Lys Leu Gly Asn Ala Met Ala
          180          185          190
Ala Pro Arg Val Asn Ser Gln Ile Pro Leu Pro Ser Gly Val Gln Gly
          195          200          205
Lys Leu Lys Phe Gln Thr Val Asn Asp Tyr Gly Ser Val Thr Pro Val
210          215          220
Arg Glu Val Asn Leu Asn
225          230

```

<210> 357

<211> 867

<212> PRT

<213> Escherichia coli

<400> 357

```

Met Lys Ile Pro Thr Thr Thr Asp Ile Pro Gln Arg Tyr Thr Trp Cys
 1          5          10          15
Leu Ala Gly Ile Cys Tyr Ser Ser Leu Ala Ile Leu Pro Ser Phe Leu
          20          25          30
Ser Tyr Ala Glu Ser Tyr Phe Asn Pro Ala Phe Leu Leu Glu Asn Gly
          35          40          45
Thr Ser Val Ala Asp Leu Ser Arg Phe Glu Arg Gly Asn His Gln Pro
50          55          60
Ala Gly Val Tyr Arg Val Asp Leu Trp Arg Asn Asp Glu Phe Ile Gly
65          70          75          80
Ser Gln Asp Ile Val Phe Glu Ser Thr Thr Glu Asn Thr Gly Asp Lys
          85          90          95
Ser Gly Gly Leu Met Pro Cys Phe Asn Gln Val Leu Leu Glu Arg Ile
          100          105          110
Gly Leu Asn Ser Ser Ala Phe Pro Glu Leu Ala Gln Gln Asn Asn
          115          120          125
Lys Cys Ile Asn Leu Leu Lys Ala Val Pro Asp Ala Thr Ile Asn Phe
130          135          140
Asp Phe Ala Ala Met Arg Leu Asn Ile Thr Ile Pro Gln Ile Ala Leu
145          150          155          160

```

Leu Ser Ser Ala His Gly Tyr Ile Pro Pro Glu Glu Trp Asp Glu Gly
 165 170 175
 Ile Pro Ala Leu Leu Leu Asn Tyr Asn Phe Thr Gly Asn Arg Gly Asn
 180 185 190
 Gly Asn Asp Ser Tyr Phe Phe Ser Glu Leu Ser Gly Ile Asn Ile Gly
 195 200 205
 Pro Trp Arg Leu Arg Asn Asn Gly Ser Trp Asn Tyr Phe Arg Gly Asn
 210 215 220
 Gly Tyr His Ser Glu Gln Trp Asn Asn Ile Gly Thr Trp Val Gln Arg
 225 230 235 240
 Ala Ile Ile Pro Leu Lys Ser Glu Leu Val Met Gly Asp Gly Asn Thr
 245 250 255
 Gly Ser Asp Ile Phe Asp Gly Val Gly Phe Arg Gly Val Arg Leu Tyr
 260 265 270
 Ser Ser Asp Asn Met Tyr Pro Asp Ser Gln Gln Gly Phe Ala Pro Thr
 275 280 285
 Val Arg Gly Ile Ala Arg Thr Ala Ala Gln Leu Thr Ile Arg Gln Asn
 290 295 300
 Gly Phe Ile Ile Tyr Gln Ser Tyr Val Ser Pro Gly Ala Phe Glu Ile
 305 310 315 320
 Thr Asp Leu His Pro Thr Ser Ser Asn Gly Asp Leu Asp Val Thr Ile
 325 330 335
 Asp Glu Arg Asp Gly Asn Gln Gln Asn Tyr Thr Ile Pro Tyr Ser Thr
 340 345 350
 Val Pro Ile Leu Gln Arg Glu Gly Arg Phe Lys Phe Asp Leu Thr Ala
 355 360 365
 Gly Asp Phe Arg Ser Gly Asn Ser Gln Gln Ser Ser Pro Phe Phe Phe
 370 375 380
 Gln Gly Thr Ala Leu Gly Gly Leu Pro Gln Glu Phe Thr Ala Tyr Gly
 385 390 395 400
 Gly Thr Gln Leu Ser Ala Asn Tyr Thr Ala Phe Leu Leu Gly Leu Gly
 405 410 415
 Arg Asn Leu Gly Asn Trp Gly Ala Val Ser Leu Asp Val Thr His Ala
 420 425 430
 Arg Ser Gln Leu Ala Asp Ala Ser Arg His Glu Gly Asp Ser Ile Arg
 435 440 445
 Phe Leu Tyr Ala Lys Ser Met Asn Thr Phe Gly Thr Asn Phe Gln Leu
 450 455 460
 Met Gly Tyr Arg Tyr Ser Thr Gln Gly Phe Tyr Thr Leu Asp Asp Val
 465 470 475 480
 Ala Tyr Arg Arg Met Glu Gly Tyr Glu Tyr Asp Tyr Asp Gly Glu His
 485 490 495
 Arg Asp Glu Pro Ile Ile Val Asn Tyr His Asn Leu Arg Phe Ser Arg
 500 505 510
 Lys Asp Arg Leu Gln Leu Asn Val Ser Gln Ser Leu Asn Asp Phe Gly
 515 520 525
 Ser Leu Tyr Ile Ser Gly Thr His Gln Lys Tyr Trp Asn Thr Ser Asp
 530 535 540
 Ser Asp Thr Trp Tyr Gln Val Gly Tyr Thr Ser Ser Trp Val Gly Ile
 545 550 555 560
 Ser Tyr Ser Leu Ser Phe Ser Trp Asn Glu Ser Val Gly Ile Pro Asp
 565 570 575
 Asn Glu Arg Ile Val Gly Leu Asn Val Ser Val Pro Phe Asn Val Leu
 580 585 590
 Thr Lys Arg Arg Tyr Thr Arg Glu Asn Ala Leu Asp Arg Ala Tyr Ala
 595 600 605
 Ser Phe Asn Ala Asn Arg Asn Ser Asn Gly Gln Asn Ser Trp Leu Ala
 610 615 620
 Gly Val Gly Gly Thr Leu Leu Glu Gly His Asn Leu Ser Tyr His Val
 625 630 635 640

Ser Gln Gly Asp Thr Ser Asn Asn Gly Tyr Thr Gly Ser Ala Thr Ala
 645 650 655
 Asn Trp Gln Ala Ala Tyr Gly Thr Leu Gly Gly Gly Tyr Asn Tyr Asp
 660 665 670
 Arg Asp Gln His Asp Val Asn Trp Gln Leu Ser Gly Gly Val Val Gly
 675 680 685
 His Glu Asn Gly Ile Thr Leu Ser Gln Pro Leu Gly Asp Thr Asn Val
 690 695 700
 Leu Ile Lys Ala Pro Gly Ala Gly Gly Val Arg Ile Glu Asn Gln Thr
 705 710 715 720
 Gly Ile Leu Thr Asp Trp Arg Gly Tyr Ala Val Met Leu Tyr Ala Thr
 725 730 735
 Val Tyr Arg Tyr Asn Arg Ile Ala Leu Asp Thr Asn Thr Met Gly Asn
 740 745 750
 Ser Ile Asp Val Glu Lys Asn Ile Ser Ser Val Val Pro Thr Gln Gly
 755 760 765
 Ala Leu Val Arg Ala Asn Phe Asp Thr Arg Ile Gly Val Arg Ala Leu
 770 775 780
 Ile Thr Val Thr Gln Gly Gly Lys Pro Val Pro Phe Gly Ser Leu Val
 785 790 795 800
 Arg Glu Asn Ser Thr Gly Ile Thr Ser Met Val Gly Asp Asp Gly Gln
 805 810 815
 Val Tyr Leu Ser Gly Ala Pro Leu Ser Gly Glu Leu Leu Val Gln Trp
 820 825 830
 Gly Asp Gly Ala Asn Ser Arg Cys Ile Ala His Tyr Val Leu Pro Lys
 835 840 845
 Gln Ser Leu Gln Gln Ala Val Thr Val Ile Ser Ala Val Cys Thr His
 850 855 860
 Pro Gly Ser
 865

<210> 358

<211> 325

<212> PRT

<213> Escherichia coli

<400> 358

Met Ala Cys Leu Cys Leu Ala Asn Ile Ser Trp Ala Thr Val Cys Ala
 1 5 10 15
 Asn Ser Thr Gly Val Ala Glu Asp Glu His Tyr Asp Leu Ser Asn Ile
 20 25 30
 Phe Asn Ser Thr Asn Asn Gln Pro Gly Gln Ile Val Val Leu Pro Glu
 35 40 45
 Lys Ser Gly Trp Val Gly Val Ser Ala Ile Cys Pro Pro Gly Thr Leu
 50 55 60
 Val Asn Tyr Thr Tyr Arg Ser Tyr Val Thr Asn Phe Ile Val Gln Glu
 65 70 75 80
 Thr Ile Asp Asn Tyr Lys Tyr Met Gln Leu His Asp Tyr Leu Leu Gly
 85 90 95
 Ala Met Ser Leu Val Asp Ser Val Met Asp Ile Gln Phe Pro Pro Gln
 100 105 110
 Asn Tyr Ile Arg Met Gly Thr Asp Pro Asn Val Ser Gln Asn Leu Pro
 115 120 125
 Phe Gly Val Met Asp Ser Arg Leu Ile Phe Arg Leu Lys Val Ile Arg
 130 135 140
 Pro Phe Ile Asn Met Val Glu Ile Pro Arg Gln Val Met Phe Thr Val
 145 150 155 160
 Tyr Val Thr Ser Thr Pro Tyr Asp Pro Leu Val Thr Pro Val Tyr Thr
 165 170 175
 Ile Ser Phe Gly Gly Arg Val Glu Val Pro Gln Asn Cys Glu Leu Asn

```
<210> 359
<211> 171
<212> PRT
<213> Escherichia coli
```

```
<210> 360
<211> 194
<212> PRT
<213> Escherichia coli
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-333-

```

      35      40      45
Arg Asp Glu Ser His Cys Tyr Pro Ser Gly Trp Gln Ala Arg Leu Gly
  50      55      60
Met Ile Asn Glu Phe His Lys Gln Gly Ser Ala Phe Tyr Phe Gly Leu
65      70      75      80
Phe Asp Pro Asp Glu Lys Glu Ile Ile Gly Val Ala Asn Phe Ser Asn
      85      90      95
Val Val Arg Gly Ser Phe His Ala Cys Tyr Leu Gly Tyr Ser Ile Gly
      100      105      110
Gln Lys Trp Gln Gly Lys Gly Leu Met Phe Glu Ala Leu Thr Ala Ala
      115      120      125
Ile Arg Tyr Met Gln Arg Thr Gln His Ile His Arg Ile Met Ala Asn
      130      135      140
Tyr Met Pro His Asn Lys Arg Ser Gly Asp Leu Leu Ala Arg Leu Gly
145      150      155      160
Phe Glu Lys Glu Gly Tyr Ala Lys Asp Tyr Leu Leu Ile Asp Gly Gln
      165      170      175
Trp Arg Asp His Val Leu Thr Ala Leu Thr Thr Pro Asp Trp Thr Pro
      180      185      190
Gly Arg

```

<210> 361

<211> 215

<212> PRT

<213> Escherichia coli

<400> 361

```

Met Lys Tyr Gln Leu Thr Ala Leu Glu Ala Arg Val Ile Gly Cys Leu
  1      5      10      15
Leu Glu Lys Gln Val Thr Thr Pro Glu Gln Tyr Pro Leu Ser Val Asn
      20      25      30
Gly Val Val Thr Ala Cys Asn Gln Lys Thr Asn Arg Glu Pro Val Met
      35      40      45
Asn Leu Ser Glu Ser Glu Val Gln Glu Gln Leu Asp Asn Leu Val Lys
      50      55      60
Arg His Tyr Leu Arg Thr Val Ser Gly Phe Gly Asn Arg Val Thr Lys
65      70      75      80
Tyr Glu Gln Arg Phe Cys Asn Ser Glu Phe Gly Asp Leu Lys Leu Ser
      85      90      95
Ala Ala Glu Val Ala Leu Ile Thr Thr Leu Leu Leu Arg Gly Ala Gln
      100      105      110
Thr Pro Gly Glu Leu Arg Ser Arg Ala Ala Arg Met Tyr Glu Phe Ser
      115      120      125
Asp Met Ala Glu Val Glu Ser Thr Leu Glu Gln Leu Ala Asn Arg Glu
      130      135      140
Asp Gly Pro Phe Val Val Arg Leu Ala Arg Glu Pro Gly Lys Arg Glu
145      150      155      160
Asn Arg Tyr Met His Leu Phe Ser Gly Glu Val Glu Asp Gln Pro Ala
      165      170      175
Val Thr Asp Met Ser Asn Ala Val Asp Gly Asp Leu Gln Ala Arg Val
      180      185      190
Glu Ala Leu Glu Ile Glu Val Ala Glu Leu Lys Gln Arg Leu Asp Ser
      195      200      205
Leu Leu Ala His Leu Gly Asp
      210      215

```

<210> 362

<211> 307

<212> PRT

<213> Escherichia coli

<400> 362

```

Met Lys Lys Leu Arg Ile Gly Val Val Gly Leu Gly Gly Ile Ala Gln
 1           5           10           15
Lys Ala Trp Leu Pro Val Leu Ala Ala Ser Asp Trp Thr Leu Gln
 20           25           30
Gly Ala Trp Ser Pro Thr Arg Ala Lys Ala Leu Pro Ile Cys Glu Ser
 35           40           45
Trp Arg Ile Pro Tyr Ala Asp Ser Leu Ser Ser Leu Ala Ala Ser Cys
 50           55           60
Asp Ala Val Phe Val His Ser Ser Thr Ala Ser His Phe Asp Val Val
 65           70           75           80
Ser Thr Leu Leu Asn Ala Gly Val His Val Cys Val Asp Lys Pro Leu
 85           90           95
Ala Glu Asn Leu Arg Asp Ala Glu Arg Leu Val Glu Leu Ala Ala Arg
100          105          110
Lys Lys Leu Thr Leu Met Val Gly Phe Asn Arg Arg Phe Ala Pro Leu
115          120          125
Tyr Gly Glu Leu Lys Thr Gln Leu Ala Thr Ala Ala Ser Leu Arg Met
130          135          140
Asp Lys His Arg Ser Asn Ser Val Gly Pro His Asp Leu Tyr Phe Thr
145          150          155          160
Leu Leu Asp Asp Tyr Leu His Val Val Asp Thr Ala Leu Trp Leu Ser
165          170          175
Gly Gly Lys Ala Ser Leu Asp Gly Gly Thr Leu Leu Thr Asn Asp Ala
180          185          190
Gly Glu Met Leu Phe Ala Glu His His Phe Ser Ala Gly Pro Leu Gln
195          200          205
Ile Thr Thr Cys Met His Arg Arg Ala Gly Ser Gln Arg Glu Thr Val
210          215          220
Gln Ala Val Thr Asp Gly Ala Leu Ile Asp Ile Thr Asp Met Arg Glu
225          230          235          240
Trp Arg Glu Glu Arg Gly Gln Gly Val Val His Lys Pro Ile Pro Gly
245          250          255
Trp Gln Ser Thr Leu Glu Gln Arg Gly Phe Val Gly Cys Ala Arg His
260          265          270
Phe Ile Glu Cys Val Gln Asn Gln Thr Val Pro Gln Thr Ala Gly Glu
275          280          285
Gln Ala Val Leu Ala Gln Arg Ile Val Asp Lys Ile Trp Arg Asp Ala
290          295          300
Met Ser Glu
305

```

<210> 363

<211> 239

<212> PRT

<213> Escherichia coli

<400> 363

```

Met Leu Lys Arg Val Phe Leu Ser Leu Leu Val Leu Ile Gly Leu Leu
 1           5           10           15
Leu Leu Thr Val Leu Gly Leu Asp Arg Trp Met Ser Trp Lys Thr Ala
 20           25           30
Pro Tyr Ile Tyr Asp Glu Leu Gln Asp Leu Pro Tyr Arg Gln Val Gly
 35           40           45
Val Val Leu Gly Thr Ala Lys Tyr Tyr Arg Thr Gly Val Ile Asn Gln
 50           55           60
Tyr Tyr Arg Tyr Arg Ile Gln Gly Ala Ile Asn Ala Tyr Asn Ser Gly
 65           70           75           80

```

Lys Val Asn Tyr Leu Leu Leu Ser Gly Asp Asn Ala Leu Gln Ser Tyr
 85 90 95
 Asn Glu Pro Met Thr Met Arg Lys Asp Leu Ile Ala Ala Gly Val Asp
 100 105 110
 Pro Ser Asp Ile Val Leu Asp Tyr Ala Gly Phe Arg Thr Leu Asp Ser
 115 120 125
 Ile Val Arg Thr Arg Lys Val Phe Asp Thr Asn Asp Phe Ile Ile Ile
 130 135 140
 Thr Gln Arg Phe His Cys Glu Arg Ala Leu Phe Ile Ala Leu His Met
 145 150 155 160
 Gly Ile Gln Ala Gln Cys Tyr Ala Val Pro Ser Pro Lys Asp Met Leu
 165 170 175
 Ser Val Arg Ile Arg Glu Phe Ala Ala Arg Phe Gly Ala Leu Ala Asp
 180 185 190
 Leu Tyr Ile Phe Lys Arg Glu Pro Arg Phe Leu Gly Pro Leu Val Pro
 195 200 205
 Ile Pro Ala Met His Gln Val Pro Glu Asp Ala Gln Gly Tyr Pro Ala
 210 215 220
 Val Thr Pro Glu Gln Leu Leu Glu Leu Gln Lys Lys Gln Gly Lys
 225 230 235

<210> 364

<211> 79

<212> PRT

<213> Escherichia coli

<400> 364

Met Asp Val Gln Gln Phe Phe Val Val Ala Val Phe Phe Leu Ile Pro
 1 5 10 15
 Ile Phe Cys Phe Arg Glu Ala Trp Lys Gly Trp Arg Ala Gly Ala Ile
 20 25 30
 Asp Lys Arg Val Lys Asn Ala Pro Glu Pro Val Tyr Val Trp Arg Ala
 35 40 45
 Lys Asn Pro Gly Leu Phe Phe Ala Tyr Met Val Ala Tyr Ile Gly Phe
 50 55 60
 Gly Ile Leu Ser Ile Gly Met Ile Val Tyr Leu Ile Phe Tyr Arg
 65 70 75

<210> 365

<211> 510

<212> PRT

<213> Escherichia coli

<400> 365

Met Ala Thr Ile Asp Ser Met Asn Lys Asp Thr Thr Arg Leu Ser Asp
 1 5 10 15
 Gly Pro Asp Trp Thr Phe Asp Leu Leu Asp Val Tyr Leu Ala Glu Ile
 20 25 30
 Asp Arg Val Ala Lys Leu Tyr Arg Leu Asp Thr Tyr Pro His Gln Ile
 35 40 45
 Glu Val Ile Thr Ser Glu Gln Met Met Asp Ala Tyr Ser Ser Val Gly
 50 55 60
 Met Pro Ile Asn Tyr Pro His Trp Ser Phe Gly Lys Lys⁴⁹ Phe Ile Glu
 65 70 75 80
 Thr Glu Arg Leu Tyr Lys His Gly Gln Gln Gly Leu Ala Tyr Glu Ile
 85 90 95
 Val Ile Asn Ser Asn Pro Cys Ile Ala Tyr Leu Met Glu Glu Asn Thr
 100 105 110
 Ile Thr Met Gln Ala Leu Val Met Ala His Ala Cys Tyr Gly His Asn
 115 120 125

Ser Phe Phe Lys Asn Asn Tyr Leu Phe Arg Ser Trp Thr Asp Ala Ser
 130 135 140
 Ser Ile Val Asp Tyr Leu Ile Phe Ala Arg Lys Tyr Ile Thr Glu Cys
 145 150 155 160
 Glu Glu Arg Tyr Gly Val Asp Glu Val Glu Arg Leu Leu Asp Ser Cys
 165 170 175
 His Ala Leu Met Asn Tyr Gly Val Asp Arg Tyr Lys Arg Pro Gln Lys
 180 185 190
 Ile Ser Leu Gln Glu Glu Lys Ala Arg Gln Lys Ser Arg Glu Glu Tyr
 195 200 205
 Leu Gln Ser Gln Val Asn Met Leu Trp Arg Thr Leu Pro Lys Arg Glu
 210 215 220
 Glu Glu Lys Thr Val Ala Glu Ala Arg Arg Tyr Pro Ser Glu Pro Gln
 225 230 235 240
 Glu Asn Leu Leu Tyr Phe Met Glu Lys Asn Ala Pro Leu Leu Glu Ser
 245 250 255
 Trp Gln Arg Glu Ile Leu Arg Ile Val Arg Lys Val Ser Gln Tyr Phe
 260 265 270
 Tyr Pro Gln Lys Gln Thr Gln Val Met Asn Glu Gly Trp Ala Thr Phe
 275 280 285
 Trp His Tyr Thr Ile Leu Asn His Leu Tyr Asp Glu Gly Lys Val Thr
 290 295 300
 Glu Arg Phe Met Leu Glu Phe Leu His Ser His Thr Asn Val Val Phe
 305 310 315 320
 Gln Pro Pro Tyr Asn Ser Pro Trp Tyr Ser Gly Ile Asn Pro Tyr Ala
 325 330 335
 Leu Gly Phe Ala Met Phe Gln Asp Ile Lys Arg Ile Cys Gln Ser Pro
 340 345 350
 Thr Glu Glu Asp Lys Tyr Trp Phe Pro Asp Ile Ala Gly Ser Asp Trp
 355 360 365
 Leu Glu Thr Leu His Phe Ala Met Arg Asp Phe Lys Asp Glu Ser Phe
 370 375 380
 Ile Ser Gln Phe Leu Ser Pro Lys Val Met Arg Asp Phe Arg Phe Phe
 385 390 395 400
 Thr Val Leu Asp Asp Asp Arg His Asn Tyr Leu Glu Ile Ser Ala Ile
 405 410 415
 His Asn Glu Glu Gly Tyr Arg Glu Ile Arg Asn Arg Leu Ser Ser Gln
 420 425 430
 Tyr Asn Leu Ser Asn Leu Glu Pro Asn Ile Gln Ile Trp Asn Val Asp
 435 440 445
 Leu Arg Gly Asp Arg Ser Leu Thr Leu Arg Tyr Ile Pro His Asn Arg
 450 455 460
 Ala Pro Leu Asp Arg Gly Arg Lys Glu Val Leu Lys His Val His Arg
 465 470 475 480
 Leu Trp Gly Phe Asp Val Met Leu Glu Gln Gln Asn Glu Asp Gly Ser
 485 490 495
 Ile Glu Leu Leu Glu Arg Cys Pro Pro Arg Met Gly Asn Leu
 500 505 510

<210> 366

<211> 452

<212> PRT

<213> Escherichia coli

<400> 366

Met Lys Arg Leu Ser Ile Thr Val Arg Leu Thr Leu Leu Phe Ile Leu
 1 5 10 15
 Leu Leu Ser Val Ala Gly Ala Gly Ile Val Trp Thr Leu Tyr Asn Gly
 20 25 30
 Leu Ala Ser Glu Leu Lys Trp Arg Asp Asp Thr Thr Leu Ile Asn Arg

35	40	45
Thr Ala Gln Ile Lys Gln Leu Leu Ile Asp Gly Val Asn Pro Asp Thr		
50	55	60
Leu Pro Val Tyr Phe Asn Arg Met Met Asp Val Ser Gln Asp Ile Leu		
65	70	75
Ile Ile His Gly Asp Ser Ile Asn Lys Ile Val Asn Arg Thr Asn Val		
85	90	95
Ser Asp Gly Met Leu Asn Asn Ile Pro Ala Ser Glu Thr Ile Ser Ala		
100	105	110
Ala Gly Ile Tyr Arg Ser Ile Ile Asn Asp Thr Glu Ile Asp Ala Leu		
115	120	125
Arg Ile Asn Ile Asp Glu Val Ser Pro Ser Leu Thr Val Thr Val Ala		
130	135	140
Lys Leu Ala Ser Ala Arg His Asn Met Leu Glu Gln Tyr Lys Ile Asn		
145	150	155
Ser Ile Ile Ile Cys Ile Val Ala Ile Val Leu Cys Ser Val Leu Ser		
165	170	175
Pro Leu Leu Ile Arg Thr Gly Leu Arg Glu Ile Lys Lys Leu Ser Gly		
180	185	190
Val Thr Glu Ala Leu Asn Tyr Asn Asp Ser Arg Glu Pro Val Glu Val		
195	200	205
Ser Ala Leu Pro Arg Glu Leu Lys Pro Leu Gly Gln Ala Leu Asn Lys		
210	215	220
Met His His Ala Leu Val Lys Asp Phe Glu Arg Leu Ser Gln Phe Ala		
225	230	235
Asp Asp Leu Ala His Glu Leu Arg Thr Pro Ile Asn Ala Leu Leu Gly		
245	250	255
Gln Asn Gln Val Thr Leu Ser Gln Thr Arg Ser Ile Ala Glu Tyr Gln		
260	265	270
Lys Thr Ile Ala Gly Asn Ile Glu Glu Leu Glu Asn Ile Ser Arg Leu		
275	280	285
Thr Glu Asn Ile Leu Phe Leu Ala Arg Ala Asp Lys Asn Asn Val Leu		
290	295	300
Val Lys Leu Asp Ser Leu Ser Leu Asn Lys Glu Val Glu Asn Leu Leu		
305	310	315
Asp Tyr Leu Glu Tyr Leu Ser Asp Glu Lys Glu Ile Cys Phe Lys Val		
325	330	335
Glu Cys Asn Gln Gln Ile Phe Ala Asp Lys Ile Leu Leu Gln Arg Met		
340	345	350
Leu Ser Asn Leu Ile Val Asn Ala Ile Arg Tyr Ser Pro Glu Lys Ser		
355	360	365
Arg Ile His Ile Thr Ser Phe Leu Asp Thr Asn Ser Tyr Leu Asn Ile		
370	375	380
Asp Ile Ala Ser Pro Gly Thr Lys Ile Asn Glu Pro Glu Lys Leu Phe		
385	390	395
Arg Arg Phe Trp Arg Gly Asp Asn Ser Arg His Ser Val Gly Gln Gly		
405	410	415
Leu Gly Leu Ser Leu Val Lys Ala Ile Ala Glu Leu His Gly Gly Ser		
420	425	430
Ala Thr Tyr His Tyr Leu Asn Lys His Asn Val Phe Arg Ile Thr Leu		
435	440	445
Pro Gln Arg Asn		
450		

<210> 367

<211> 239

<212> PRT

<213> Escherichia coli

<400> 367

```

Met Asn Gln Ala Val Ser Ile Thr Tyr Asp Leu Trp His Ile Ile Phe
 1           5           10           15
Met Lys Ile Leu Leu Ile Glu Asp Asn Gln Arg Thr Gln Glu Trp Val
           20           25           30
Thr Gln Gly Leu Ser Glu Ala Gly Tyr Val Ile Asp Ala Val Ser Asp
           35           40           45
Gly Arg Asp Gly Leu Tyr Leu Ala Leu Lys Asp Asp Tyr Ala Leu Ile
           50           55           60
Ile Leu Asp Ile Met Leu Pro Gly Met Asp Gly Trp Gln Ile Leu Gln
65           70           75           80
Thr Leu Arg Thr Ala Lys Gln Thr Pro Val Ile Cys Leu Thr Ala Arg
           85           90           95
Asp Ser Val Asp Asp Arg Val Arg Gly Leu Asp Ser Gly Ala Asn Asp
           100          105          110
Tyr Leu Val Lys Pro Phe Ser Phe Ser Glu Leu Leu Ala Arg Val Arg
           115          120          125
Ala Gln Leu Arg Gln His His Ala Leu Asn Ser Thr Leu Glu Ile Ser
           130          135          140
Gly Leu Arg Met Asp Ser Val Ser His Ser Val Ser Arg Asp Asn Ile
145          150          155          160
Ser Ile Thr Leu Thr Arg Lys Glu Phe Gln Leu Leu Trp Leu Leu Ala
           165          170          175
Ser Arg Ala Gly Glu Ile Ile Pro Arg Thr Val Ile Ala Ser Glu Ile
           180          185          190
Trp Gly Ile Asn Phe Asp Ser Asp Thr Asn Thr Val Asp Val Ala Ile
           195          200          205
Arg Arg Leu Arg Ala Lys Val Asp Asp Pro Phe Pro Glu Lys Leu Ile
           210          215          220
Ala Thr Ile Arg Gly Met Gly Tyr Ser Phe Val Ala Val Lys Lys
225          230          235

```

<210> 368

<211> 172

<212> PRT

<213> Escherichia coli

<400> 368

```

Met Ile Leu Lys Ser Ala Ile Ser Ala Asp Ser Leu Leu Ala Lys Asp
 1           5           10           15
Ala Phe Arg Ala Ser Phe His Leu His Phe Leu Arg Asn His Gly Ile
           20           25           30
Thr Asn Lys Ile Ser Leu Val Ser Tyr Ile Val Trp Gln Glu Arg Tyr
           35           40           45
Ala Thr Asp Ile Thr Asp Pro Gln Ser Gly Glu Phe Met Thr Ile Lys
           50           55           60
Asn Lys Met Leu Leu Gly Ala Leu Leu Leu Val Thr Ser Ala Ala Trp
65           70           75           80
Ala Ala Pro Ala Thr Ala Gly Ser Thr Asn Thr Ser Gly Ile Ser Lys
           85           90           95
Tyr Glu Leu Ser Ser Phe Ile Ala Asp Phe Lys His Phe Lys Pro Gly
           100          105          110
Asp Thr Val Pro Glu Met Tyr Arg Thr Asp Glu Tyr Asn Ile Lys Gln
           115          120          125
Trp Gln Leu Arg Asn Leu Pro Ala Pro Asp Ala Gly Thr His Trp Thr
           130          135          140
Tyr Met Gly Gly Ala Tyr Val Leu Ile Ser Asp Thr Asp Gly Lys Ile
145          150          155          160
Ile Lys Ala Tyr Asp Gly Glu Ile Phe Tyr His Arg
           165          170

```

<210> 369
 <211> 274
 <212> PRT
 <213> Escherichia coli

<400> 369

```

Met Thr Glu Phe Thr Thr Leu Leu Gln Gln Gly Asn Ala Trp Phe Phe
 1      5      10      15
Ile Pro Ser Ala Ile Leu Leu Gly Ala Leu His Gly Leu Glu Pro Gly
      20      25      30
His Ser Lys Thr Met Met Ala Ala Phe Ile Ile Ala Ile Lys Gly Thr
      35      40      45
Ile Lys Gln Ala Val Met Leu Gly Leu Ala Ala Thr Ile Ser His Thr
      50      55      60
Ala Val Val Trp Leu Ile Ala Phe Gly Gly Met Val Ile Ser Lys Arg
65      70      75      80
Phe Thr Ala Gln Ser Ala Glu Pro Trp Leu Gln Leu Ile Ser Ala Val
      85      90      95
Ile Ile Ile Ser Thr Ala Phe Trp Met Phe Trp Arg Thr Trp Arg Gly
      100     105     110
Glu Arg Asn Trp Leu Glu Asn Met His Gly His Asp Tyr Glu His His
      115     120     125
His His Asp His Glu His His His Asp His Gly His His His His
      130     135     140
Glu His Gly Glu Tyr Gln Asp Ala His Ala Arg Ala His Ala Asn Asp
145     150     155     160
Ile Lys Arg Arg Phe Asp Gly Arg Glu Val Thr Asn Trp Gln Ile Leu
      165     170     175
Leu Phe Gly Leu Thr Gly Gly Leu Ile Pro Cys Pro Ala Ala Ile Thr
      180     185     190
Val Leu Leu Ile Cys Ile Gln Leu Lys Ala Leu Thr Leu Gly Ala Thr
      195     200     205
Leu Val Val Ser Phe Ser Ile Gly Leu Ala Leu Thr Leu Val Thr Val
      210     215     220
Gly Val Gly Ala Ala Ile Ser Val Gln Gln Val Ala Lys Arg Trp Ser
225     230     235     240
Gly Phe Asn Thr Leu Ala Lys Arg Ala Pro Tyr Phe Ser Ser Leu Leu
      245     250     255
Ile Gly Leu Val Gly Val Tyr Met Gly Val His Gly Phe Met Gly Ile
      260     265     270
Met Arg

```

<210> 370
 <211> 82
 <212> PRT
 <213> Escherichia coli

<400> 370

```

Met Cys Ile Gly Val Pro Gly Gln Val Leu Ala Val Gly Glu Asp Ile
 1      5      10      15
His Gln Leu Ala Gln Val Glu Val Cys Gly Ile Lys Arg Asp Val Asn
      20      25      30
Ile Ala Leu Ile Cys Glu Gly Asn Pro Ala Asp Leu Leu Gly Gln Trp
      35      40      45
Val Leu Val His Val Gly Phe Ala Met Ser Ile Ile Asp Glu Asp Glu
      50      55      60
Ala Lys Ala Thr Leu Asp Ala Leu Arg Gln Met Asp Tyr Asp Ile Thr
65      70      75      80
Ser Ala

```

<210> 371
 <211> 113
 <212> PRT
 <213> Escherichia coli

<400> 371
 Met His Glu Leu Ser Leu Cys Gln Ser Ala Val Glu Ile Ile Gln Arg
 1 5 10 15
 Gln Ala Glu Gln His Asp Val Lys Arg Val Thr Ala Val Trp Leu Glu
 20 25 30
 Ile Gly Ala Leu Ser Cys Val Glu Glu Ser Ala Val Arg Phe Ser Phe
 35 40 45
 Glu Ile Val Cys His Gly Thr Val Ala Gln Gly Cys Asp Leu His Ile
 50 55 60
 Val Tyr Lys Pro Ala Gln Ala Trp Cys Trp Asp Cys Ser Gln Val Val
 65 70 75 80
 Glu Ile His Gln His Asp Ala Gln Cys Pro Leu Cys His Gly Glu Arg
 85 90 95
 Leu Arg Val Asp Thr Gly Asp Ser Leu Ile Val Lys Ser Ile Glu Val
 100 105 110
 Glu

<210> 372
 <211> 162
 <212> PRT
 <213> Escherichia coli

<400> 372
 Met Thr Glu Glu Ile Ala Gly Phe Gln Thr Ser Pro Lys Ala Gln Val
 1 5 10 15
 Gln Ala Ala Phe Glu Glu Ile Ala Arg Ser Met His Asp Leu Ser
 20 25 30
 Phe Leu His Pro Ser Met Pro Val Tyr Val Ser Asp Phe Thr Leu Phe
 35 40 45
 Glu Gly Gln Trp Thr Gly Cys Val Ile Thr Pro Trp Met Leu Ser Ala
 50 55 60
 Val Ile Phe Pro Gly Pro Asp Gln Leu Trp Pro Leu Arg Lys Val Ser
 65 70 75 80
 Glu Lys Ile Gly Leu Gln Leu Pro Tyr Gly Thr Met Thr Phe Thr Val
 85 90 95
 Gly Glu Leu Asp Gly Val Ser Gln Tyr Leu Ser Cys Ser Leu Met Ser
 100 105 110
 Pro Leu Ser His Ser Met Ser Ile Glu Glu Gly Gln Arg Leu Thr Asp
 115 120 125
 Asp Cys Ala Arg Met Ile Leu Ser Leu Pro Val Thr Asn Pro Asp Val
 130 135 140
 Pro His Ala Gly Arg Arg Ala Leu Leu Phe Gly Arg Arg Ser Gly Glu
 145 150 155 160
 Asn Ala

<210> 373
 <211> 164
 <212> PRT
 <213> Escherichia coli

<400> 373

```

Met Arg Ile Leu Val Leu Gly Val Gly Asn Ile Leu Leu Thr Asp Glu
 1      5      10      15
Ala Ile Gly Val Arg Ile Val Glu Ala Leu Glu Gln Arg Tyr Ile Leu
 20      25      30
Pro Asp Tyr Val Glu Ile Leu Asp Gly Gly Thr Ala Gly Met Glu Leu
 35      40      45
Leu Gly Asp Met Ala Asn Arg Asp His Leu Ile Ile Ala Asp Ala Ile
 50      55      60
Val Ser Lys Lys Asn Ala Pro Gly Thr Met Met Ile Leu Arg Asp Glu
 65      70      75      80
Glu Val Pro Ala Leu Phe Thr Asn Lys Ile Ser Pro His Gln Leu Gly
 85      90      95
Leu Ala Asp Val Leu Ser Ala Leu Arg Phe Thr Gly Glu Phe Pro Lys
100      105      110
Lys Leu Thr Leu Val Gly Val Ile Pro Glu Ser Leu Glu Pro His Ile
115      120      125
Gly Leu Thr Pro Thr Val Glu Ala Met Ile Glu Pro Ala Leu Glu Gln
130      135      140
Val Leu Ala Ala Leu Arg Glu Ser Gly Val Glu Ala Ile Pro Arg Glu
145      150      155      160
Ala Ile His Asp

```

<210> 374

<211> 567

<212> PRT

<213> Escherichia coli

<400> 374

```

Met Ser Gln Arg Ile Thr Ile Asp Pro Val Thr Arg Ile Glu Gly His
 1      5      10      15
Leu Arg Ile Asp Cys Glu Ile Glu Asn Gly Val Val Ser Lys Ala Trp
 20      25      30
Ala Ser Gly Thr Met Trp Arg Gly Met Glu Glu Ile Val Lys Asn Arg
 35      40      45
Asp Pro Arg Asp Ala Trp Met Ile Val Gln Arg Ile Cys Gly Val Cys
 50      55      60
Thr Thr Thr His Ala Leu Ser Ser Val Arg Ala Ala Glu Ser Ala Leu
 65      70      75      80
Asn Ile Asp Val Pro Val Asn Ala Gln Tyr Ile Arg Asn Ile Ile Leu
 85      90      95
Ala Ala His Thr Thr His Asp His Ile Val His Phe Tyr Gln Leu Ser
100      105      110
Ala Leu Asp Trp Val Asp Ile Thr Ser Ala Leu Gln Ala Asp Pro Thr
115      120      125
Lys Ala Ser Glu Met Leu Lys Gly Val Ser Thr Trp His Leu Asn Ser
130      135      140
Pro Glu Glu Phe Thr Lys Val Gln Asn Lys Ile Lys Asp Leu Val Ala
145      150      155      160
Ser Gly Gln Leu Gly Ile Phe Ala Asn Gly Tyr Trp Gly His Pro Ala
165      170      175
Met Lys Leu Pro Pro Glu Val Asn Leu Ile Ala Val Ala His Tyr Leu
180      185      190
Gln Ala Leu Glu Cys Gln Arg Asp Ala Asn Arg Val Val Ala Leu Leu
195      200      205
Gly Gly Lys Thr Pro His Ile Gln Asn Leu Ala Val Gly Gly Val Ala
210      215      220
Asn Pro Ile Asn Leu Asp Gly Leu Gly Val Leu Asn Leu Glu Arg Leu
225      230      235      240
Met Tyr Ile Lys Ser Phe Ile Asp Lys Leu Ser Asp Phe Val Glu Gln

```



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<210> 375
<211> 392
<212> PRT
<213> Escherichia coli
```

```

<400> 375
Met Ser His Asp Pro Gln Pro Leu Gly Gly Lys Ile Ile Ser Lys Pro
 1          5          10
Val Met Ile Phe Gly Pro Leu Ile Val Ile Cys Met Leu Leu Ile Val
 20          25          30
Lys Arg Leu Val Phe Gly Leu Gly Ser Val Ser Asp Leu Asn Gly Gly
 35          40          45
Phe Pro Trp Gly Val Trp Ile Ala Phe Asp Leu Leu Ile Gly Thr Gly
 50          55          60
Phe Ala Cys Gly Gly Trp Ala Leu Ala Trp Ala Val Tyr Val Phe Asn
 65          70          75          80
Arg Gly Gln Tyr His Pro Leu Val Arg Pro Ala Leu Leu Ala Ser Leu
 85          90          95

```

Phe Gly Tyr Ser Leu Gly Gly Leu Ser Ile Thr Ile Asp Val Gly Arg
 100 105 110
 Tyr Trp Asn Leu Pro Tyr Phe Tyr Ile Pro Gly His Phe Asn Val Asn
 115 120 125
 Ser Val Leu Phe Glu Thr Ala Val Cys Met Thr Ile Tyr Ile Gly Val
 130 135 140
 Met Ala Leu Glu Phe Ala Pro Ala Leu Phe Glu Arg Leu Gly Trp Lys
 145 150 155 160
 Val Ser Leu Gln Arg Leu Asn Lys Val Met Phe Phe Ile Ile Ala Leu
 165 170 175
 Gly Ala Leu Leu Pro Thr Met His Gln Ser Ser Met Gly Ser Leu Met
 180 185 190
 Ile Ser Ala Gly Tyr Lys Val His Pro Leu Trp Gln Ser Tyr Glu Met
 195 200 205
 Leu Pro Leu Phe Ser Leu Leu Thr Ala Phe Ile Met Gly Phe Ser Ile
 210 215 220
 Val Ile Phe Glu Gly Ser Leu Val Gln Ala Gly Leu Arg Gly Asn Gly
 225 230 235 240
 Pro Asp Glu Lys Ser Leu Phe Val Lys Leu Thr Asn Thr Ile Ser Val
 245 250 255
 Leu Leu Ala Ile Phe Ile Val Leu Arg Phe Gly Glu Leu Ile Tyr Arg
 260 265 270
 Asp Lys Leu Ser Leu Ala Phe Ala Gly Asp Phe Tyr Ser Val Met Phe
 275 280 285
 Trp Ile Glu Val Leu Leu Met Leu Phe Pro Leu Val Val Leu Arg Val
 290 295 300
 Ala Lys Leu Arg Asn Asp Ser Arg Met Leu Phe Leu Ser Ala Leu Ser
 305 310 315 320
 Ala Leu Leu Gly Cys Ala Thr Trp Arg Leu Thr Tyr Ser Leu Val Ala
 325 330 335
 Phe Asn Pro Gly Gly Gly Tyr Ala Tyr Phe Pro Thr Trp Glu Glu Leu
 340 345 350
 Leu Ile Ser Ile Gly Phe Val Ala Ile Glu Ile Cys Ala Tyr Ile Val
 355 360 365
 Leu Ile Arg Leu Leu Pro Ile Leu Pro Pro Leu Lys Gln Asn Asp His
 370 375 380
 Asn Arg His Glu Ala Ser Lys Ala
 385 390

<210> 376

<211> 328

<212> PRT

<213> Escherichia coli

<400> 376

Met Asn Arg Arg Asn Phe Ile Lys Ala Ala Ser Cys Gly Ala Leu Leu
 1 5 10 15
 Thr Gly Ala Leu Pro Ser Val Ser His Ala Ala Ala Glu Asn Arg Pro
 20 25 30
 Pro Ile Pro Gly Ser Leu Gly Met Leu Tyr Asp Ser Thr Leu Cys Val
 35 40 45
 Gly Cys Gln Ala Cys Val Thr Lys Cys Gln Asp Ile Asn Phe Pro Glu
 50 55 60
 Arg Asn Pro Gln Gly Glu Gln Thr Trp Ser Asn Asn Asp Lys Leu Ser
 65 70 75 80
 Pro Tyr Thr Asn Asn Ile Ile Gln Val Trp Thr Ser Gly Thr Gly Val
 85 90 95
 Asn Lys Asp Gln Glu Glu Asn Gly Tyr Ala Tyr Ile Lys Lys Gln Cys
 100 105 110
 Met His Cys Val Asp Pro Asn Cys Val Ser Val Cys Pro Val Ser Ala

```

      115              120              125
Leu Lys Lys Asp Pro Lys Thr Gly Ile Val His Tyr Asp Lys Asp Val
  130              135              140
Cys Thr Gly Cys Arg Tyr Cys Met Val Ala Cys Pro Tyr Asn Val Pro
  145              150              155              160
Lys Tyr Asp Tyr Asn Asn Pro Phe Gly Ala Leu His Lys Cys Glu Leu
      165              170              175
Cys Asn Gln Lys Gly Val Glu Arg Leu Asp Lys Gly Gly Leu Pro Gly
      180              185              190
Cys Val Glu Val Cys Pro Ala Gly Ala Val Ile Phe Gly Thr Arg Glu
      195              200              205
Glu Leu Met Ala Glu Ala Lys Lys Arg Leu Ala Leu Lys Pro Gly Ser
      210              215              220
Glu Tyr His Tyr Pro Arg Gln Thr Leu Lys Ser Gly Asp Thr Tyr Leu
  225              230              235              240
His Thr Val Pro Lys Tyr Tyr Pro His Leu Tyr Gly Glu Lys Glu Gly
      245              250              255
Gly Gly Thr Gln Val Leu Val Leu Thr Gly Val Pro Tyr Glu Asn Leu
      260              265              270
Asp Leu Pro Lys Leu Asp Asp Leu Ser Thr Gly Ala Arg Ser Glu Asn
      275              280              285
Ile Gln His Thr Leu Tyr Lys Gly Met Met Leu Pro Leu Ala Val Leu
      290              295              300
Ala Gly Leu Thr Val Leu Val Arg Arg Asn Thr Lys Asn Asp His His
  305              310              315              320
Asp Gly Gly Asp Asp His Glu Ser
      325

```

<210> 377

<211> 824

<212> PRT

<213> Escherichia coli

<400> 377

```

Met Leu Gln Cys Gly Ala Lys Asn Val Asn Pro Leu Glu Arg Phe Val
  1              5              10              15
Ser Ser Leu Pro Val Ala Ala Val Leu Pro Glu Leu Leu Thr Ala Leu
      20              25              30
Asp Cys Ala Pro Gln Val Leu Leu Ser Ala Pro Thr Gly Ala Gly Lys
      35              40              45
Ser Thr Trp Leu Pro Leu Gln Leu Leu Ala His Pro Gly Ile Asn Gly
      50              55              60
Lys Ile Ile Leu Leu Glu Pro Arg Arg Leu Ala Ala Arg Asn Val Ala
      65              70              75              80
Gln Arg Leu Ala Glu Leu Leu Asn Glu Lys Pro Gly Asp Thr Val Gly
      85              90              95
Tyr Arg Met Arg Ala Gln Asn Cys Val Gly Pro Asn Thr Arg Leu Glu
      100              105              110
Val Val Thr Glu Gly Val Leu Thr Arg Met Ile Gln Arg Asp Pro Glu
      115              120              125
Leu Ser Gly Val Gly Leu Val Ile Leu Asp Glu Phe His Glu Arg Ser
      130              135              140
Leu Gln Ala Asp Leu Ala Leu Ala Leu Leu Asp Val Gln Gln Gly
      145              150              155              160
Leu Arg Asp Asp Leu Lys Leu Leu Ile Met Ser Ala Thr Leu Asp Asn
      165              170              175
Asp Arg Leu Gln Gln Met Leu Pro Glu Ala Pro Val Val Ile Ser Glu
      180              185              190
Gly Arg Ser Phe Pro Val Glu Arg Arg Tyr Leu Pro Leu Pro Ala His
      195              200              205

```

Gln	Arg	Phe	Asp	Asp	Ala	Val	Ala	Val	Ala	Thr	Ala	Glu	Met	Leu	Arg
210						215					220				
Gln	Glu	Ser	Gly	Ser	Leu	Leu	Phe	Leu	Pro	Gly	Val	Gly	Glu	Ile	
225					230				235					240	
Gln	Arg	Val	Gln	Glu	Gln	Leu	Ala	Ser	Arg	Ile	Gly	Ser	Asp	Val	Leu
				245					250					255	
Leu	Cys	Pro	Leu	Tyr	Gly	Ala	Leu	Ser	Leu	Asn	Asp	Gln	Arg	Lys	Ala
			260					265					270		
Ile	Leu	Pro	Ala	Pro	Gln	Gly	Met	Arg	Lys	Val	Val	Leu	Ala	Thr	Asn
		275					280						285		
Ile	Ala	Glu	Thr	Ser	Leu	Thr	Ile	Glu	Gly	Ile	Arg	Leu	Val	Val	Asp
	290					295					300				
Cys	Ala	Gln	Glu	Arg	Val	Ala	Arg	Phe	Asp	Pro	Arg	Thr	Gly	Leu	Thr
305					310					315					320
Arg	Leu	Ile	Thr	Gln	Arg	Val	Ser	Gln	Ala	Ser	Met	Thr	Gln	Arg	Ala
				325					330					335	
Gly	Arg	Ala	Gly	Arg	Leu	Glu	Pro	Gly	Ile	Ser	Leu	His	Leu	Ile	Ala
			340					345					350		
Lys	Glu	Gln	Ala	Glu	Arg	Ala	Ala	Ala	Gln	Ser	Glu	Pro	Glu	Ile	Leu
		355					360					365			
Gln	Ser	Asp	Leu	Ser	Gly	Leu	Leu	Met	Glu	Leu	Leu	Gln	Trp	Gly	Cys
370						375					380				
Ser	Asp	Pro	Ala	Gln	Met	Ser	Trp	Leu	Asp	Gln	Pro	Pro	Val	Val	Asn
385				390					395						400
Leu	Leu	Ala	Ala	Lys	Arg	Leu	Leu	Gln	Met	Leu	Gly	Ala	Leu	Glu	Gly
				405					410					415	
Glu	Arg	Leu	Ser	Ala	Gln	Gly	Gln	Lys	Met	Ala	Ala	Leu	Gly	Asn	Asp
			420					425					430		
Pro	Arg	Leu	Ala	Ala	Met	Leu	Val	Ser	Ala	Lys	Asn	Asp	Asp	Glu	Ala
		435					440					445			
Ala	Thr	Ala	Ala	Lys	Ile	Ala	Ala	Ile	Leu	Glu	Glu	Pro	Pro	Arg	Met
	450					455					460				
Gly	Asn	Ser	Asp	Leu	Gly	Val	Ala	Phe	Ser	Arg	Asn	Gln	Pro	Ala	Trp
465					470				475						480
Gln	Gln	Arg	Ser	Gln	Gln	Leu	Leu	Lys	Arg	Leu	Asn	Val	Arg	Gly	Gly
				485					490					495	
Glu	Ala	Asp	Ser	Ser	Leu	Ile	Ala	Pro	Leu	Leu	Ala	Gly	Ala	Phe	Ala
			500					505					510		
Asp	Arg	Ile	Ala	Arg	Arg	Arg	Gly	Gln	Asp	Gly	Arg	Tyr	Gln	Leu	Ala
		515					520					525			
Asn	Gly	Met	Gly	Ala	Met	Leu	Asp	Ala	Asn	Asp	Ala	Leu	Ser	Arg	His
530						535					540				
Glu	Trp	Leu	Ile	Ala	Pro	Leu	Leu	Gln	Gly	Ser	Ala	Ser	Pro	Asp	
545				550					555					560	
Ala	Arg	Ile	Leu	Leu	Ala	Leu	Leu	Val	Asp	Ile	Asp	Glu	Leu	Val	Gln
				565					570					575	
Arg	Cys	Pro	Gln	Leu	Val	Gln	Gln	Ser	Asp	Thr	Val	Glu	Trp	Asp	Asp
			580					585					590		
Ala	Gln	Gly	Thr	Leu	Lys	Ala	Trp	Arg	Arg	Leu	Gln	Ile	Gly	Gln	Leu
		595					600					605			
Thr	Val	Lys	Val	Gln	Pro	Leu	Ala	Lys	Pro	Ser	Glu	Asp	Glu	Leu	His
	610					615					620				
Gln	Ala	Met	Leu	Asn	Gly	Ile	Arg	Asp	Lys	Gly	Leu	Ser	Val	Leu	Asn
625					630					635					640
Trp	Thr	Ala	Glu	Ala	Glu	Gln	Leu	Arg	Leu	Arg	Leu	Leu	Cys	Ala	Ala
				645					650					655	
Lys	Trp	Leu	Pro	Glu	Tyr	Asp	Trp	Pro	Ala	Val	Asp	Asp	Glu	Ser	Leu
			660					665					670		
Leu	Ala	Ala	Leu	Glu	Thr	Trp	Leu	Leu	Pro	His	Met	Thr	Gly	Val	His
			675				680						685		

Ser Leu Arg Gly Leu Lys Ser Leu Asp Ile Tyr Gln Ala Leu Arg Gly
 690 695 700
 Leu Leu Asp Trp Gly Met Gln Gln Arg Leu Asp Ser Glu Leu Pro Ala
 705 710 715 720
 His Tyr Thr Val Pro Thr Gly Ser Arg Ile Ala Ile Arg Tyr His Glu
 725 730 735
 Asp Asn Pro Pro Ala Leu Ala Val Arg Met Gln Glu Met Phe Gly Glu
 740 745 750
 Ala Thr Asn Pro Thr Ile Ala Gln Gly Arg Val Pro Leu Val Leu Glu
 755 760 765
 Leu Leu Ser Pro Ala Gln Arg Pro Leu Gln Ile Thr Arg Asp Leu Ser
 770 775 780
 Asp Phe Trp Lys Gly Ala Tyr Arg Glu Val Gln Lys Glu Met Lys Gly
 785 790 795 800
 Arg Tyr Pro Lys His Val Trp Pro Asp Asp Pro Ala Asn Thr Ala Pro
 805 810 815
 Thr Arg Arg Thr Lys Lys Tyr Ser
 820

<210> 378

<211> 316

<212> PRT

<213> Escherichia coli

<400> 378

Met Ser Lys Leu Asp Thr Phe Ile Gln His Ala Val Asn Ala Val Pro
 1 5 10 15
 Val Ser Gly Thr Ser Leu Ile Ser Ser Leu Tyr Gly Asp Ser Leu Ser
 20 25 30
 His Arg Gly Gly Glu Ile Trp Leu Gly Ser Leu Ala Ala Leu Leu Glu
 35 40 45
 Gly Leu Gly Phe Gly Glu Arg Phe Val Arg Thr Ala Leu Phe Arg Leu
 50 55 60
 Asn Lys Glu Gly Trp Leu Asp Val Ser Arg Ile Gly Arg Arg Ser Phe
 65 70 75 80
 Tyr Ser Leu Ser Asp Lys Gly Leu Arg Leu Thr Arg Arg Ala Glu Ser
 85 90 95
 Lys Ile Tyr Arg Ala Glu Gln Pro Ala Trp Asp Gly Lys Trp Leu Leu
 100 105 110
 Leu Leu Ser Glu Gly Leu Asp Lys Ser Thr Leu Ala Asp Val Lys Lys
 115 120 125
 Gln Leu Ile Trp Gln Gly Phe Gly Ala Leu Ala Pro Ser Leu Met Ala
 130 135 140
 Ser Pro Ser Gln Lys Leu Ala Asp Val Gln Thr Leu Leu His Glu Ala
 145 150 155 160
 Gly Val Ala Asp Asn Val Ile Cys Phe Glu Ala Gln Ile Pro Leu Ala
 165 170 175
 Leu Ser Arg Ala Ala Leu Arg Ala Arg Val Glu Glu Cys Trp His Leu
 180 185 190
 Thr Glu Gln Asn Ala Met Tyr Glu Thr Phe Ile Gln Ser Phe Arg Pro
 195 200 205
 Leu Val Pro Leu Leu Lys Glu Ala Ala Asp Glu Leu Thr Pro Glu Arg
 210 215 220
 Ala Phe His Ile Gln Leu Leu Leu Ile His Phe Tyr Arg Arg Val Val
 225 230 235 240
 Leu Lys Asp Pro Leu Leu Pro Glu Glu Leu Leu Pro Ala His Trp Ala
 245 250 255
 Gly His Thr Ala Arg Gln Leu Cys Ile Asn Ile Tyr Gln Arg Val Ala
 260 265 270
 Pro Ala Ala Leu Ala Phe Val Ser Glu Lys Gly Glu Thr Ser Val Gly

275 280 285
 Glu Leu Pro Ala Pro Gly Ser Leu Tyr Phe Gln Arg Phe Gly Gly Leu
 290 295 300
 Asn Ile Glu Gln Glu Ala Leu Cys Gln Phe Ile Arg
 305 310 315

<210> 379

<211> 196

<212> PRT

<213> Escherichia coli

<400> 379

Met Pro Ile Tyr Gln Ile Asp Gly Leu Thr Pro Val Val Pro Glu Glu
 1 5 10 15
 Ser Phe Val His Pro Thr Ala Val Leu Ile Gly Asp Val Ile Leu Gly
 20 25 30
 Lys Gly Val Tyr Val Gly Pro Asn Ala Ser Leu Arg Gly Asp Phe Gly
 35 40 45
 Arg Ile Val Val Lys Asp Gly Ala Asn Ile Gln Asp Asn Cys Val Met
 50 55 60
 His Gly Phe Pro Glu Gln Asp Thr Val Val Gly Glu Asp Gly His Ile
 65 70 75 80
 Gly His Ser Ala Ile Leu His Gly Cys Ile Ile Arg Arg Asn Ala Leu
 85 90 95
 Val Gly Met Asn Ala Val Val Met Asp Gly Ala Val Ile Gly Glu Asn
 100 105 110
 Ser Ile Val Gly Ala Ser Ala Phe Val Lys Ala Lys Ala Glu Met Pro
 115 120 125
 Ala Asn Tyr Leu Ile Val Gly Ser Pro Ala Lys Ala Ile Arg Glu Leu
 130 135 140
 Ser Glu Gln Glu Leu Ala Trp Lys Lys Gln Gly Thr His Glu Tyr Gln
 145 150 155 160
 Val Leu Val Thr Arg Cys Lys Gln Thr Leu His Gln Val Glu Pro Leu
 165 170 175
 Arg Glu Ile Glu Pro Gly Arg Lys Arg Leu Val Phe Asp Glu Asn Leu
 180 185 190
 Arg Pro Lys Gln
 195

<210> 380

<211> 426

<212> PRT

<213> Escherichia coli

<400> 380

Met Lys His Leu Thr Glu Met Val Arg Gln His Lys Ala Gly Lys Thr
 1 5 10 15
 Asn Gly Ile Tyr Ala Val Cys Ser Ala His Pro Leu Val Leu Glu Ala
 20 25 30
 Ala Ile Arg Tyr Ala Ser Ala Asn Gln Thr Pro Leu Leu Ile Glu Ala
 35 40 45
 Thr Ser Asn Gln Val Asp Gln Phe Gly Gly Tyr Thr Gly Met Thr Pro
 50 55 60
 Ala Asp Phe Arg Gly Phe Val Cys Gln Leu Ala Asp Ser Leu Asn Phe
 65 70 75 80
 Pro Gln Asp Ala Leu Ile Leu Gly Gly Asp His Leu Gly Pro Asn Arg
 85 90 95
 Trp Gln Asn Leu Pro Ala Ala Gln Ala Met Ala Asn Ala Asp Asp Leu
 100 105 110
 Ile Lys Ser Tyr Val Ala Ala Gly Phe Lys Lys Ile His Leu Asp Cys

```

      115      120      125
Ser Met Ser Cys Gln Asp Asp Pro Ile Pro Leu Thr Asp Asp Ile Val
130      135      140
Ala Glu Arg Ala Ala Arg Leu Ala Lys Val Ala Glu Glu Thr Cys Leu
145      150      155      160
Glu His Phe Gly Glu Ala Asp Leu Glu Tyr Val Ile Gly Thr Glu Val
      165      170      175
Pro Val Pro Gly Gly Ala His Glu Thr Leu Ser Glu Leu Ala Val Thr
      180      185      190
Thr Pro Asp Ala Ala Arg Ala Thr Leu Glu Ala His Arg His Ala Phe
      195      200      205
Glu Lys Gln Gly Leu Asn Ala Ile Trp Pro Arg Ile Ile Ala Leu Val
      210      215      220
Val Gln Pro Gly Val Glu Phe Asp His Thr Asn Val Ile Asp Tyr Gln
225      230      235      240
Pro Ala Lys Ala Ser Ala Leu Ser Gln Met Val Glu Asn Tyr Glu Thr
      245      250      255
Leu Ile Phe Glu Ala His Ser Thr Asp Tyr Gln Thr Pro Gln Ser Leu
      260      265      270
Arg Gln Leu Val Ile Asp His Phe Ala Ile Leu Lys Val Gly Pro Ala
      275      280      285
Leu Thr Phe Ala Leu Arg Glu Ala Leu Phe Ser Leu Ala Ala Ile Glu
      290      295      300
Glu Glu Leu Val Pro Ala Lys Ala Cys Ser Gly Leu Arg Gln Val Leu
305      310      315      320
Glu Asp Val Met Leu Asp Arg Pro Glu Tyr Trp Gln Ser His Tyr His
      325      330      335
Gly Asp Gly Asn Ala Arg Arg Leu Ala Arg Gly Tyr Ser Tyr Ser Asp
      340      345      350
Arg Val Arg Tyr Tyr Trp Pro Asp Ser Gln Ile Asp Asp Ala Phe Ala
      355      360      365
His Leu Val Arg Asn Leu Ala Asp Ser Pro Ile Pro Leu Pro Leu Ile
      370      375      380
Ser Gln Tyr Leu Pro Leu Gln Tyr Val Lys Val Arg Ser Gly Glu Leu
385      390      395      400
Gln Pro Thr Pro Arg Glu Leu Ile Ile Asn His Ile Gln Asp Ile Leu
      405      410      415
Ala Gln Tyr His Thr Ala Cys Glu Gly Gln
      420      425

```

<210> 381

<211> 169

<212> PRT

<213> Escherichia coli

<400> 381

```

Met Lys Ala Asn Lys Gln Asn Lys Glu Glu His Ala Met Pro Asn Ile
1      5      10      15
Val Leu Ser Arg Ile Asp Glu Arg Leu Ile His Gly Gln Val Gly Val
      20      25      30
Gln Trp Val Gly Phe Ala Gly Ala Asn Leu Val Leu Val Ala Asn Asp
      35      40      45
Glu Val Ala Glu Asp Pro Val Gln Gln Asn Leu Met Glu Met Val Leu
      50      55      60
Ala Glu Gly Ile Ala Val Arg Phe Trp Thr Leu Gln Lys Val Ile Asp
      65      70      75      80
Asn Ile His Arg Ala Ala Asp Arg Gln Lys Ile Leu Leu Val Cys Lys
      85      90      95
Thr Pro Ala Asp Phe Leu Thr Leu Val Lys Gly Gly Val Pro Val Asn
      100      105      110

```

Arg Ile Asn Val Gly Asn Met His Tyr Ala Asn Gly Lys Gln Gln Ile
 115 120 125
 Ala Lys Thr Val Ser Val Asp Ala Gly Asp Ile Ala Ala Phe Asn Asp
 130 135 140
 Leu Lys Thr Ala Gly Val Glu Cys Phe Val Gln Gly Val Pro Thr Glu
 145 150 155 160
 Pro Ala Val Asp Leu Phe Lys Leu Leu
 165

<210> 382

<211> 133

<212> PRT

<213> Escherichia coli

<400> 382

Met Glu Ile Ser Leu Leu Gln Ala Phe Ala Leu Gly Ile Ile Ala Phe
 1 5 10 15
 Ile Ala Gly Leu Asp Met Phe Asn Gly Leu Thr His Met His Arg Pro
 20 25 30
 Val Val Leu Gly Pro Leu Val Gly Leu Val Leu Gly Asp Leu His Thr
 35 40 45
 Gly Ile Leu Thr Gly Gly Thr Leu Glu Leu Val Trp Met Gly Leu Ala
 50 55 60
 Pro Leu Ala Gly Ala Gln Pro Pro Asn Val Ile Ile Gly Thr Ile Val
 65 70 75 80
 Gly Thr Ala Phe Ala Ile Thr Thr Gly Val Lys Pro Asp Val Ala Val
 85 90 95
 Gly Val Ala Val Pro Phe Ala Val Ala Val Gln Met Gly Ile Thr Phe
 100 105 110
 Leu Phe Ser Val Met Ser Gly Val Met Ser Arg Cys Asp Leu Ala Thr
 115 120 125
 Asn Pro Arg Arg Ile
 130

<210> 383

<211> 167

<212> PRT

<213> Escherichia coli

<400> 383

Met His Cys Tyr Asn Gly Met Thr Gly Leu His His Arg Glu Pro Gly
 1 5 10 15
 Met Val Gly Ala Gly Leu Thr Asp Lys Arg Ala Trp Leu Glu Leu Ile
 20 25 30
 Ala Asp Gly His His Val His Pro Ala Ala Met Ser Leu Cys Cys Cys
 35 40 45
 Cys Ala Lys Glu Arg Ile Val Leu Ile Thr Asp Ala Met Gln Ala Ala
 50 55 60
 Gly Met Pro Asp Gly Arg Tyr Thr Leu Cys Gly Glu Glu Val Gln Met
 65 70 75 80
 His Gly Gly Val Val Arg Thr Ala Ser Gly Gly Leu Ala Gly Ser Thr
 85 90 95
 Leu Ser Val Asp Ala Ala Val Arg Asn Met Val Glu Leu Thr Gly Val
 100 105 110
 Thr Pro Ala Glu Ala Ile His Met Ala Ser Leu His Pro Ala Arg Met
 115 120 125
 Leu Gly Val Asp Gly Val Leu Gly Ser Leu Lys Pro Gly Lys Arg Ala
 130 135 140
 Arg Val Val Ala Leu Asp Ser Gly Leu His Val Gln Gln Ile Trp Ile
 145 150 155 160

Gln Gly Gln Leu Ala Ser Phe
165

<210> 384

<211> 384

<212> PRT

<213> Escherichia coli

<400> 384

```

Met Pro Glu Asn Tyr Thr Pro Ala Ala Ala Ala Thr Gly Thr Trp Thr
 1          5          10          15
Glu Glu Glu Ile Arg His Gln Pro Arg Ala Trp Ile Arg Ser Leu Thr
 20          25          30
Asn Ile Asp Ala Leu Arg Ser Ala Leu Asn Asn Phe Leu Glu Pro Leu
 35          40          45
Leu Arg Lys Glu Asn Leu Arg Ile Ile Leu Thr Gly Ala Gly Thr Ser
 50          55          60
Ala Phe Ile Gly Asp Ile Ile Ala Pro Trp Leu Ala Ser His Thr Gly
 65          70          75          80
Lys Asn Phe Ser Ala Val Pro Thr Thr Asp Leu Val Thr Asn Pro Met
 85          90          95
Asp Tyr Leu Asn Pro Ala His Pro Leu Leu Leu Ile Ser Phe Gly Arg
100          105          110
Ser Gly Asn Ser Pro Glu Ser Val Ala Ala Val Glu Leu Ala Asn Gln
115          120          125
Phe Val Pro Glu Cys Tyr His Leu Pro Ile Thr Cys Asn Glu Ala Gly
130          135          140
Ala Leu Tyr Gln Asn Ala Ile Asn Ser Asp Asn Ala Phe Ala Leu Leu
145          150          155          160
Met Pro Ala Glu Thr His Asp Arg Gly Phe Ala Met Thr Ser Ser Ile
165          170          175
Thr Thr Met Met Ala Ser Cys Leu Ala Val Phe Ala Pro Glu Thr Ile
180          185          190
Asn Ser Gln Thr Phe Arg Asp Val Ala Asp Arg Cys Gln Ala Ile Leu
195          200          205
Thr Ser Leu Gly Asp Phe Ser Glu Gly Val Phe Gly Tyr Ala Pro Trp
210          215          220
Lys Arg Ile Val Tyr Leu Gly Ser Gly Gly Leu Gln Gly Ala Ala Arg
225          230          235          240
Glu Ser Ala Leu Lys Val Leu Glu Leu Thr Ala Gly Lys Leu Ala Ala
245          250          255
Phe Tyr Asp Ser Pro Thr Gly Phe Arg His Gly Pro Lys Ser Leu Val
260          265          270
Asp Asp Glu Thr Leu Val Val Val Phe Val Ser Ser His Pro Tyr Thr
275          280          285
Arg Gln Tyr Asp Leu Asp Leu Leu Ala Glu Leu Arg Arg Asp Asn Gln
290          295          300
Ala Met Arg Val Ile Ala Ile Ala Ala Glu Ser Ser Asp Ile Val Ala
305          310          315          320
Ala Gly Pro His Ile Ile Leu Pro Pro Ser Arg His Phe Ile Asp Val
325          330          335
Glu Gln Ala Phe Cys Phe Leu Met Tyr Ala Gln Thr Phe Ala Leu Met
340          345          350
Gln Ser Leu His Met Gly Asn Thr Pro Asp Thr Pro Ser Ala Ser Gly
355          360          365
Thr Val Asn Arg Val Val Gln Gly Val Ile Ile His Pro Trp Gln Ala
370          375          380

```

<210> 385

<211> 286

<212> PRT

<213> Escherichia coli

<400> 385

```

Met Ser Ile Ile Ser Thr Lys Tyr Leu Leu Gln Asp Ala Gln Ala Asn
 1           5           10           15
Gly Tyr Ala Val Pro Ala Phe Asn Ile His Asn Ala Glu Thr Ile Gln
          20           25           30
Ala Ile Leu Glu Val Cys Ser Glu Met Arg Ser Pro Val Ile Leu Ala
      35           40           45
Gly Thr Pro Gly Thr Phe Lys His Ile Ala Leu Glu Glu Ile Tyr Ala
      50           55           60
Leu Cys Ser Ala Tyr Ser Thr Thr Tyr Asn Met Pro Leu Ala Leu His
      65           70           75           80
Leu Asp His His Glu Ser Leu Asp Asp Ile Arg Arg Lys Val His Ala
          85           90           95
Gly Val Arg Ser Ala Met Ile Asp Gly Ser His Phe Pro Phe Ala Glu
          100          105          110
Asn Val Lys Leu Val Lys Ser Val Val Asp Phe Cys His Ser Gln Asp
          115          120          125
Cys Ser Val Glu Ala Glu Leu Gly Arg Leu Gly Gly Val Glu Asp Asp
      130          135          140
Met Ser Val Asp Ala Glu Ser Ala Phe Leu Thr Asp Pro Gln Glu Ala
      145          150          155          160
Lys Arg Phe Val Glu Leu Thr Gly Val Asp Ser Leu Ala Val Ala Ile
          165          170          175
Gly Thr Ala His Gly Leu Tyr Ser Lys Thr Pro Lys Ile Asp Phe Gln
          180          185          190
Arg Leu Ala Glu Ile Arg Glu Val Val Asp Val Pro Leu Val Leu His
          195          200          205
Gly Ala Ser Asp Val Pro Asp Glu Phe Val Arg Arg Thr Ile Glu Leu
          210          215          220
Gly Val Thr Lys Val Asn Val Ala Thr Glu Leu Lys Ile Ala Phe Ala
      225          230          235          240
Gly Ala Val Lys Ala Trp Phe Ala Glu Asn Pro Gln Gly Asn Asp Pro
          245          250          255
Arg Tyr Tyr Met Arg Val Gly Met Asp Ala Met Lys Glu Val Val Arg
          260          265          270
Asn Lys Ile Asn Val Cys Gly Ser Ala Asn Arg Ile Ser Ala
          275          280          285

```

<210> 386

<211> 118

<212> PRT

<213> Escherichia coli

<400> 386

```

Met Ala Arg Ile Ala Gly Ile Asn Ile Pro Asp His Lys His Ala Val
 1           5           10           15
Ile Ala Leu Thr Ser Ile Tyr Gly Val Gly Lys Thr Arg Ser Lys Ala
          20           25           30
Ile Leu Ala Ala Ala Gly Ile Ala Glu Asp Val Lys Ile Ser Glu Leu
          35           40           45
Ser Glu Gly Gln Ile Asp Thr Leu Arg Asp Glu Val Ala Lys Phe Val
          50           55           60
Val Glu Gly Asp Leu Arg Arg Glu Ile Ser Met Ser Ile Lys Arg Leu
      65           70           75           80
Met Asp Leu Gly Cys Tyr Arg Gly Leu Arg His Arg Arg Gly Leu Pro
          85           90           95
Val Arg Gly Gln Arg Thr Lys Thr Asn Ala Arg Thr Arg Lys Gly Pro

```

100 105 110
 Arg Lys Pro Ile Lys Lys
 115

<210> 387
 <211> 129
 <212> PRT
 <213> Escherichia coli

<400> 387
 Met Ala Lys Ala Pro Ile Arg Ala Arg Lys Arg Val Arg Lys Gln Val
 1 5 10 15
 Ser Asp Gly Val Ala His Ile His Ala Ser Phe Asn Asn Thr Ile Val
 20 25 30
 Thr Ile Thr Asp Arg Gln Gly Asn Ala Leu Gly Trp Ala Thr Ala Gly
 35 40 45
 Gly Ser Gly Phe Arg Gly Ser Arg Lys Ser Thr Pro Phe Ala Ala Gln
 50 55 60
 Val Ala Ala Glu Arg Cys Ala Asp Ala Val Lys Glu Tyr Gly Ile Lys
 65 70 75 80
 Asn Leu Glu Val Met Val Lys Gly Pro Gly Pro Gly Arg Glu Ser Thr
 85 90 95
 Ile Arg Ala Leu Asn Ala Ala Gly Phe Arg Ile Thr Asn Ile Thr Asp
 100 105 110
 Val Thr Pro Ile Pro His Asn Gly Cys Arg Pro Pro Lys Lys Arg Arg
 115 120 125
 Val

<210> 388
 <211> 206
 <212> PRT
 <213> Escherichia coli

<400> 388
 Met Ala Arg Tyr Leu Gly Pro Lys Leu Lys Leu Ser Arg Arg Glu Gly
 1 5 10 15
 Thr Asp Leu Phe Leu Lys Ser Gly Val Arg Ala Ile Asp Thr Lys Cys
 20 25 30
 Lys Ile Glu Gln Ala Pro Gly Gln His Gly Ala Arg Lys Pro Arg Leu
 35 40 45
 Ser Asp Tyr Gly Val Gln Leu Arg Glu Lys Gln Lys Val Arg Arg Ile
 50 55 60
 Tyr Gly Val Leu Glu Arg Gln Phe Arg Asn Tyr Tyr Lys Glu Ala Ala
 65 70 75 80
 Arg Leu Lys Gly Asn Thr Gly Glu Asn Leu Leu Ala Leu Leu Glu Gly
 85 90 95
 Arg Leu Asp Asn Val Val Tyr Arg Met Gly Phe Gly Ala Thr Arg Ala
 100 105 110
 Glu Ala Arg Gln Leu Val Ser His Lys Ala Ile Met Val Asn Gly Arg
 115 120 125
 Val Val Asn Ile Ala Ser Tyr Gln Val Ser Pro Asn Asp Val Val Ser
 130 135 140
 Ile Arg Glu Lys Ala Lys Lys Gln Ser Arg Val Lys Ala Ala Leu Glu
 145 150 155 160
 Leu Ala Glu Gln Arg Glu Lys Pro Thr Trp Leu Glu Val Asp Ala Gly
 165 170 175
 Lys Met Glu Gly Thr Phe Lys Arg Lys Pro Glu Arg Ser Asp Leu Ser
 180 185 190
 Ala Asp Ile Asn Glu His Leu Ile Val Glu Leu Tyr Ser Lys

195

200

205

<210> 389

<211> 329

<212> PRT

<213> Escherichia coli

<400> 389

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Met Gln Gly Ser Val Thr Glu Phe Leu Lys Pro Arg Leu Val Asp Ile
 1              5              10              15
Glu Gln Val Ser Ser Thr His Ala Lys Val Thr Leu Glu Pro Leu Glu
      20              25              30
Arg Gly Phe Gly His Thr Leu Gly Asn Ala Leu Arg Arg Ile Leu Leu
      35              40              45
Ser Ser Met Pro Gly Cys Ala Val Thr Glu Val Glu Ile Asp Gly Val
 50              55              60
Leu His Glu Tyr Ser Thr Lys Glu Gly Val Gln Glu Asp Ile Leu Glu
65              70              75              80
Ile Leu Leu Asn Leu Lys Gly Leu Ala Val Arg Val Gln Gly Lys Asp
      85              90              95
Glu Val Ile Leu Thr Leu Asn Lys Ser Gly Ile Gly Pro Val Thr Ala
      100              105              110
Ala Asp Ile Thr His Asp Gly Asp Val Glu Ile Val Lys Pro Gln His
      115              120              125
Val Ile Cys His Leu Thr Asp Glu Asn Ala Ser Ile Ser Met Arg Ile
      130              135              140
Lys Val Gln Arg Gly Arg Gly Tyr Val Pro Ala Ser Thr Arg Ile His
      145              150              155              160
Ser Glu Glu Asp Glu Arg Pro Ile Gly Arg Leu Leu Val Asp Ala Cys
      165              170              175
Tyr Ser Pro Val Glu Arg Ile Ala Tyr Asn Val Glu Ala Ala Arg Val
      180              185              190
Glu Gln Arg Thr Asp Leu Asp Lys Leu Val Ile Glu Met Glu Thr Asn
      195              200              205
Gly Thr Ile Asp Pro Glu Glu Ala Ile Arg Arg Ala Ala Thr Ile Leu
      210              215              220
Ala Glu Gln Leu Glu Ala Phe Val Asp Leu Arg Asp Val Arg Gln Pro
      225              230              235              240
Glu Val Lys Glu Glu Lys Pro Glu Phe Asp Pro Ile Leu Leu Arg Pro
      245              250              255
Val Asp Asp Leu Glu Leu Thr Val Arg Ser Ala Asn Cys Leu Lys Ala
      260              265              270
Glu Ala Ile His Tyr Ile Gly Asp Leu Val Gln Arg Thr Glu Val Glu
      275              280              285
Leu Leu Lys Thr Pro Asn Leu Gly Lys Lys Ser Leu Thr Glu Ile Lys
      290              295              300
Asp Val Leu Ala Ser Arg Gly Leu Ser Leu Gly Met Arg Leu Glu Asn
      305              310              315              320
Trp Pro Pro Ala Ser Ile Ala Asp Glu
      325

```

<210> 390

<211> 127

<212> PRT

<213> Escherichia coli

<400> 390

```

Met Arg His Arg Lys Ser Gly Arg Gln Leu Asn Arg Asn Ser Ser His
 1              5              10              15
Arg Gln Ala Met Phe Arg Asn Met Ala Gly Ser Leu Val Arg His Glu

```

			20					25				30				
Ile	Ile	Lys	Thr	Thr	Leu	Pro	Lys	Ala	Lys	Glu	Leu	Arg	Arg	Val	Val	
		35					40					45				
Glu	Pro	Leu	Ile	Thr	Leu	Ala	Lys	Thr	Asp	Ser	Val	Ala	Asn	Arg	Arg	
	50					55					60					
Leu	Ala	Phe	Ala	Arg	Thr	Arg	Asp	Asn	Glu	Ile	Val	Ala	Lys	Leu	Phe	
65					70					75					80	
Asn	Glu	Leu	Gly	Pro	Arg	Phe	Ala	Ser	Arg	Ala	Gly	Gly	Tyr	Thr	Arg	
				85					90						95	
Ile	Leu	Lys	Cys	Gly	Phe	Arg	Ala	Gly	Asp	Asn	Ala	Pro	Met	Ala	Tyr	
		100						105					110			
Ile	Glu	Leu	Val	Asp	Arg	Ser	Glu	Lys	Ala	Glu	Ala	Ala	Ala	Glu		
		115					120					125				

```
<210> 391
<211> 243
<212> PRT
<213> Escherichia coli
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[illegible]

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<210> 392
<211> 308
<212> PRT
<213> Escherichia coli
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<400> 392
Met Ile Glu Phe Ser His Val Ser Lys Leu Phe Gly Ala Gln Lys Ala

```

1           5           10           15
Val Asn Asp Leu Asn Leu Asn Phe Gln Glu Gly Ser Phe Ser Val Leu
20           25           30
Ile Gly Thr Ser Gly Ser Gly Lys Ser Thr Thr Leu Lys Met Ile Asn
35           40           45
Arg Leu Val Glu His Asp Ser Gly Glu Ile Arg Phe Ala Gly Glu Glu
50           55           60
Ile Arg Ser Leu Pro Val Leu Glu Leu Arg Arg Arg Met Gly Tyr Ala
65           70           75           80
Ile Gln Ser Ile Gly Leu Phe Pro His Trp Ser Val Ala Gln Asn Ile
85           90           95
Ala Thr Val Pro Gln Leu Gln Lys Trp Ser Arg Ala Arg Ile Asp Asp
100          105          110
Arg Ile Asp Glu Leu Met Ala Leu Leu Gly Leu Glu Ser Asn Leu Arg
115          120          125
Glu Arg Tyr Pro His Gln Leu Ser Gly Gly Gln Gln Arg Val Gly
130          135          140
Val Ala Arg Ala Leu Ala Ala Asp Pro Gln Val Leu Leu Met Asp Glu
145          150          155          160
Pro Phe Gly Ala Leu Asp Pro Val Thr Arg Gly Ala Leu Gln Gln Glu
165          170          175
Met Thr Arg Ile His Arg Leu Leu Gly Arg Thr Ile Val Leu Val Thr
180          185          190
His Asp Ile Asp Glu Ala Leu Arg Leu Ala Glu His Leu Val Leu Met
195          200          205
Asp His Gly Glu Val Val Gln Gln Gly Asn Pro Leu Thr Met Leu Thr
210          215          220
Arg Pro Ala Asn Asp Phe Val Arg Gln Phe Phe Gly Arg Ser Glu Leu
225          230          235          240
Gly Val Arg Leu Leu Ser Leu Arg Ser Val Ala Asp Tyr Val Arg Arg
245          250          255
Glu Glu Arg Ala Asp Gly Glu Ala Leu Ala Glu Glu Met Thr Leu Arg
260          265          270
Asp Ala Leu Ser Leu Phe Val Ala Arg Gly Cys Glu Val Leu Pro Val
275          280          285
Val Asn Met Gln Gly Gln Pro Cys Gly Thr Leu His Phe Gln Asp Leu
290          295          300
Leu Val Glu Ala
305

```

<210> 393

<211> 385

<212> PRT

<213> Escherichia coli

<400> 393

```

Met Thr Tyr Phe Arg Ile Asn Pro Val Leu Ala Leu Leu Leu Leu
1           5           10           15
Thr Ala Ile Ala Ala Leu Pro Phe Ile Ser Tyr Ala Pro Asn Arg
20           25           30
Leu Val Ser Gly Glu Gly Arg His Leu Trp Gln Leu Trp Pro Gln Thr
35           40           45
Ile Trp Met Leu Val Gly Val Gly Cys Ala Trp Leu Thr Ala Cys Phe
50           55           60
Ile Pro Gly Lys Lys Gly Ser Ile Cys Ala Leu Ile Leu Ala Gln Phe
65           70           75           80
Val Phe Val Leu Leu Val Trp Gly Ala Gly Lys Ala Ala Thr Gln Leu
85           90           95
Ala Gln Asn Gly Ser Ala Leu Ala Arg Thr Ser Leu Gly Ser Gly Phe
100          105          110

```

Trp Leu Ala Ala Ala Leu Ala Leu Leu Ala Cys Ser Asp Ala Ile Arg
 115 120 125
 Arg Ile Ser Thr His Pro Leu Trp Arg Trp Leu Leu His Met Gln Ile
 130 135 140
 Ala Ile Ile Pro Leu Trp Leu Leu Tyr Ser Gly Thr Leu Asn Asp Leu
 145 150 155 160
 Ser Leu Met Lys Glu Tyr Ala Asn Arg Gln Asp Val Phe Asp Asp Ala
 165 170 175
 Leu Ala Gln His Leu Thr Leu Leu Phe Gly Ala Val Leu Pro Ala Leu
 180 185 190
 Val Ile Gly Val Pro Leu Gly Ile Trp Cys Tyr Phe Ser Thr Ala Arg
 195 200 205
 Gln Gly Ala Ile Phe Ser Leu Leu Asn Val Ile Gln Thr Val Pro Ser
 210 215 220
 Val Ala Leu Phe Gly Leu Leu Ile Ala Pro Leu Ala Ala Leu Val Thr
 225 230 235 240
 Ala Phe Pro Trp Leu Gly Thr Leu Gly Ile Ala Gly Thr Gly Met Thr
 245 250 255
 Pro Ala Leu Ile Ala Leu Val Leu Tyr Ala Leu Leu Pro Leu Val Arg
 260 265 270
 Gly Val Val Val Gly Leu Asn Gln Ile Pro Arg Asp Val Leu Glu Ser
 275 280 285
 Ala Arg Ala Met Gly Met Ser Gly Ala Gln Arg Phe Leu His Val Gln
 290 295 300
 Leu Pro Leu Ala Leu Pro Val Phe Leu Arg Ser Leu Arg Val Val Met
 305 310 315 320
 Val Gln Thr Val Gly Met Ala Val Ile Ala Ala Leu Ile Gly Ala Gly
 325 330 335
 Gly Phe Gly Ala Leu Val Phe Gln Gly Leu Leu Ser Ser Ala Ile Asp
 340 345 350
 Leu Val Leu Leu Gly Val Ile Pro Val Ile Val Leu Ala Val Leu Thr
 355 360 365
 Asp Ala Leu Phe Asp Leu Leu Ile Ala Leu Leu Lys Val Lys Arg Asn
 370 375 380
 Asp
 385

<210> 394
 <211> 305
 <212> PRT
 <213> Escherichia coli

<400> 394
 Met Pro Leu Leu Lys Leu Trp Ala Gly Ser Leu Val Met Leu Ala Ala
 1 5 10 15
 Val Ser Leu Pro Leu Gln Ala Ala Ser Pro Val Lys Val Gly Ser Lys
 20 25 30
 Ile Asp Thr Glu Gly Ala Leu Leu Gly Asn Ile Ile Leu Gln Val Leu
 35 40 45
 Glu Ser His Gly Val Pro Thr Val Asn Lys Val Gln Leu Gly Thr Thr
 50 55 60
 Pro Val Val Arg Gly Ala Ile Thr Ser Gly Glu Leu Asp Ile Tyr Pro
 65 70 75 80
 Glu Tyr Thr Gly Asn Gly Ala Phe Phe Phe Lys Asp Glu Asn Asp Ala
 85 90 95
 Ala Trp Lys Asn Ala Gln Gln Gly Tyr Glu Lys Val Lys Lys Leu Asp
 100 105 110
 Ser Glu His Asn Lys Leu Ile Trp Leu Thr Pro Ala Pro Ala Asn Asn
 115 120 125
 Thr Trp Thr Ile Ala Val Arg Gln Asp Val Ala Glu Lys Asn Lys Leu

```

      130              135              140
Thr Ser Leu Ala Asp Leu Ser Arg Tyr Leu Gln Glu Gly Gly Thr Phe
145              150              155              160
Lys Leu Ala Ala Ser Ala Glu Phe Ile Glu Arg Ala Asp Ala Leu Pro
      165              170              175
Ala Phe Glu Lys Ala Tyr Gly Phe Lys Leu Gly Gln Asp Gln Leu Leu
      180              185              190
Ser Leu Ala Gly Gly Asp Thr Ala Val Thr Ile Lys Ala Ala Ala Gln
      195              200              205
Gln Thr Ser Gly Val Asn Ala Ala Met Ala Tyr Gly Thr Asp Gly Pro
      210              215              220
Val Ala Ala Leu Gly Leu Gln Thr Leu Ser Asp Pro Gln Gly Val Gln
225              230              235              240
Pro Ile Tyr Ala Pro Ala Pro Val Val Arg Glu Ser Val Leu Arg Glu
      245              250              255
Tyr Pro Gln Met Ala Gln Trp Leu Gln Pro Val Phe Ala Ser Leu Asp
      260              265              270
Ala Lys Thr Leu Gln Gln Leu Asn Ala Ser Ile Ala Val Glu Gly Leu
      275              280              285
Asp Ala Lys Lys Val Ala Ala Asp Tyr Leu Lys Gln Lys Gly Trp Thr
290              295              300
Lys
305

```

<210> 395

<211> 207

<212> PRT

<213> Escherichia coli

<400> 395

```

Met Leu Val Tyr Trp Leu Asp Ile Val Gly Thr Ala Val Phe Ala Ile
 1      5      10      15
Ser Gly Val Leu Leu Ala Gly Lys Leu Arg Met Asp Pro Phe Gly Val
      20      25      30
Leu Val Leu Gly Val Val Thr Ala Val Gly Gly Gly Thr Ile Arg Asp
      35      40      45
Met Ala Leu Asp His Gly Pro Val Phe Trp Val Lys Asp Pro Thr Asp
50      55      60
Leu Val Val Ala Met Val Thr Ser Met Leu Thr Ile Val Leu Val Arg
65      70      75      80
Gln Pro Arg Arg Leu Pro Lys Trp Met Leu Pro Val Leu Asp Ala Val
      85      90      95
Gly Leu Ala Val Phe Val Gly Ile Gly Val Asn Lys Ala Phe Asn Ala
      100      105      110
Glu Ala Gly Pro Leu Ile Ala Val Cys Met Gly Val Ile Thr Gly Val
      115      120      125
Gly Gly Gly Ile Ile Arg Asp Val Leu Ala Arg Glu Ile Pro Met Ile
130      135      140
Leu Arg Thr Glu Ile Tyr Ala Thr Ala Cys Ile Ile Gly Gly Ile Val
145      150      155      160
His Ala Thr Ala Tyr Tyr Thr Phe Ser Val Pro Leu Glu Thr Ala Ser
      165      170      175
Met Met Gly Met Val Val Thr Leu Leu Ile Arg Leu Ala Ala Ile Arg
      180      185      190
Trp His Leu Lys Leu Pro Thr Phe Ala Leu Asp Glu Asn Gly Arg
195      200      205

```

<210> 396

<211> 266

<212> PRT

<213> Escherichia coli

<400> 396

```

Met Ala Lys Ser Leu Phe Arg Ala Leu Val Ala Leu Ser Phe Leu Ala
 1           5           10           15
Pro Leu Trp Leu Asn Ala Ala Pro Arg Val Ile Thr Leu Ser Pro Ala
      20           25           30
Asn Thr Glu Leu Ala Phe Ala Ala Gly Ile Thr Pro Val Gly Val Ser
      35           40           45
Ser Tyr Ser Asp Tyr Pro Pro Gln Ala Gln Lys Ile Glu Gln Val Ser
      50           55           60
Thr Trp Gln Gly Met Asn Leu Glu Arg Ile Val Ala Leu Lys Pro Asp
      65           70           75           80
Leu Val Ile Ala Trp Arg Gly Gly Asn Ala Glu Arg Gln Val Asp Gln
      85           90           95
Leu Ala Ser Leu Gly Ile Lys Val Met Trp Val Asp Ala Thr Ser Ile
      100          105          110
Glu Gln Ile Ala Asn Ala Leu Arg Gln Leu Ala Pro Trp Ser Pro Gln
      115          120          125
Pro Asp Lys Ala Glu Gln Ala Ala Gln Ser Leu Leu Asp Gln Tyr Ala
      130          135          140
Gln Leu Lys Ala Gln Tyr Ala Asp Lys Pro Lys Lys Arg Val Phe Leu
      145          150          155          160
Gln Phe Gly Ile Asn Pro Pro Phe Thr Ser Gly Lys Glu Ser Ile Gln
      165          170          175
Asn Gln Val Leu Glu Val Cys Gly Gly Glu Asn Ile Phe Lys Asp Ser
      180          185          190
Arg Val Pro Trp Pro Gln Val Ser Arg Glu Gln Val Leu Ala Arg Ser
      195          200          205
Pro Gln Ala Ile Val Ile Thr Gly Gly Pro Asp Gln Ile Pro Lys Ile
      210          215          220
Lys Gln Tyr Trp Gly Glu Gln Leu Lys Ile Pro Val Ile Pro Leu Thr
      225          230          235          240
Ser Asp Trp Phe Glu Arg Ala Ser Pro Arg Ile Ile Leu Ala Ala Gln
      245          250          255
Gln Leu Cys Asn Ala Leu Ser Gln Val Asp
      260          265

```

<210> 397

<211> 232

<212> PRT

<213> Escherichia coli

<400> 397

```

Met Lys Ile Gly Ile Ile Gly Ala Met Glu Glu Glu Val Thr Leu Leu
 1           5           10           15
Arg Asp Lys Ile Glu Asn Arg Gln Thr Ile Ser Leu Gly Gly Cys Glu
      20           25           30
Ile Tyr Thr Gly Gln Leu Asn Gly Thr Glu Val Ala Leu Leu Lys Ser
      35           40           45
Gly Ile Gly Lys Val Ala Ala Ala Leu Gly Ala Thr Leu Leu Leu Glu
      50           55           60
His Cys Lys Pro Asp Val Ile Ile Asn Thr Gly Ser Ala Gly Gly Leu
      65           70           75           80
Ala Pro Thr Leu Lys Val Gly Asp Ile Val Val Ser Asp Glu Ala Arg
      85           90           95
Tyr His Asp Ala Asp Val Thr Ala Phe Gly Tyr Glu Tyr Gly Gln Leu
      100          105          110
Pro Gly Cys Pro Ala Gly Phe Lys Ala Asp Asp Lys Leu Ile Ala Ala
      115          120          125

```

Ala Glu Ala Cys Ile Ala Glu Leu Asn Leu Asn Ala Val Arg Gly Leu
 130 135 140
 Ile Val Ser Gly Asp Ala Phe Ile Asn Gly Ser Val Gly Leu Ala Lys
 145 150 155 160
 Ile Arg His Asn Phe Pro Gln Ala Ile Ala Val Glu Met Glu Ala Thr
 165 170 175
 Ala Ile Ala His Val Cys His Asn Phe Asn Val Pro Phe Val Val Val
 180 185 190
 Arg Ala Ile Ser Asp Val Ala Asp Gln Gln Ser His Leu Ser Phe Asp
 195 200 205
 Glu Phe Leu Ala Val Ala Ala Lys Gln Ser Ser Leu Met Val Glu Ser
 210 215 220
 Leu Val Gln Lys Leu Ala His Gly
 225 230

<210> 398

<211> 262

<212> PRT

<213> Escherichia coli

<400> 398

Met Ile Asp Lys Ser Ala Phe Val His Pro Thr Ala Ile Val Glu Glu
 1 5 10 15
 Gly Ala Ser Ile Gly Ala Asn Ala His Ile Gly Pro Phe Cys Ile Val
 20 25 30
 Gly Pro His Val Glu Ile Gly Glu Gly Thr Val Leu Lys Ser His Val
 35 40 45
 Val Val Asn Gly His Thr Lys Ile Gly Arg Asp Asn Glu Ile Tyr Gln
 50 55 60
 Phe Ala Ser Ile Gly Glu Val Asn Gln Asp Leu Lys Tyr Ala Gly Glu
 65 70 75 80
 Pro Thr Arg Val Glu Ile Gly Asp Arg Asn Arg Ile Arg Glu Ser Val
 85 90 95
 Thr Ile His Arg Gly Thr Val Gln Gly Gly Leu Thr Lys Val Gly
 100 105 110
 Ser Asp Asn Leu Leu Met Ile Asn Ala His Ile Ala His Asp Cys Thr
 115 120 125
 Val Gly Asn Arg Cys Ile Leu Ala Asn Asn Ala Thr Leu Ala Gly His
 130 135 140
 Val Ser Val Asp Asp Phe Ala Ile Ile Gly Gly Met Thr Ala Val His
 145 150 155 160
 Gln Phe Cys Ile Ile Gly Ala His Val Met Val Gly Gly Cys Ser Gly
 165 170 175
 Val Ala Gln Asp Val Pro Pro Tyr Val Ile Ala Gln Gly Asn His Ala
 180 185 190
 Thr Pro Phe Gly Val Asn Ile Glu Gly Leu Lys Arg Arg Gly Phe Ser
 195 200 205
 Arg Glu Ala Ile Thr Ala Ile Arg Asn Ala Tyr Lys Leu Ile Tyr Arg
 210 215 220
 Ser Gly Lys Thr Leu Asp Glu Val Lys Pro Glu Ile Ala Glu Leu Ala
 225 230 235 240
 Glu Thr Tyr Pro Glu Val Lys Ala Phe Thr Asp Phe Phe Ala Arg Ser
 245 250 255
 Thr Arg Gly Leu Ile Arg
 260

<210> 399

<211> 382

<212> PRT

<213> Escherichia coli

<400> 399

```

Met Thr Glu Gln Arg Pro Leu Thr Ile Ala Leu Val Ala Gly Glu Thr
 1           5           10           15
Ser Gly Asp Ile Leu Gly Ala Gly Leu Ile Arg Ala Leu Lys Glu His
 20           25           30
Val Pro Asn Ala Arg Phe Val Gly Val Ala Gly Pro Arg Met Gln Ala
 35           40           45
Glu Gly Cys Glu Ala Trp Tyr Glu Met Glu Glu Leu Ala Val Met Gly
 50           55           60
Ile Val Glu Val Leu Gly Arg Leu Arg Arg Leu Leu His Ile Arg Ala
 65           70           75           80
Asp Leu Thr Lys Arg Phe Gly Glu Leu Lys Pro Asp Val Phe Val Gly
 85           90           95
Ile Asp Ala Pro Asp Phe Asn Ile Thr Leu Glu Gly Asn Leu Lys Lys
 100          105          110
Gln Gly Ile Lys Thr Ile His Tyr Val Ser Pro Ser Val Trp Ala Trp
 115          120          125
Arg Gln Lys Arg Val Phe Lys Ile Gly Arg Ala Thr Asp Leu Val Leu
 130          135          140
Ala Phe Leu Pro Phe Glu Lys Ala Phe Tyr Asp Lys Tyr Asn Val Pro
 145          150          155          160
Cys Arg Phe Ile Gly His Thr Met Ala Asp Ala Met Pro Leu Asp Pro
 165          170          175
Asp Lys Asn Ala Ala Arg Asp Val Leu Gly Ile Pro His Asp Ala His
 180          185          190
Cys Leu Ala Leu Leu Pro Gly Ser Arg Gly Ala Glu Val Glu Met Leu
 195          200          205
Ser Ala Asp Phe Leu Lys Thr Ala Gln Leu Leu Arg Gln Thr Tyr Pro
 210          215          220
Asp Leu Glu Ile Val Val Pro Leu Val Asn Ala Lys Arg Arg Glu Gln
 225          230          235          240
Phe Glu Arg Ile Lys Ala Glu Val Ala Pro Asp Leu Ser Val His Leu
 245          250          255
Leu Asp Gly Met Gly Arg Glu Ala Met Val Ala Ser Asp Ala Ala Leu
 260          265          270
Leu Ala Ser Gly Thr Ala Ala Leu Glu Cys Met Leu Ala Lys Cys Pro
 275          280          285
Met Val Val Gly Tyr Arg Met Lys Pro Phe Thr Phe Trp Leu Ala Lys
 290          295          300
Arg Leu Val Lys Thr Asp Tyr Val Ser Leu Pro Asn Leu Leu Ala Gly
 305          310          315          320
Arg Glu Leu Val Lys Glu Leu Leu Gln Glu Glu Cys Glu Pro Gln Lys
 325          330          335
Leu Ala Ala Ala Leu Leu Pro Leu Leu Ala Asn Gly Lys Thr Ser His
 340          345          350
Ala Met His Asp Thr Phe Arg Glu Leu His Gln Gln Ile Arg Cys Asn
 355          360          365
Ala Asp Glu Gln Ala Ala Gln Ala Val Leu Glu Leu Ala Gln
 370          375          380

```

<210> 400

<211> 198

<212> PRT

<213> Escherichia coli

<400> 400

```

Met Ile Glu Phe Val Tyr Pro His Thr Gln Leu Val Ala Gly Val Asp
 1           5           10           15
Glu Val Gly Arg Gly Pro Leu Val Gly Ala Val Val Thr Ala Ala Val

```

```

      20      25      30
Ile Leu Asp Pro Ala Arg Pro Ile Ala Gly Leu Asn Asp Ser Lys Lys
      35      40      45
Leu Ser Glu Lys Arg Arg Leu Ala Leu Tyr Glu Glu Ile Lys Glu Lys
      50      55      60
Ala Leu Ser Trp Ser Leu Gly Arg Ala Glu Pro His Glu Ile Asp Glu
65      70      75      80
Leu Asn Ile Leu His Ala Thr Met Leu Ala Met Gln Arg Ala Val Ala
      85      90      95
Gly Leu His Ile Ala Pro Glu Tyr Val Leu Ile Asp Gly Asn Arg Cys
      100      105      110
Pro Lys Leu Pro Met Pro Ala Met Ala Val Val Lys Gly Asp Ser Arg
      115      120      125
Val Pro Glu Ile Ser Ala Ala Ser Ile Leu Ala Lys Val Thr Arg Asp
      130      135      140
Ala Glu Met Ala Ala Leu Asp Ile Val Phe Pro Gln Tyr Gly Phe Ala
145      150      155      160
Gln His Lys Gly Tyr Pro Thr Ala Phe His Leu Glu Lys Leu Ala Glu
      165      170      175
His Gly Ala Thr Glu His His Arg Arg Ser Phe Gly Pro Val Lys Arg
      180      185      190
Ala Leu Gly Leu Ala Ser
      195

```

<210> 401

<211> 1160

<212> PRT

<213> Escherichia coli

<400> 401

```

Met Ser Glu Pro Arg Phe Val His Leu Arg Val His Ser Asp Tyr Ser
1      5      10      15
Met Ile Asp Gly Leu Ala Lys Thr Ala Pro Leu Val Lys Lys Ala Ala
      20      25      30
Ala Leu Gly Met Pro Ala Leu Ala Ile Thr Asp Phe Thr Asn Leu Cys
      35      40      45
Gly Leu Val Lys Phe Tyr Gly Ala Gly His Gly Ala Gly Ile Lys Pro
      50      55      60
Ile Val Gly Ala Asp Phe Asn Val Gln Cys Asp Leu Leu Gly Asp Glu
65      70      75      80
Leu Thr His Leu Thr Val Leu Ala Ala Asn Thr Gly Tyr Gln Asn
      85      90      95
Leu Thr Leu Leu Ile Ser Lys Ala Tyr Gln Arg Gly Tyr Gly Ala Ala
      100      105      110
Gly Pro Ile Ile Asp Arg Asp Trp Leu Ile Glu Leu Asn Glu Gly Leu
      115      120      125
Ile Leu Leu Ser Gly Gly Arg Met Gly Asp Val Gly Arg Ser Leu Leu
      130      135      140
Arg Gly Asn Ser Ala Leu Val Asp Glu Cys Val Ala Phe Tyr Glu Glu
145      150      155      160
His Phe Pro Asp Arg Tyr Phe Leu Glu Leu Ile Arg Thr Gly Arg Pro
      165      170      175
Asp Glu Glu Ser Tyr Leu His Ala Ala Val Glu Leu Ala Glu Ala Arg
      180      185      190
Gly Leu Pro Val Val Ala Thr Asn Asp Val Arg Phe Ile Asp Ser Ser
      195      200      205
Asp Phe Asp Ala His Glu Ile Arg Val Ala Ile His Asp Gly Phe Thr
      210      215      220
Leu Asp Asp Pro Lys Arg Pro Arg Asn Tyr Ser Pro Gln Gln Tyr Met
225      230      235      240

```

Arg Ser Glu Glu Glu Met Cys Glu Leu Phe Ala Asp Ile Pro Glu Ala
 245 250 255
 Leu Ala Asn Thr Val Glu Ile Ala Lys Arg Cys Asn Val Thr Val Arg
 260 265 270
 Leu Gly Glu Tyr Phe Leu Pro Gln Phe Pro Thr Gly Asp Met Ser Thr
 275 280 285
 Glu Asp Tyr Leu Val Lys Arg Ala Lys Glu Gly Leu Glu Glu Arg Leu
 290 295 300
 Ala Phe Leu Phe Pro Asp Glu Glu Glu Arg Leu Lys Arg Arg Pro Glu
 305 310 315 320
 Tyr Asp Glu Arg Leu Glu Thr Glu Leu Gln Val Ile Asn Gln Met Gly
 325 330 335
 Phe Pro Gly Tyr Phe Leu Ile Val Met Glu Phe Ile Gln Trp Ser Lys
 340 345 350
 Asp Asn Gly Val Pro Val Gly Pro Gly Arg Gly Ser Gly Ala Gly Ser
 355 360 365
 Leu Val Ala Tyr Ala Leu Lys Ile Thr Asp Leu Asp Pro Leu Glu Phe
 370 375 380
 Asp Leu Leu Phe Glu Arg Phe Leu Asn Pro Glu Arg Val Ser Met Pro
 385 390 395 400
 Asp Phe Asp Val Asp Phe Cys Met Glu Lys Arg Asp Gln Val Ile Glu
 405 410 415
 His Val Ala Asp Met Tyr Gly Arg Asp Ala Val Ser Gln Ile Ile Thr
 420 425 430
 Phe Gly Thr Met Ala Ala Lys Ala Val Ile Arg Asp Val Gly Arg Val
 435 440 445
 Leu Gly His Pro Tyr Gly Phe Val Asp Arg Ile Ser Lys Leu Ile Pro
 450 455 460
 Pro Asp Pro Gly Met Thr Leu Ala Lys Ala Phe Glu Ala Glu Pro Gln
 465 470 475 480
 Leu Pro Glu Ile Tyr Glu Ala Asp Glu Glu Val Lys Ala Leu Ile Asp
 485 490 495
 Met Ala Arg Lys Leu Glu Gly Val Thr Arg Asn Ala Gly Lys His Ala
 500 505 510
 Gly Gly Val Val Ile Ala Pro Thr Lys Ile Thr Asp Phe Ala Pro Leu
 515 520 525
 Tyr Cys Asp Glu Glu Gly Lys His Pro Val Thr Gln Phe Asp Lys Ser
 530 535 540
 Asp Val Glu Tyr Ala Gly Leu Val Lys Phe Asp Phe Leu Gly Leu Arg
 545 550 555 560
 Thr Leu Thr Ile Ile Asn Trp Ala Leu Glu Met Ile Asn Lys Arg Arg
 565 570 575
 Ala Lys Asn Gly Glu Pro Pro Leu Asp Ile Ala Ala Ile Pro Leu Asp
 580 585 590
 Asp Lys Lys Ser Phe Asp Met Leu Gln Arg Ser Glu Thr Thr Ala Val
 595 600 605
 Phe Gln Leu Glu Ser Arg Gly Met Lys Asp Leu Ile Lys Arg Leu Gln
 610 615 620
 Pro Asp Cys Phe Glu Asp Met Ile Ala Leu Val Ala Leu Phe Arg Pro
 625 630 635 640
 Gly Pro Leu Gln Ser Gly Met Val Asp Asn Phe Ile Asp Arg Lys His
 645 650 655
 Gly Arg Glu Glu Ile Ser Tyr Pro Asp Val Gln Trp Gln His Glu Ser
 660 665 670
 Leu Lys Pro Val Leu Glu Pro Thr Tyr Gly Ile Ile Leu Tyr Gln Glu
 675 680 685
 Gln Val Met Gln Ile Ala Gln Val Leu Ser Gly Tyr Thr Leu Gly Gly
 690 695 700
 Ala Asp Met Leu Arg Arg Ala Met Gly Lys Lys Lys Pro Glu Glu Met
 705 710 715 720

Ala Lys Gln Arg Ser Val Phe Ala Glu Gly Ala Glu Lys Asn Gly Ile
 725 730 735
 Asn Ala Glu Leu Ala Met Lys Ile Phe Asp Leu Val Glu Lys Phe Ala
 740 745 750
 Gly Tyr Gly Phe Asn Lys Ser His Ser Ala Ala Tyr Ala Leu Val Ser
 755 760 765
 Tyr Gln Thr Leu Trp Leu Lys Ala His Tyr Pro Ala Glu Phe Met Ala
 770 775 780
 Ala Val Met Thr Ala Asp Met Asp Asn Thr Glu Lys Val Val Gly Leu
 785 790 795 800
 Val Asp Glu Cys Trp Arg Met Gly Leu Lys Ile Leu Pro Pro Asp Ile
 805 810 815
 Asn Ser Gly Leu Tyr His Phe His Val Asn Asp Asp Gly Glu Ile Val
 820 825 830
 Tyr Gly Ile Gly Ala Ile Lys Gly Val Gly Glu Gly Pro Ile Glu Ala
 835 840 845
 Ile Ile Glu Ala Arg Asn Lys Gly Gly Tyr Phe Arg Glu Leu Phe Asp
 850 855 860
 Leu Cys Ala Arg Thr Asp Thr Lys Lys Leu Asn Arg Arg Val Leu Glu
 865 870 875 880
 Lys Leu Ile Met Ser Gly Ala Phe Asp Arg Leu Gly Pro His Arg Ala
 885 890 895
 Ala Leu Met Asn Ser Leu Gly Asp Ala Leu Lys Ala Ala Asp Gln His
 900 905 910
 Ala Lys Ala Glu Ala Ile Gly Gln Ala Asp Met Phe Gly Val Leu Ala
 915 920 925
 Glu Glu Pro Glu Gln Ile Glu Gln Ser Tyr Ala Ser Cys Gln Pro Trp
 930 935 940
 Pro Glu Gln Val Val Leu Asp Gly Glu Arg Glu Thr Leu Gly Leu Tyr
 945 950 955 960
 Leu Thr Gly His Pro Ile Asn Gln Tyr Leu Lys Glu Ile Glu Arg Tyr
 965 970 975
 Val Gly Gly Val Arg Leu Lys Asp Met His Pro Thr Glu Arg Gly Lys
 980 985 990
 Val Ile Thr Ala Ala Gly Leu Val Val Ala Ala Arg Val Met Val Thr
 995 1000 1005
 Lys Arg Gly Asn Arg Ile Gly Ile Cys Thr Leu Asp Asp Arg Ser Gly
 1010 1015 1020
 Arg Leu Glu Val Met Leu Phe Thr Asp Ala Leu Asp Lys Tyr Gln Gln
 1025 1030 1035 1040
 Leu Leu Glu Lys Asp Arg Ile Leu Ile Val Ser Gly Gln Val Ser Phe
 1045 1050 1055
 Asp Asp Phe Ser Gly Gly Leu Lys Met Thr Ala Arg Glu Val Met Asp
 1060 1065 1070
 Ile Asp Glu Ala Arg Glu Lys Tyr Ala Arg Gly Leu Ala Ile Ser Leu
 1075 1080 1085
 Thr Asp Arg Gln Ile Asp Asp Gln Leu Leu Asn Arg Leu Arg Gln Ser
 1090 1095 1100
 Leu Glu Pro His Arg Ser Gly Thr Ile Pro Val His Leu Tyr Tyr Gln
 1105 1110 1115 1120
 Arg Ala Asp Ala Arg Ala Arg Leu Arg Phe Gly Ala Thr Trp Arg Val
 1125 1130 1135
 Ser Pro Ser Asp Arg Leu Leu Asn Asp Leu Arg Gly Leu Ile Gly Ser
 1140 1145 1150
 Glu Gln Val Glu Leu Glu Phe Asp
 1155 1160

<210> 402

<211> 239

<212> PRT

<213> Escherichia coli

<400> 402

```

Met Asn Val Asn Phe Phe Val Thr Cys Ile Gly Asp Ala Leu Lys Ser
 1           5           10           15
Arg Met Ala Arg Asp Ser Val Leu Leu Glu Lys Leu Gly Cys Arg
      20           25           30
Val Asn Phe Pro Glu Lys Gln Gly Cys Cys Gly Gln Pro Ala Ile Asn
      35           40           45
Ser Gly Tyr Ile Lys Glu Ala Ile Pro Gly Met Lys Asn Leu Ile Ala
      50           55           60
Ala Leu Glu Asp Asn Asp Asp Pro Ile Ile Ser Pro Ala Gly Ser Cys
      65           70           75           80
Thr Tyr Ala Val Lys Ser Tyr Pro Thr Tyr Leu Ala Asp Glu Pro Glu
      85           90           95
Trp Ala Ser Arg Ala Ala Lys Val Ala Ala Arg Met Gln Asp Leu Thr
      100          105          110
Ser Phe Ile Val Asn Lys Leu Gly Val Val Asp Val Gly Ala Ser Leu
      115          120          125
Gln Gly Arg Ala Val Tyr His Pro Ser Cys Ser Leu Ala Arg Lys Leu
      130          135          140
Gly Val Lys Asp Glu Pro Leu Thr Leu Leu Lys Asn Val Arg Gly Leu
      145          150          155          160
Glu Leu Leu Thr Phe Ala Glu Gln Asp Thr Cys Cys Gly Phe Gly Gly
      165          170          175
Thr Phe Ser Val Lys Met Ala Glu Ile Ser Gly Glu Met Val Lys Glu
      180          185          190
Lys Val Ala His Leu Met Glu Val Arg Pro Glu Tyr Leu Ile Gly Ala
      195          200          205
Asp Val Ser Cys Leu Leu Asn Ile Ser Gly Arg Leu Gln Arg Glu Gly
      210          215          220
Gln Lys Val Lys Val Met His Ile Ala Glu Val Leu Met Ser Arg
      225          230          235

```

<210> 403

<211> 475

<212> PRT

<213> Escherichia coli

<400> 403

```

Met Ser Ile Lys Thr Ser Asn Thr Asp Phe Lys Thr Arg Ile Arg Gln
 1           5           10           15
Gln Ile Glu Asp Pro Ile Met Arg Lys Ala Val Ala Asn Ala Gln Gln
      20           25           30
Arg Ile Gly Ala Asn Arg Gln Lys Met Val Asp Glu Leu Gly His Trp
      35           40           45
Glu Glu Trp Arg Asp Arg Ala Ala Gln Ile Arg Asp His Val Leu Ser
      50           55           60
Asn Leu Asp Ala Tyr Leu Tyr Gln Leu Ser Glu Lys Val Thr Gln Asn
      65           70           75           80
Gly Gly His Val Tyr Phe Ala Arg Thr Lys Glu Asp Ala Thr Arg Tyr
      85           90           95
Ile Leu Gln Val Ala Gln Arg Lys Asn Ala Arg Lys Val Val Lys Ser
      100          105          110
Lys Ser Met Val Thr Glu Glu Ile Gly Val Asn His Val Leu Gln Asp
      115          120          125
Ala Gly Ile Gln Val Ile Glu Thr Asp Leu Gly Glu Tyr Ile Leu Gln
      130          135          140
Leu Asp Gln Asp Pro Pro Ser His Val Val Val Pro Ala Ile His Lys
      145          150          155          160

```

Asp Arg His Gln Ile Arg Arg Val Leu His Glu Arg Leu Gly Tyr Glu
 165 170 175
 Gly Pro Glu Thr Pro Glu Ala Met Thr Leu Phe Ile Arg Gln Lys Ile
 180 185 190
 Arg Glu Asp Phe Leu Ser Ala Glu Ile Gly Ile Thr Gly Cys Asn Phe
 195 200 205
 Ala Val Ala Glu Thr Gly Ser Val Cys Leu Val Thr Asn Glu Gly Asn
 210 215 220
 Ala Arg Met Cys Thr Thr Leu Pro Lys Thr His Ile Ala Val Met Gly
 225 230 235 240
 Met Glu Arg Ile Ala Pro Thr Phe Ala Glu Val Asp Val Leu Ile Thr
 245 250 255
 Met Leu Ala Arg Ser Ala Val Gly Ala Arg Leu Thr Gly Tyr Asn Thr
 260 265 270
 Trp Leu Thr Gly Pro Arg Glu Ala Gly His Val Asp Gly Pro Glu Glu
 275 280 285
 Phe His Leu Val Ile Val Asp Asn Gly Arg Ser Glu Val Leu Ala Ser
 290 295 300
 Glu Phe Arg Asp Val Leu Arg Cys Ile Arg Cys Gly Ala Cys Met Asn
 305 310 315 320
 Thr Cys Pro Ala Tyr Arg His Ile Gly Gly His Gly Tyr Gly Ser Ile
 325 330 335
 Tyr Pro Gly Pro Ile Gly Ala Val Ile Ser Pro Leu Leu Gly Gly Tyr
 340 345 350
 Lys Asp Phe Lys Asp Leu Pro Tyr Ala Cys Ser Leu Cys Thr Ala Cys
 355 360 365
 Asp Asn Val Cys Pro Val Arg Ile Pro Leu Ser Lys Leu Ile Leu Arg
 370 375 380
 His Arg Arg Val Met Ala Glu Lys Gly Ile Thr Ala Lys Ala Glu Gln
 385 390 395 400
 Arg Ala Ile Lys Met Phe Ala Tyr Ala Asn Ser His Pro Gly Leu Trp
 405 410 415
 Lys Val Gly Met Met Ala Gly Ala His Ala Ala Ser Trp Phe Ile Asn
 420 425 430
 Gly Gly Lys Thr Pro Leu Lys Phe Gly Ala Ile Ser Asp Trp Met Glu
 435 440 445
 Ala Arg Asp Leu Pro Glu Ala Asp Gly Glu Ser Phe Arg Ser Trp Phe
 450 455 460
 Lys Lys His Gln Ala Gln Glu Lys Lys Asn Gly
 465 470 475

<210> 404

<211> 282

<212> PRT

<213> Escherichia coli

<400> 404

Met Leu Met Arg Gln Ala Gly Leu Ser Met Ala Ala Lys His His Ser
 1 5 10 15
 Asn Leu Ala Arg Leu Ala Thr Gly Trp Lys His Ala Ile Phe Leu Lys
 20 25 30
 Leu Thr Glu Arg Val Ser Val Val Gly Leu Arg Asn Ile Arg Arg Arg
 35 40 45
 Arg Lys Arg Met Asp Asn Arg Gly Glu Phe Leu Asn Asn Val Ala Gln
 50 55 60
 Ala Leu Gly Arg Pro Leu Arg Leu Glu Pro Gln Ala Glu Asp Ala Pro
 65 70 75 80
 Leu Asn Asn Tyr Ala Asn Glu Arg Leu Thr Gln Leu Asn Gln Gln Gln
 85 90 95
 Arg Cys Asp Ala Phe Ile Gln Phe Ala Ser Asp Val Met Leu Thr Arg

[illegible]

<210> 405

<211> 390

<212> PRT

<213> Escherichia coli

<400> 405

Met 1	Ser	Glu	Ile	Ala 5	Met	His	Val	Thr	Ala 10	Lys	Pro	Ser	Ser	Phe 15	Gln
Cys	Asn	Leu	Lys 20	Cys	Asp	Tyr	Cys	Phe 25	Tyr	Leu	Glu	Lys	Glu 30	Ser	Gln
Phe	Thr	His 35	Glu	Lys	Trp	Met	Asp 40	Asp	Ser	Thr	Leu	Lys 45	Glu	Phe	Ile
Lys	Gln	Tyr 50	Ile	Ala	Ala	Ser	Gly 55	Asn	Gln	Val	Tyr 60	Phe	Thr	Trp	Gln
Gly 65	Gly	Glu	Pro	Thr 70	Leu	Ala	Gly	Leu	Asp 75	Phe	Phe	Arg	Lys	Val 80	Ile
His	Tyr	Gln	Gln	Arg 85	Tyr	Ala	Gly	Gln	Lys 90	Arg	Ile	Phe	Asn	Ala 95	Leu
Gln	Thr	Asn 100	Gly	Ile	Leu	Leu	Asn 105	Asn	Glu	Trp	Cys	Ala 110	Phe	Leu	Lys
Glu	His	Glu 115	Phe	Leu	Val	Gly	Ile 120	Ser	Ile	Asp	Gly	Pro 125	Gln	Glu	Leu
His	Asp 130	Arg	Tyr	Arg	Arg	Ser	Asn 135	Ser	Gly	Asn	Gly 140	Thr	Phe	Ala	Lys
Val 145	Ile	Ala	Ala	Ile 150	Glu	Arg	Leu	Lys	Ser 155	Tyr	Gln	Val	Glu	Phe 160	Asn
Thr	Leu	Thr	Val 165	Ile	Asn	Asn	Val 170	Asn	Val 175	His	Tyr	Pro	Leu	Glu 175	Val
Tyr	His	Phe 180	Leu	Lys	Ser	Ile	Gly 185	Ser	Lys	His	Met	Gln 190	Phe	Ile	Glu
Leu	Leu	Glu 195	Thr	Gly	Thr	Pro	Asn 200	Ile	Asp	Phe	Ser	Gly 205	His	Ser	Glu
Asn	Thr 210	Phe	Arg	Ile	Ile	Asp 215	Phe	Ser	Val	Pro	Pro 220	Thr	Ala	Tyr	Gly
Lys 225	Phe	Met	Ser	Thr 230	Ile	Phe	Met	Gln	Trp 235	Val	Lys	Asn	Asp	Val	Gly 240

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<210> 406
<211> 571
<212> PRT
<213> Escherichia coli
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<400> 406															
Met	Glu	Leu	Ser	Thr	Ile	Arg	Arg	Gly	Thr	Phe	Met	Lys	Ser	Ala	Leu
1				5					10					15	
Lys	Lys	Ser	Val	Val	Ser	Thr	Ser	Ile	Ser	Leu	Ile	Leu	Ala	Ser	Gly
			20					25					30		
Met	Ala	Ala	Phe	Ala	Ala	His	Ala	Ala	Asp	Asp	Val	Lys	Leu	Lys	Ala
		35					40					45			
Thr	Lys	Thr	Asn	Val	Ala	Phe	Ser	Asp	Phe	Thr	Pro	Thr	Glu	Tyr	Ser
	50					55					60				
Thr	Lys	Gly	Lys	Pro	Asn	Ile	Ile	Val	Leu	Thr	Met	Asp	Asp	Leu	Gly
65					70					75				80	
Tyr	Gly	Gln	Leu	Pro	Phe	Asp	Lys	Gly	Ser	Phe	Asp	Pro	Lys	Thr	Met
				85					90					95	
Glu	Asn	Arg	Glu	Val	Val	Asp	Thr	Tyr	Lys	Ile	Gly	Ile	Asp	Lys	Ala
			100					105					110		
Ile	Glu	Ala	Ala	Gln	Lys	Ser	Thr	Pro	Thr	Leu	Leu	Ser	Leu	Met	Asp
		115					120					125			
Glu	Gly	Val	Arg	Phe	Thr	Asn	Gly	Tyr	Val	Ala	His	Gly	Val	Ser	Gly
	130					135					140				
Pro	Ser	Arg	Ala	Ala	Ile	Met	Thr	Gly	Arg	Ala	Pro	Ala	Arg	Phe	Gly
145					150				155					160	
Val	Tyr	Ser	Asn	Thr	Asp	Ala	Gln	Asp	Gly	Ile	Pro	Leu	Thr	Glu	Thr
			165						170					175	
Phe	Leu	Pro	Glu	Leu	Phe	Gln	Asn	His	Gly	Tyr	Tyr	Thr	Ala	Ala	Val
			180					185					190		
Gly	Lys	Trp	His	Leu	Ser	Lys	Ile	Ser	Asn	Val	Pro	Val	Pro	Glu	Asp
		195					200					205			
Lys	Gln	Thr	Arg	Asp	Tyr	His	Asp	Asn	Phe	Thr	Thr	Phe	Ser	Ala	Glu
		210				215					220				
Glu	Trp	Gln	Pro	Gln	Asn	Arg	Gly	Phe	Asp	Tyr	Phe	Met	Gly	Phe	His
225					230				235					240	
Ala	Ala	Gly	Thr	Ala	Tyr	Tyr	Asn	Ser	Pro	Ser	Leu	Phe	Lys	Asn	Arg
				245					250					255	
Glu	Arg	Val	Pro	Ala	Lys	Gly	Tyr	Ile	Ser	Asp	Gln	Leu	Thr	Asp	Glu

260	265	270
Ala Ile Gly Val Val Asp Arg	Ala Lys Thr Leu Asp Gln Pro Phe Met	
275	280	285
Leu Tyr Leu Ala Tyr Asn Ala Pro His Leu Pro Asn Asp Asn Pro Ala		
290	295	300
Pro Asp Gln Tyr Gln Lys Gln Phe Asn Thr Gly Ser Gln Thr Ala Asp		
305	310	315
Asn Tyr Tyr Ala Ser Val Tyr Ser Val Asp Gln Gly Val Lys Arg Ile		
325	330	335
Leu Glu Gln Leu Lys Lys Asn Gly Gln Tyr Asp Asn Thr Ile Ile Leu		
340	345	350
Phe Thr Ser Asp Asn Gly Ala Val Ile Asp Gly Pro Leu Pro Leu Asn		
355	360	365
Gly Ala Gln Lys Gly Tyr Lys Ser Gln Thr Tyr Pro Gly Gly Thr His		
370	375	380
Thr Pro Met Phe Met Trp Trp Lys Gly Lys Leu Gln Pro Gly Asn Tyr		
385	390	395
Asp Lys Leu Ile Ser Ala Met Asp Phe Tyr Pro Thr Ala Leu Asp Ala		
405	410	415
Ala Asp Ile Ser Ile Pro Lys Asp Leu Lys Leu Asp Gly Val Ser Leu		
420	425	430
Leu Pro Trp Leu Gln Asp Lys Lys Gln Gly Glu Pro His Lys Asn Leu		
435	440	445
Thr Trp Ile Thr Ser Tyr Ser His Trp Phe Asp Glu Glu Asn Ile Pro		
450	455	460
Phe Trp Asp Asn Tyr His Lys Phe Val Arg His Gln Ser Asp Asp Tyr		
465	470	475
Pro His Asn Pro Asn Thr Glu Asp Leu Ser Gln Phe Ser Tyr Thr Val		
485	490	495
Arg Asn Asn Asp Tyr Ser Leu Val Tyr Thr Val Glu Asn Asn Gln Leu		
500	505	510
Gly Leu Tyr Lys Leu Thr Asp Leu Gln Gln Lys Asp Asn Leu Ala Ala		
515	520	525
Ala Asn Pro Gln Val Val Lys Glu Met Gln Gly Val Val Arg Glu Phe		
530	535	540
Ile Asp Ser Ser Gln Pro Pro Leu Ser Glu Val Asn Gln Glu Lys Phe		
545	550	555
Asn Asn Ile Lys Lys Ala Leu Ser Glu Ala Lys		
565	570	

<210> 407

<211> 274

<212> PRT

<213> Escherichia coli

<400> 407

Met Thr Glu Phe Thr Thr Leu Leu Gln Gln Gly Asn Ala Trp Phe Phe	
1	15
Ile Pro Ser Ala Ile Leu Leu Gly Ala Leu His Gly Leu Glu Pro Gly	
20	30
His Ser Lys Thr Met Met Ala Ala Phe Ile Ile Ala Ile Lys Gly Thr	
35	45
Ile Lys Gln Ala Val Met Leu Gly Leu Ala Ala Thr Ile Ser His Thr	
50	60
Ala Val Val Trp Leu Ile Ala Phe Gly Gly Met Val Ile Ser Lys Arg	
65	80
Phe Thr Ala Gln Ser Ala Glu Pro Trp Leu Gln Leu Ile Ser Ala Val	
85	95
Ile Ile Ile Ser Thr Ala Phe Trp Met Phe Trp Arg Thr Trp Arg Gly	
100	110

Glu Arg Asn Trp Leu Glu Asn Met His Gly His Asp Tyr Glu His His
 115 120 125
 His His Asp His Glu His His His Asp His Gly His His His His
 130 135 140
 Glu His Gly Glu Tyr Gln Asp Ala His Ala Arg Ala His Ala Asn Asp
 145 150 155 160
 Ile Lys Arg Arg Phe Asp Gly Arg Glu Val Thr Asn Trp Gln Ile Leu
 165 170 175
 Leu Phe Gly Leu Thr Gly Gly Leu Ile Pro Cys Pro Ala Ala Ile Thr
 180 185 190
 Val Leu Leu Ile Cys Ile Gln Leu Lys Ala Leu Thr Leu Gly Ala Thr
 195 200 205
 Leu Val Val Ser Phe Ser Ile Gly Leu Ala Leu Thr Leu Val Thr Val
 210 215 220
 Gly Val Gly Ala Ala Ile Ser Val Gln Gln Val Ala Lys Arg Trp Ser
 225 230 235 240
 Gly Phe Asn Thr Leu Ala Lys Arg Ala Pro Tyr Phe Ser Ser Leu Leu
 245 250 255
 Ile Gly Leu Val Gly Val Tyr Met Gly Val His Gly Phe Met Gly Ile
 260 265 270
 Met Arg

<210> 408
 <211> 172
 <212> PRT
 <213> Escherichia coli

<400> 408
 Met Ile Leu Lys Ser Ala Ile Ser Ala Asp Ser Leu Leu Ala Lys Asp
 1 5 10 15
 Ala Phe Arg Ala Ser Phe His Leu His Phe Leu Arg Asn His Gly Ile
 20 25 30
 Thr Asn Lys Ile Ser Leu Val Ser Tyr Ile Val Trp Gln Glu Arg Tyr
 35 40 45
 Ala Thr Asp Ile Thr Asp Pro Gln Ser Gly Glu Phe Met Thr Ile Lys
 50 55 60
 Asn Lys Met Leu Leu Gly Ala Leu Leu Leu Val Thr Ser Ala Ala Trp
 65 70 75 80
 Ala Ala Pro Ala Thr Ala Gly Ser Thr Asn Thr Ser Gly Ile Ser Lys
 85 90 95
 Tyr Glu Leu Ser Ser Phe Ile Ala Asp Phe Lys His Phe Lys Pro Gly
 100 105 110
 Asp Thr Val Pro Glu Met Tyr Arg Thr Asp Glu Tyr Asn Ile Lys Gln
 115 120 125
 Trp Gln Leu Arg Asn Leu Pro Ala Pro Asp Ala Gly Thr His Trp Thr
 130 135 140
 Tyr Met Gly Gly Ala Tyr Val Leu Ile Ser Asp Thr Asp Gly Lys Ile
 145 150 155 160
 Ile Lys Ala Tyr Asp Gly Glu Ile Phe Tyr His Arg
 165 170

<210> 409
 <211> 567
 <212> PRT
 <213> Escherichia coli

<400> 409
 Met Ala Phe Val Ser Glu Arg Glu Ile Val Arg Lys Ile Phe Ser Lys
 1 5 10 15

Lys Ile Asp Phe Thr Ile Leu Ala Phe Phe Tyr Ile Ser Ser Ile Phe
 20 25 30
 Phe Leu Leu Cys Ser Gly Val Leu Phe Gln Tyr Phe Thr Ala Ala Phe
 35 40 45
 Thr Lys Gly Asn Cys Tyr Glu Cys Ser Met Lys Leu Asp Tyr Ile Lys
 50 55 60
 Gln Phe Tyr Phe Ser Leu Glu Thr Ala Trp Tyr Leu Ile Ser Ala Val
 65 70 75 80
 Ala Val Phe Ile Ala Ser Val Phe Ile Gln His Arg Ile Lys Ala Tyr
 85 90 95
 Leu Thr Leu Leu Ala Ile Thr Trp Ile Val Leu Thr Ile Thr Asp Val
 100 105 110
 Ala Leu Ile His Ala Leu Asp Asn Ile Ala Met Asn Asn Ile Leu Leu
 115 120 125
 Asn Ile Leu Tyr Asn Leu Phe Gly Ala Ile Leu Leu Ser Leu Phe Met
 130 135 140
 Cys Leu Ser Asn Ser Leu Leu Phe His Leu Asn Lys Ile Lys His Ile
 145 150 155 160
 Pro Met Ile Leu Ser Ala Met Ile Pro Leu Val Ser Ala Ile Ile Ile
 165 170 175
 Ala Ile Leu Ile Thr Ala Val Ile Tyr Leu Leu Phe Ala Arg Gln Ala
 180 185 190
 Val Glu Ile Glu Met Asp Ile Ser Glu Gly Ser Asp Ile Ala Tyr Val
 195 200 205
 Gly Val Lys Asp Asn Glu Glu Ser Phe Gly Phe Leu Asn Asp Lys Lys
 210 215 220
 Thr Asp Thr Pro Thr Tyr Leu Asp Val Ile Lys Asn Gly Ser Leu Ile
 225 230 235 240
 Tyr Asn Asp Thr Gln Gly Leu Ser Gly Ala Asp Ile Tyr Ile Val Ser
 245 250 255
 Gly Cys Tyr Ala Leu Pro Asp Leu Leu Arg Asn Val Pro Leu Asp Ala
 260 265 270
 Lys Lys Ser Phe Leu Asn Val Lys Lys Leu Glu Ile Thr Gln Lys Leu
 275 280 285
 Pro Met Met Gly Phe Ile Gln Gly Glu Ser Ala Asp Val Met Pro Lys
 290 295 300
 Ala Ala Ser Arg Leu Ser Leu Ser Lys Gln Asp Asp Lys Phe Met Leu
 305 310 315 320
 Ala Ser Ser Val Thr Asp Ser Gln Ile Lys Phe Lys Ser Asn Asn Ala
 325 330 335
 Gln Leu Met Val Ala Phe Ala Phe Met Pro Ile Thr Thr Asn Gly Ile
 340 345 350
 Leu His Asp Tyr Thr Tyr Asp Ile Ile Ile Asn Asp Lys Lys Tyr Lys
 355 360 365
 Ile Glu Asn His Val Ala Pro Leu Ser Arg Leu Asp Lys Asn Lys Lys
 370 375 380
 Met Lys Cys Glu Tyr Gln Gln Ile Ser Asp Leu Thr Asn Thr Tyr Asn
 385 390 395 400
 Ile Asn Ala Asn Tyr Leu Thr Gly Phe Leu Leu Val Leu Lys Pro Asp
 405 410 415
 Asp Ile Ile Asn Tyr Asn Asn Ser Pro Ser Val Leu Leu Lys Thr Asp
 420 425 430
 Phe Ala Phe Tyr Lys Lys Thr Tyr Gln Lys Leu Asp Lys Ile Tyr Asp
 435 440 445
 Asp Ile Ser Asn Gly Lys Leu Ser Ser Leu Arg Ala Thr Gly Ile Ser
 450 455 460
 Gln Phe Ser Ile Asn Gly Lys His Leu Ser Leu Arg Pro Glu Ser Glu
 465 470 475 480
 Ile Ile Ile Ser Glu Gly Ser Leu Tyr Gly Leu Val Asn Lys Ser Lys
 485 490 495

Lys Ile Lys Ile Tyr Gly Thr Ala Asp Leu Val Phe Val Asp Asn Lys
 500 505 510
 Ile Met Asn Leu Arg Lys Ile Thr Tyr Leu Gln Ser Lys Leu Glu Ile
 515 520 525
 Phe Gly Ser Ser Ile Met Asp Ile Leu Lys Tyr Ile Phe Gly Leu Gly
 530 535 540
 Leu Leu Ala Ile Ser Ile Lys Phe Ile His Ser Tyr Phe Lys Asn Asp
 545 550 555 560
 Val Asn Glu Asn Leu Phe Leu
 565

<210> 410

<211> 363

<212> PRT

<213> Escherichia coli

<400> 410

Met Ser Asn Phe Ile Asn Ile His Val Leu Ile Ser His Ser Pro Ser
 1 5 10 15
 Cys Leu Asn Arg Asp Asp Met Asn Met Gln Lys Asp Ala Ile Phe Gly
 20 25 30
 Gly Lys Arg Arg Val Arg Ile Ser Ser Gln Ser Leu Lys Arg Ala Met
 35 40 45
 Arg Lys Ser Gly Tyr Tyr Ala Gln Asn Ile Gly Glu Ser Ser Leu Arg
 50 55 60
 Thr Ile His Leu Ala Gln Leu Arg Asp Val Leu Arg Gln Lys Leu Gly
 65 70 75 80
 Glu Arg Phe Asp Gln Lys Ile Ile Asp Lys Thr Leu Ala Leu Leu Ser
 85 90 95
 Gly Lys Ser Val Asp Glu Ala Glu Lys Ile Ser Ala Asp Ala Val Thr
 100 105 110
 Pro Trp Val Val Gly Glu Ile Ala Trp Phe Cys Glu Gln Val Ala Lys
 115 120 125
 Ala Glu Ala Asp Asn Leu Asp Asp Lys Lys Leu Leu Lys Val Leu Lys
 130 135 140
 Glu Asp Ile Ala Ala Ile Arg Val Asn Leu Gln Gln Gly Val Asp Ile
 145 150 155 160
 Ala Leu Ser Gly Arg Met Ala Thr Ser Gly Met Met Thr Glu Leu Gly
 165 170 175
 Lys Val Asp Gly Ala Met Ser Ile Ala His Ala Ile Thr Thr His Gln
 180 185 190
 Val Asp Ser Asp Ile Asp Trp Phe Thr Ala Val Asp Asp Leu Gln Glu
 195 200 205
 Gln Gly Ser Ala His Leu Gly Thr Gln Glu Phe Ser Ser Gly Val Phe
 210 215 220
 Tyr Arg Tyr Ala Asn Ile Asn Leu Ala Gln Leu Gln Glu Asn Leu Gly
 225 230 235 240
 Gly Ala Ser Arg Glu Gln Ala Leu Glu Ile Ala Thr His Val Val His
 245 250 255
 Met Leu Ala Thr Glu Val Pro Gly Ala Lys Gln Arg Thr Tyr Ala Ala
 260 265 270
 Phe Asn Pro Ala Asp Met Val Met Val Asn Phe Ser Asp Met Pro Leu
 275 280 285
 Ser Met Ala Asn Ala Phe Glu Lys Ala Val Lys Ala Lys Asp Gly Phe
 290 295 300
 Leu Gln Pro Ser Ile Gln Ala Phe Asn Gln Tyr Trp Asp Arg Val Ala
 305 310 315 320
 Asn Gly Tyr Gly Leu Asn Gly Ala Ala Ala Gln Phe Ser Leu Ser Asp
 325 330 335
 Val Asp Pro Ile Thr Ala Gln Val Lys Gln Met Pro Thr Leu Glu Gln


```

      210              215              220
Pro Gly Gly Ala Phe Leu Tyr Thr Asn Gln Gln Thr Leu Ser Leu Gly
225              230              235              240
Ile Val Cys Pro Leu Ser Ser Leu Thr Gln Ser Arg Val Pro Ala Ser
      245              250              255
Glu Leu Leu Thr Arg Phe Lys Ala His Pro Ala Val Arg Pro Leu Ile
      260              265              270
Lys Asn Thr Glu Ser Leu Glu Tyr Gly Ala His Leu Val Pro Glu Gly
      275              280              285
Gly Leu His Ser Met Pro Val Gln Tyr Ala Gly Asn Gly Trp Leu Leu
      290              295              300
Val Gly Asp Ala Leu Arg Ser Cys Val Asn Thr Gly Ile Ser Val Arg
305              310              315              320
Gly Met Asp Met Ala Leu Thr Gly Ala Gln Ala Ala Ala Gln Thr Leu
      325              330              335
Ile Ser Ala Cys Gln His Arg Glu Pro Gln Asn Leu Phe Pro Leu Tyr
      340              345              350
His His Asn Val Glu Arg Ser Leu Leu Trp Asp Val Leu Gln Arg Tyr
      355              360              365
Gln His Val Pro Ala Leu Leu Gln Arg Pro Gly Trp Tyr Arg Thr Trp
      370              375              380
Pro Ala Leu Met Gln Asp Ile Ser Arg Asp Leu Trp Asp Gln Gly Asp
385              390              395              400
Lys Pro Val Pro Pro Leu Arg Gln Leu Phe Trp His His Leu Arg Arg
      405              410              415
His Gly Leu Trp His Leu Ala Gly Asp Val Ile Arg Ser Leu Arg Cys
      420              425              430
Leu

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<210> 413
 <211> 98
 <212> PRT
 <213> Escherichia coli

```

<400> 413
Met Ala Ser Gly Gly Arg Cys Tyr Gln Glu Ser Ala Met Ser Val Ala
  1              5              10              15
Arg Asn Leu Trp Arg Val Ala Asp Ala Pro His Ile Val Pro Ala Asp
      20              25              30
Ser Val Glu Arg Gln Thr Ala Glu Arg Leu Ile Asn Ala Cys Pro Ala
      35              40              45
Gly Leu Phe Ser Leu Thr Pro Glu Gly Asn Leu Arg Ile Asp Tyr Arg
      50              55              60
Ser Cys Leu Glu Cys Gly Thr Cys Arg Leu Leu Cys Asp Glu Ser Thr
      65              70              75              80
Leu Gln Gln Trp Arg Tyr Pro Pro Ser Gly Phe Gly Ile Thr Tyr Arg
      85              90              95
Phe Gly

```

<210> 414
 <211> 191
 <212> PRT
 <213> Escherichia coli

```

<400> 414
Met Pro Leu Leu His Leu Leu Arg Gln Asn Pro Val Ile Ala Ala Val
  1              5              10              15
Lys Asp Asn Ala Ser Leu Gln Leu Ala Ile Asp Ser Glu Cys Gln Phe

```


			20					25					30				
Ile	Ser	Val	Leu	Tyr	Gly	Asn	Ile	Cys	Thr	Ile	Ser	Asn	Ile	Val	Lys		
		35					40					45					
Lys	Ile	Lys	Asn	Ala	Gly	Lys	Tyr	Ala	Phe	Ile	His	Val	Asp	Leu	Leu		
		50				55					60						
Glu	Gly	Ala	Ser	Asn	Lys	Glu	Val	Val	Ile	Gln	Phe	Leu	Lys	Leu	Val		
65					70				75					80			
Thr	Glu	Ala	Asp	Gly	Ile	Ile	Ser	Thr	Lys	Ala	Ser	Met	Leu	Lys	Ala		
				85				90					95				
Ala	Arg	Ala	Glu	Gly	Phe	Phe	Cys	Ile	His	Arg	Leu	Phe	Ile	Val	Asp		
		100					105					110					
Ser	Ile	Ser	Phe	His	Asn	Ile	Asp	Lys	Gln	Val	Ala	Gln	Ser	Asn	Pro		
		115				120						125					
Asp	Cys	Ile	Glu	Ile	Leu	Pro	Gly	Cys	Met	Pro	Lys	Val	Leu	Gly	Trp		
		130				135					140						
Val	Thr	Glu	Lys	Ile	Arg	Gln	Pro	Leu	Ile	Ala	Gly	Gly	Leu	Val	Cys		
145					150					155					160		
Asp	Glu	Glu	Asp	Ala	Arg	Asn	Ala	Ile	Asn	Ala	Gly	Val	Val	Ala	Leu		
				165					170					175			
Ser	Thr	Thr	Asn	Thr	Gly	Val	Trp	Thr	Leu	Ala	Lys	Lys	Leu	Leu			
			180					185					190				

<210> 415

<211> 134

<212> PRT

<213> Escherichia coli

<400> 415

Met	Phe	Met	Thr	Trp	Glu	Tyr	Ala	Leu	Ile	Gly	Leu	Val	Val	Gly	Ile		
1				5					10					15			
Ile	Ile	Gly	Ala	Val	Ala	Met	Arg	Phe	Gly	Asn	Arg	Lys	Leu	Arg	Gln		
		20						25					30				
Gln	Gln	Ala	Leu	Gln	Tyr	Glu	Leu	Glu	Lys	Asn	Lys	Ala	Glu	Leu	Asp		
		35				40						45					
Glu	Tyr	Arg	Glu	Glu	Leu	Val	Ser	His	Phe	Ala	Arg	Ser	Ala	Glu	Leu		
		50				55				60							
Leu	Asp	Thr	Met	Ala	His	Asp	Tyr	Arg	Gln	Leu	Tyr	Gln	His	Met	Ala		
65					70				75					80			
Lys	Ser	Ser	Ser	Ser	Leu	Leu	Pro	Glu	Leu	Ser	Ala	Glu	Ala	Asn	Pro		
				85				90						95			
Phe	Arg	Asn	Arg	Leu	Ala	Glu	Ser	Glu	Ala	Ser	Asn	Asp	Gln	Ala	Pro		
		100						105					110				
Val	Gln	Met	Pro	Arg	Asp	Tyr	Ser	Glu	Gly	Ala	Ser	Gly	Leu	Leu	Arg		
		115					120					125					
Thr	Gly	Ala	Lys	Arg	Asp												
		130															

<210> 416

<211> 455

<212> PRT

<213> Escherichia coli

<400> 416

Met	Lys	Lys	Gln	Thr	Gln	Leu	Leu	Ser	Ala	Leu	Ala	Leu	Ser	Val	Gly		
1				5					10					15			
Leu	Thr	Leu	Ser	Ala	Ser	Phe	Gln	Ala	Val	Ala	Ser	Ile	Pro	Gly	Gln		
		20						25					30				
Val	Ala	Asp	Gln	Ala	Pro	Leu	Pro	Ser	Leu	Ala	Pro	Met	Leu	Glu	Lys		
		35				40						45					
Val	Leu	Pro	Ala	Val	Val	Ser	Val	Arg	Val	Glu	Gly	Thr	Ala	Ser	Gln		

50	55	60
Gly Gln Lys Ile Pro Glu	Glu Phe Lys Lys Phe	Gly Asp Asp Leu
65	70	75
Pro Asp Gln Pro Ala Gln	Pro Phe Glu Gly Leu Gly	Ser Gly Val Ile
85	90	95
Ile Asn Ala Ser Lys Gly	Tyr Val Leu Thr Asn Asn	His Val Ile Asn
100	105	110
Gln Ala Gln Lys Ile Ser	Ile Gln Leu Asn Asp Gly	Arg Glu Phe Asp
115	120	125
Ala Lys Leu Ile Gly Ser	Asp Asp Gln Ser Asp Ile	Ala Leu Leu Gln
130	135	140
Ile Gln Asn Pro Ser Lys	Leu Thr Gln Ile Ala Ile	Ala Asp Ser Asp
145	150	155
Lys Leu Arg Val Gly Asp	Phe Ala Val Ala Val Gly	Asn Pro Phe Gly
165	170	175
Leu Gly Gln Thr Ala Thr	Ser Gly Ile Val Ser Ala	Leu Gly Arg Ser
180	185	190
Gly Leu Asn Leu Glu Gly	Leu Glu Asn Phe Ile Gln	Thr Asp Ala Ser
195	200	205
Ile Asn Arg Gly Asn Ser	Gly Gly Ala Leu Leu Asn	Leu Asn Gly Glu
210	215	220
Leu Ile Gly Ile Asn Thr	Ala Ile Leu Ala Pro Gly	Gly Gly Ser Val
225	230	235
Gly Ile Gly Phe Ala Ile	Pro Ser Asn Met Ala Arg	Thr Leu Ala Gln
245	250	255
Gln Leu Ile Asp Phe Gly	Glu Ile Lys Arg Gly Leu	Leu Gly Ile Lys
260	265	270
Gly Thr Glu Met Ser Ala	Asp Ile Ala Lys Ala Phe	Asn Leu Asp Val
275	280	285
Gln Arg Gly Ala Phe Val	Ser Glu Val Leu Pro Gly	Ser Gly Ser Ala
290	295	300
Lys Ala Gly Val Lys Ala	Gly Asp Ile Ile Thr Ser	Leu Asn Gly Lys
305	310	315
Pro Leu Asn Ser Phe Ala	Glu Leu Arg Ser Arg Ile	Ala Thr Thr Glu
325	330	335
Pro Gly Thr Lys Val Lys	Leu Gly Leu Leu Arg Asn	Gly Lys Pro Leu
340	345	350
Glu Val Glu Val Thr Leu	Asp Thr Ser Thr Ser Ser	Ser Ala Ser Ala
355	360	365
Glu Met Ile Thr Pro Ala	Leu Glu Gly Ala Thr Leu	Ser Asp Gly Gln
370	375	380
Leu Lys Asp Gly Gly Lys	Gly Ile Lys Ile Asp Glu	Val Val Lys Gly
385	390	395
Ser Pro Ala Ala Gln Ala	Gly Leu Gln Lys Asp Asp	Val Ile Ile Gly
405	410	415
Val Asn Arg Asp Arg Val	Asn Ser Ile Ala Glu Met	Arg Lys Val Leu
420	425	430
Ala Ala Lys Pro Ala Ile	Ile Ala Leu Gln Ile Val	Arg Gly Asn Glu
435	440	445
Ser Ile Tyr Leu Leu Met	Arg	
450	455	

<210> 417

<211> 355

<212> PRT

<213> Escherichia coli

<400> 417

Met Phe Val Lys Leu Leu	Arg Ser Val Ala Ile Gly Leu	Ile Val Gly
1	5	10
		15

Ala Ile Leu Leu Val Ala Met Pro Ser Leu Arg Ser Leu Asn Pro Leu
 20 25 30
 Ser Thr Pro Gln Phe Asp Ser Thr Asp Glu Thr Pro Ala Ser Tyr Asn
 35 40 45
 Leu Ala Val Arg Arg Ala Ala Pro Ala Val Val Asn Val Tyr Asn Arg
 50 55 60
 Gly Leu Asn Thr Asn Ser His Asn Gln Leu Glu Ile Arg Thr Leu Gly
 65 70 75 80
 Ser Gly Val Ile Met Asp Gln Arg Gly Tyr Ile Ile Thr Asn Lys His
 85 90 95
 Val Ile Asn Asp Ala Asp Gln Ile Ile Val Ala Leu Gln Asp Gly Arg
 100 105 110
 Val Phe Glu Ala Leu Leu Val Gly Ser Asp Ser Leu Thr Asp Leu Ala
 115 120 125
 Val Leu Lys Ile Asn Ala Thr Gly Gly Leu Pro Thr Ile Pro Ile Asn
 130 135 140
 Ala Arg Arg Val Pro His Ile Gly Asp Val Val Leu Ala Ile Gly Asn
 145 150 155 160
 Pro Tyr Asn Leu Gly Gln Thr Ile Thr Gln Gly Ile Ile Ser Ala Thr
 165 170 175
 Gly Arg Ile Gly Leu Asn Pro Thr Gly Arg Gln Asn Phe Leu Gln Thr
 180 185 190
 Asp Ala Ser Ile Asn His Gly Asn Ser Gly Gly Ala Leu Val Asn Ser
 195 200 205
 Leu Gly Glu Leu Met Gly Ile Asn Thr Leu Ser Phe Asp Lys Ser Asn
 210 215 220
 Asp Gly Glu Thr Pro Glu Gly Ile Gly Phe Ala Ile Pro Phe Gln Leu
 225 230 235 240
 Ala Thr Lys Ile Met Asp Lys Leu Ile Arg Asp Gly Arg Val Ile Arg
 245 250 255
 Gly Tyr Ile Gly Ile Gly Gly Arg Glu Ile Ala Pro Leu His Ala Gln
 260 265 270
 Gly Gly Gly Ile Asp Gln Leu Gln Gly Ile Val Val Asn Glu Val Ser
 275 280 285
 Pro Asp Gly Pro Ala Ala Asn Ala Gly Ile Gln Val Asn Asp Leu Ile
 290 295 300
 Ile Ser Val Asp Asn Lys Pro Ala Ile Ser Ala Leu Glu Thr Met Asp
 305 310 315 320
 Gln Val Ala Glu Ile Arg Pro Gly Ser Val Ile Pro Val Val Met
 325 330 335
 Arg Asp Asp Lys Gln Leu Thr Leu Gln Val Thr Ile Gln Glu Tyr Pro
 340 345 350
 Ala Thr Asn
 355

<210> 418

<211> 118

<212> PRT

<213> Escherichia coli

<400> 418

Met Ala Arg Ile Ala Gly Ile Asn Ile Pro Asp His Lys His Ala Val
 1 5 10 15
 Ile Ala Leu Thr Ser Ile Tyr Gly Val Gly Lys Thr Arg Ser Lys Ala
 20 25 30
 Ile Leu Ala Ala Ala Gly Ile Ala Glu Asp Val Lys Ile Ser Glu Leu
 35 40 45
 Ser Glu Gly Gln Ile Asp Thr Leu Arg Asp Glu Val Ala Lys Phe Val
 50 55 60
 Val Glu Gly Asp Leu Arg Arg Glu Ile Ser Met Ser Ile Lys Arg Leu

```

65          70          75          80
Met Asp Leu Gly Cys Tyr Arg Gly Leu Arg His Arg Arg Gly Leu Pro
      85          90          95
Val Arg Gly Gln Arg Thr Lys Thr Asn Ala Arg Thr Arg Lys Gly Pro
      100        105        110
Arg Lys Pro Ile Lys Lys
      115

```

<210> 419

<211> 129

<212> PRT

<213> Escherichia coli

<400> 419

```

Met Ala Lys Ala Pro Ile Arg Ala Arg Lys Arg Val Arg Lys Gln Val
1          5          10          15
Ser Asp Gly Val Ala His Ile His Ala Ser Phe Asn Asn Thr Ile Val
      20        25        30
Thr Ile Thr Asp Arg Gln Gly Asn Ala Leu Gly Trp Ala Thr Ala Gly
      35        40        45
Gly Ser Gly Phe Arg Gly Ser Arg Lys Ser Thr Pro Phe Ala Ala Gln
      50        55        60
Val Ala Ala Glu Arg Cys Ala Asp Ala Val Lys Glu Tyr Gly Ile Lys
65          70          75          80
Asn Leu Glu Val Met Val Lys Gly Pro Gly Pro Gly Arg Glu Ser Thr
      85          90          95
Ile Arg Ala Leu Asn Ala Ala Gly Phe Arg Ile Thr Asn Ile Thr Asp
      100        105        110
Val Thr Pro Ile Pro His Asn Gly Cys Arg Pro Pro Lys Lys Arg Arg
      115        120        125
Val

```

<210> 420

<211> 206

<212> PRT

<213> Escherichia coli

<400> 420

```

Met Ala Arg Tyr Leu Gly Pro Lys Leu Lys Leu Ser Arg Arg Glu Gly
1          5          10          15
Thr Asp Leu Phe Leu Lys Ser Gly Val Arg Ala Ile Asp Thr Lys Cys
      20        25'       30
Lys Ile Glu Gln Ala Pro Gly Gln His Gly Ala Arg Lys Pro Arg Leu
      35        40        45
Ser Asp Tyr Gly Val Gln Leu Arg Glu Lys Gln Lys Val Arg Arg Ile
      50        55        60
Tyr Gly Val Leu Glu Arg Gln Phe Arg Asn Tyr Tyr Lys Glu Ala Ala
65          70          75          80
Arg Leu Lys Gly Asn Thr Gly Glu Asn Leu Leu Ala Leu Leu Glu Gly
      85          90          95
Arg Leu Asp Asn Val Val Tyr Arg Met Gly Phe Gly Ala Thr Arg Ala
      100        105        110
Glu Ala Arg Gln Leu Val Ser His Lys Ala Ile Met Val Asn Gly Arg
      115        120        125
Val Val Asn Ile Ala Ser Tyr Gln Val Ser Pro Asn Asp Val Val Ser
      130        135        140
Ile Arg Glu Lys Ala Lys Lys Gln Ser Arg Val Lys Ala Ala Leu Glu
145          150        155        160
Leu Ala Glu Gln Arg Glu Lys Pro Thr Trp Leu Glu Val Asp Ala Gly

```

				165					170					175			
Lys	Met	Glu	Gly	Thr	Phe	Lys	Arg	Lys	Pro	Glu	Arg	Ser	Asp	Leu	Ser		
			180					185					190				
Ala	Asp	Ile	Asn	Glu	His	Leu	Ile	Val	Glu	Leu	Tyr	Ser	Lys				
		195					200					205					

<210> 421
 <211> 329
 <212> PRT
 <213> Escherichia coli

<400> 421

Met	Gln	Gly	Ser	Val	Thr	Glu	Phe	Leu	Lys	Pro	Arg	Leu	Val	Asp	Ile		
1				5					10					15			
Glu	Gln	Val	Ser	Ser	Thr	His	Ala	Lys	Val	Thr	Leu	Glu	Pro	Leu	Glu		
		20						25					30				
Arg	Gly	Phe	Gly	His	Thr	Leu	Gly	Asn	Ala	Leu	Arg	Arg	Ile	Leu	Leu		
		35					40					45					
Ser	Ser	Met	Pro	Gly	Cys	Ala	Val	Thr	Glu	Val	Glu	Ile	Asp	Gly	Val		
	50				55						60						
Leu	His	Glu	Tyr	Ser	Thr	Lys	Glu	Gly	Val	Gln	Glu	Asp	Ile	Leu	Glu		
65					70				75						80		
Ile	Leu	Leu	Asn	Leu	Lys	Gly	Leu	Ala	Val	Arg	Val	Gln	Gly	Lys	Asp		
			85					90						95			
Glu	Val	Ile	Leu	Thr	Leu	Asn	Lys	Ser	Gly	Ile	Gly	Pro	Val	Thr	Ala		
		100						105					110				
Ala	Asp	Ile	Thr	His	Asp	Gly	Asp	Val	Glu	Ile	Val	Lys	Pro	Gln	His		
		115					120					125					
Val	Ile	Cys	His	Leu	Thr	Asp	Glu	Asn	Ala	Ser	Ile	Ser	Met	Arg	Ile		
	130					135					140						
Lys	Val	Gln	Arg	Gly	Arg	Gly	Tyr	Val	Pro	Ala	Ser	Thr	Arg	Ile	His		
145					150					155					160		
Ser	Glu	Glu	Asp	Glu	Arg	Pro	Ile	Gly	Arg	Leu	Leu	Val	Asp	Ala	Cys		
			165					170						175			
Tyr	Ser	Pro	Val	Glu	Arg	Ile	Ala	Tyr	Asn	Val	Glu	Ala	Ala	Arg	Val		
		180						185					190				
Glu	Gln	Arg	Thr	Asp	Leu	Asp	Lys	Leu	Val	Ile	Glu	Met	Glu	Thr	Asn		
		195					200					205					
Gly	Thr	Ile	Asp	Pro	Glu	Glu	Ala	Ile	Arg	Arg	Ala	Ala	Thr	Ile	Leu		
	210					215					220						
Ala	Glu	Gln	Leu	Glu	Ala	Phe	Val	Asp	Leu	Arg	Asp	Val	Arg	Gln	Pro		
225					230				235						240		
Glu	Val	Lys	Glu	Glu	Lys	Pro	Glu	Phe	Asp	Pro	Ile	Leu	Leu	Arg	Pro		
			245						250					255			
Val	Asp	Asp	Leu	Glu	Leu	Thr	Val	Arg	Ser	Ala	Asn	Cys	Leu	Lys	Ala		
		260						265					270				
Glu	Ala	Ile	His	Tyr	Ile	Gly	Asp	Leu	Val	Gln	Arg	Thr	Glu	Val	Glu		
		275					280					285					
Leu	Leu	Lys	Thr	Pro	Asn	Leu	Gly	Lys	Lys	Ser	Leu	Thr	Glu	Ile	Lys		
	290					295					300						
Asp	Val	Leu	Ala	Ser	Arg	Gly	Leu	Ser	Leu	Gly	Met	Arg	Leu	Glu	Asn		
305					310					315					320		
Trp	Pro	Pro	Ala	Ser	Ile	Ala	Asp	Glu									
				325													

<210> 422
 <211> 127
 <212> PRT
 <213> Escherichia coli

<400> 422

```

Met Arg His Arg Lys Ser Gly Arg Gln Leu Asn Arg Asn Ser Ser His
 1           5           10           15
Arg Gln Ala Met Phe Arg Asn Met Ala Gly Ser Leu Val Arg His Glu
          20           25           30
Ile Ile Lys Thr Thr Leu Pro Lys Ala Lys Glu Leu Arg Arg Val Val
          35           40           45
Glu Pro Leu Ile Thr Leu Ala Lys Thr Asp Ser Val Ala Asn Arg Arg
          50           55           60
Leu Ala Phe Ala Arg Thr Arg Asp Asn Glu Ile Val Ala Lys Leu Phe
65          70          75          80
Asn Glu Leu Gly Pro Arg Phe Ala Ser Arg Ala Gly Gly Tyr Thr Arg
          85          90          95
Ile Leu Lys Cys Gly Phe Arg Ala Gly Asp Asn Ala Pro Met Ala Tyr
          100         105         110
Ile Glu Leu Val Asp Arg Ser Glu Lys Ala Glu Ala Ala Glu
          115         120         125

```

<210> 423

<211> 46

<212> PRT

<213> Escherichia coli

<400> 423

```

Met Lys Arg Thr Phe Gln Pro Ser Val Leu Lys Arg Asn Arg Ser His
 1           5           10           15
Gly Phe Arg Ala Arg Met Ala Thr Lys Asn Gly Arg Gln Val Leu Ala
          20           25           30
Arg Arg Arg Ala Lys Gly Arg Ala Arg Leu Thr Val Ser Lys
          35           40           45

```

<210> 424

<211> 119

<212> PRT

<213> Escherichia coli

<400> 424

```

Met Val Lys Leu Ala Phe Pro Arg Glu Leu Arg Leu Leu Thr Pro Ser
 1           5           10           15
Gln Phe Thr Phe Val Phe Gln Gln Pro Gln Arg Ala Gly Thr Pro Gln
          20           25           30
Ile Thr Ile Leu Gly Arg Leu Asn Ser Leu Gly His Pro Arg Ile Gly
          35           40           45
Leu Thr Val Ala Lys Lys Asn Val Arg Arg Ala His Glu Arg Asn Arg
          50           55           60
Ile Lys Arg Leu Thr Arg Glu Ser Phe Arg Leu Arg Gln His Glu Leu
65          70          75          80
Pro Ala Met Asp Phe Val Val Val Ala Lys Lys Gly Val Ala Asp Leu
          85          90          95
Asp Asn Arg Ala Leu Ser Glu Ala Leu Glu Lys Leu Trp Arg Arg His
          100         105         110
Cys Arg Leu Ala Arg Gly Ser
          115

```

<210> 425

<211> 591

<212> PRT

<213> Escherichia coli

<400> 425

Met Ile Glu Lys Leu Arg Asn Ile Ala Ile Ile Ala His Val Asp His
 1 5 10 15
 Gly Lys Thr Thr Leu Val Asp Lys Leu Leu Gln Gln Ser Gly Thr Phe
 20 25 30
 Asp Ser Arg Ala Glu Thr Gln Glu Arg Val Met Asp Ser Asn Asp Leu
 35 40 45
 Glu Lys Glu Arg Gly Ile Thr Ile Leu Ala Lys Asn Thr Ala Ile Lys
 50 55 60
 Trp Asn Asp Tyr Arg Ile Asn Ile Val Asp Thr Pro Gly His Ala Asp
 65 70 75 80
 Phe Gly Gly Glu Val Glu Arg Val Met Ser Met Val Asp Ser Val Leu
 85 90 95
 Leu Val Val Asp Ala Phe Asp Gly Pro Met Pro Gln Thr Arg Phe Val
 100 105 110
 Thr Lys Lys Ala Phe Ala Tyr Gly Leu Lys Pro Ile Val Val Ile Asn
 115 120 125
 Lys Val Asp Arg Pro Gly Ala Arg Pro Asp Trp Val Val Asp Gln Val
 130 135 140
 Phe Asp Leu Phe Val Asn Leu Asp Ala Thr Asp Glu Gln Leu Asp Phe
 145 150 155 160
 Pro Ile Val Tyr Ala Ser Ala Leu Asn Gly Ile Ala Gly Leu Asp His
 165 170 175
 Glu Asp Met Ala Glu Asp Met Thr Pro Leu Tyr Gln Ala Ile Val Asp
 180 185 190
 His Val Pro Ala Pro Asp Val Asp Leu Asp Gly Pro Phe Gln Met Gln
 195 200 205
 Ile Ser Gln Leu Asp Tyr Asn Ser Tyr Val Gly Val Ile Gly Ile Gly
 210 215 220
 Arg Ile Lys Arg Gly Lys Val Lys Pro Asn Gln Gln Val Thr Ile Ile
 225 230 235 240
 Asp Ser Glu Gly Lys Thr Arg Asn Ala Lys Val Gly Lys Val Leu Gly
 245 250 255
 His Leu Gly Leu Glu Arg Ile Glu Thr Asp Leu Ala Glu Ala Gly Asp
 260 265 270
 Ile Val Ala Ile Thr Gly Leu Gly Glu Leu Asn Ile Ser Asp Thr Val
 275 280 285
 Cys Asp Thr Gln Asn Val Glu Ala Leu Pro Ala Leu Ser Val Asp Glu
 290 295 300
 Pro Thr Val Ser Met Phe Phe Cys Val Asn Thr Ser Pro Phe Cys Gly
 305 310 315 320
 Lys Glu Gly Lys Phe Val Thr Ser Arg Gln Ile Leu Asp Arg Leu Asn
 325 330 335
 Lys Glu Leu Val His Asn Val Ala Leu Arg Val Glu Glu Thr Glu Asp
 340 345 350
 Ala Asp Ala Phe Arg Val Ser Gly Arg Gly Glu Leu His Leu Ser Val
 355 360 365
 Leu Ile Glu Asn Met Arg Arg Glu Gly Phe Glu Leu Ala Val Ser Arg
 370 375 380
 Pro Lys Val Ile Phe Arg Glu Ile Asp Gly Arg Lys Gln Glu Pro Tyr
 385 390 395 400
 Glu Asn Val Thr Leu Asp Val Glu Glu Gln His Gln Gly Ser Val Met
 405 410 415
 Gln Ala Leu Gly Glu Arg Lys Gly Asp Leu Lys Asn Met Asn Pro Asp
 420 425 430
 Gly Lys Gly Arg Val Arg Leu Asp Tyr Val Ile Pro Ser Arg Gly Leu
 435 440 445
 Ile Gly Phe Arg Ser Glu Phe Met Thr Met Thr Ser Gly Thr Gly Leu
 450 455 460
 Leu Tyr Ser Thr Phe Ser His Tyr Asp Asp Val Arg Pro Gly Glu Val
 465 470 475 480

Gly	Gln	Arg	Gln	Asn	Gly	Val	Leu	Ile	Ser	Asn	Gly	Gln	Gly	Lys	Ala
				485					490					495	
Val	Ala	Phe	Ala	Leu	Phe	Gly	Leu	Gln	Asp	Arg	Gly	Lys	Leu	Phe	Leu
			500					505					510		
Gly	His	Gly	Ala	Glu	Val	Tyr	Glu	Gly	Gln	Ile	Ile	Gly	Ile	His	Ser
		515					520					525			
Arg	Ser	Asn	Asp	Leu	Thr	Val	Asn	Cys	Leu	Thr	Gly	Lys	Lys	Leu	Thr
	530					535					540				
Asn	Met	Arg	Ala	Ser	Gly	Thr	Asp	Glu	Ala	Val	Val	Leu	Val	Pro	Pro
545					550					555					560
Ile	Arg	Met	Thr	Leu	Glu	Gln	Ala	Leu	Glu	Phe	Ile	Asp	Asp	Asp	Glu
				565					570					575	
Leu	Val	Glu	Val	Thr	Pro	Thr	Ser	Ile	Arg	Ile	Arg	Lys	Arg	His	
			580					585					590		

<210> 426

<211> 756

<212> PRT

<213> Escherichia coli

<400> 426

Met	Met	Lys	Val	Leu	Ile	Val	Glu	Ser	Glu	Phe	Leu	His	Gln	Asp	Thr
1				5					10					15	
Trp	Val	Gly	Asn	Ala	Val	Glu	Arg	Leu	Ala	Asp	Ala	Leu	Ser	Gln	Gln
			20					25					30		
Asn	Val	Thr	Val	Ile	Lys	Ser	Thr	Ser	Phe	Asp	Asp	Gly	Phe	Ala	Ile
		35					40					45			
Leu	Ser	Ser	Asn	Glu	Ala	Ile	Asp	Cys	Leu	Met	Phe	Ser	Tyr	Gln	Met
		50				55					60				
Glu	His	Pro	Asp	Glu	His	Gln	Asn	Val	Arg	Gln	Leu	Ile	Gly	Lys	Leu
65					70					75					80
His	Glu	Arg	Gln	Gln	Asn	Val	Pro	Val	Phe	Leu	Leu	Gly	Asp	Arg	Glu
				85					90					95	
Lys	Ala	Leu	Ala	Ala	Met	Asp	Arg	Asp	Leu	Leu	Glu	Leu	Val	Asp	Glu
			100					105					110		
Phe	Ala	Trp	Ile	Leu	Glu	Asp	Thr	Ala	Asp	Phe	Ile	Ala	Gly	Arg	Ala
		115					120						125		
Val	Ala	Ala	Met	Thr	Arg	Tyr	Arg	Gln	Gln	Leu	Leu	Pro	Pro	Leu	Phe
		130				135						140			
Ser	Ala	Leu	Met	Lys	Tyr	Ser	Asp	Ile	His	Glu	Tyr	Ser	Trp	Ala	Ala
145					150					155					160
Pro	Gly	His	Gln	Gly	Gly	Val	Gly	Phe	Thr	Lys	Thr	Pro	Ala	Gly	Arg
			165					170						175	
Phe	Tyr	His	Asp	Tyr	Tyr	Gly	Glu	Asn	Leu	Phe	Arg	Thr	Asp	Met	Gly
			180					185					190		
Ile	Glu	Arg	Thr	Ser	Leu	Gly	Ser	Leu	Leu	Asp	His	Thr	Gly	Ala	Phe
		195					200						205		
Gly	Glu	Ser	Glu	Lys	Tyr	Ala	Ala	Arg	Val	Phe	Gly	Ala	Asp	Arg	Ser
		210				215					220				
Trp	Ser	Val	Val	Val	Gly	Thr	Ser	Gly	Ser	Asn	Arg	Thr	Ile	Met	Gln
225					230					235					240
Ala	Cys	Met	Thr	Asp	Asn	Asp	Val	Val	Val	Val	Asp	Arg	Asn	Cys	His
				245						250				255	
Lys	Ser	Ile	Glu	Gln	Gly	Leu	Met	Leu	Thr	Gly	Ala	Lys	Pro	Val	Tyr
			260					265					270		
Met	Val	Pro	Ser	Arg	Asn	Arg	Tyr	Gly	Ile	Ile	Gly	Pro	Ile	Tyr	Pro
		275					280					285			
Gln	Glu	Met	Gln	Pro	Glu	Thr	Leu	Gln	Lys	Lys	Ile	Ser	Glu	Ser	Pro
		290				295					300				
Leu	Thr	Lys	Asp	Lys	Ala	Gly	Gln	Lys	Pro	Ser	Tyr	Cys	Val	Val	Thr

305					310					315				320	
Asn	Cys	Thr	Tyr	Asp	Gly	Val	Cys	Tyr	Asn	Ala	Lys	Glu	Ala	Gln	Asp
				325					330					335	
Leu	Leu	Glu	Lys	Thr	Ser	Asp	Arg	Leu	His	Phe	Asp	Glu	Ala	Trp	Tyr
			340					345					350		
Gly	Tyr	Ala	Arg	Phe	Asn	Pro	Ile	Tyr	Ala	Asp	His	Tyr	Ala	Met	Arg
		355					360					365			
Gly	Glu	Pro	Gly	Asp	His	Asn	Gly	Pro	Thr	Val	Phe	Ala	Thr	His	Ser
	370						375				380				
Thr	His	Lys	Leu	Leu	Asn	Ala	Leu	Ser	Gln	Ala	Ser	Tyr	Ile	His	Val
385					390				395					400	
Arg	Glu	Gly	Arg	Gly	Ala	Ile	Asn	Phe	Ser	Arg	Phe	Asn	Gln	Ala	Tyr
				405					410					415	
Met	Met	His	Ala	Thr	Thr	Ser	Pro	Leu	Tyr	Ala	Ile	Cys	Ala	Ser	Asn
			420					425					430		
Asp	Val	Ala	Val	Ser	Met	Met	Asp	Gly	Asn	Ser	Gly	Leu	Ser	Leu	Thr
		435					440					445			
Gln	Glu	Val	Ile	Asp	Glu	Ala	Val	Asp	Phe	Arg	Gln	Ala	Met	Ala	Arg
	450					455					460				
Leu	Tyr	Lys	Glu	Phe	Thr	Ala	Asp	Gly	Ser	Trp	Phe	Phe	Lys	Pro	Trp
465					470				475					480	
Asn	Lys	Glu	Val	Val	Thr	Asp	Pro	Gln	Thr	Gly	Lys	Thr	Tyr	Asp	Phe
				485				490						495	
Ala	Asp	Ala	Pro	Thr	Lys	Leu	Leu	Thr	Thr	Val	Gln	Asp	Cys	Trp	Val
		500					505						510		
Met	His	Pro	Gly	Glu	Ser	Trp	His	Gly	Phe	Lys	Asp	Ile	Pro	Asp	Asn
		515					520					525			
Trp	Ser	Met	Leu	Asp	Pro	Ile	Lys	Val	Ser	Ile	Leu	Ala	Pro	Gly	Met
	530					535					540				
Gly	Glu	Asp	Gly	Glu	Leu	Glu	Glu	Thr	Gly	Val	Pro	Ala	Ala	Leu	Val
545					550				555					560	
Thr	Ala	Trp	Leu	Gly	Arg	His	Gly	Ile	Val	Pro	Thr	Arg	Thr	Thr	Asp
				565					570					575	
Phe	Gln	Ile	Met	Phe	Leu	Phe	Ser	Met	Gly	Val	Thr	Arg	Gly	Lys	Trp
		580						585					590		
Gly	Thr	Leu	Val	Asn	Thr	Leu	Cys	Ser	Phe	Lys	Arg	His	Tyr	Asp	Ala
		595					600					605			
Asn	Thr	Pro	Leu	Ala	Gln	Val	Met	Pro	Glu	Leu	Val	Glu	Gln	Tyr	Pro
	610					615					620				
Asp	Thr	Tyr	Ala	Asn	Met	Gly	Ile	His	Asp	Leu	Gly	Asp	Thr	Met	Phe
625					630				635					640	
Ala	Trp	Leu	Lys	Glu	Asn	Asn	Pro	Gly	Ala	Arg	Leu	Asn	Glu	Ala	Tyr
				645					650					655	
Ser	Gly	Leu	Pro	Val	Ala	Glu	Val	Thr	Pro	Arg	Glu	Ala	Tyr	Asn	Ala
		660						665					670		
Ile	Val	Asp	Asn	Asn	Val	Glu	Leu	Val	Ser	Ile	Glu	Asn	Leu	Pro	Gly
		675					680					685			
Arg	Ile	Ala	Ala	Asn	Ser	Val	Ile	Pro	Tyr	Pro	Pro	Gly	Ile	Pro	Met
	690					695					700				
Leu	Leu	Ser	Gly	Glu	Asn	Phe	Gly	Asp	Lys	Asn	Ser	Pro	Gln	Val	Ser
705					710				715					720	
Tyr	Leu	Arg	Ser	Leu	Gln	Ser	Trp	Asp	His	His	Phe	Pro	Gly	Phe	Glu
				725					730					735	
His	Glu	Thr	Glu	Gly	Thr	Glu	Ile	Ile	Asp	Gly	Ile	Tyr	His	Val	Met
			740					745					750		
Cys	Val	Lys	Ala												
			755												

<210> 427

<211> 253

<212> PRT

<213> Escherichia coli

<400> 427

```

Met Arg Ile Cys Ser Asp Gln Pro Cys Ile Val Leu Leu Thr Glu Lys
 1           5           10           15
Asp Val Trp Ile Arg Val Asn Gly Lys Glu Pro Ile Ser Leu Lys Ala
 20           25           30
Asn His Met Ala Leu Leu Asn Cys Glu Asn Asn Ile Ile Asp Val Ser
 35           40           45
Ser Leu Asn Asn Thr Leu Val Ala His Ile Ser His Asp Ile Ile Lys
 50           55           60
Asp Tyr Leu Arg Phe Leu Asn Lys Asp Leu Ser Gln Ile Pro Val Trp
 65           70           75           80
Gln Arg Ser Ala Thr Pro Ile Leu Thr Leu Pro Cys Leu Thr Pro Asp
 85           90           95
Val Phe Arg Val Ala Ala Gln His Ser Met Met Pro Ala Glu Thr Glu
100           105           110
Ser Glu Lys Glu Arg Thr Arg Ala Leu Leu Phe Thr Val Leu Ser Arg
115           120           125
Phe Leu Asp Ser Lys Lys Phe Val Ser Leu Met Met Tyr Met Leu Arg
130           135           140
Asn Cys Val Ser Asp Ser Val Tyr Gln Ile Ile Glu Ser Asp Ile His
145           150           155           160
Lys Asp Trp Asn Leu Ser Met Val Ala Ser Cys Leu Cys Leu Ser Pro
165           170           175
Ser Leu Leu Lys Lys Lys Leu Lys Ser Glu Asn Thr Ser Tyr Ser Gln
180           185           190
Ile Ile Thr Thr Cys Arg Met Arg Tyr Ala Val Asn Glu Leu Met Met
195           200           205
Asp Gly Lys Asn Ile Ser Gln Val Ser Gln Ser Cys Gly Tyr Asn Ser
210           215           220
Thr Ser Tyr Phe Ile Ser Val Phe Lys Asp Phe Tyr Gly Met Thr Pro
225           230           235           240
Leu His Tyr Val Ser Gln His Arg Glu Arg Thr Val Ala
245           250

```

<210> 428

<211> 425

<212> PRT

<213> Escherichia coli

<400> 428

```

Met Leu Arg Leu Pro Asn Ile Tyr Phe Lys Gly Tyr Ile Arg Ile Thr
 1           5           10           15
Gln Glu Thr Asn Met Ala Thr Ala Trp Tyr Lys Gln Val Asn Pro Pro
 20           25           30
Gln Arg Lys Ala Leu Phe Ser Ala Trp Leu Gly Tyr Val Phe Asp Gly
 35           40           45
Phe Asp Phe Met Met Ile Phe Tyr Ile Leu His Ile Ile Lys Ala Asp
 50           55           60
Leu Gly Ile Thr Asp Ile Gln Ala Thr Leu Ile Gly Thr Val Ala Phe
 65           70           75           80
Ile Ala Arg Pro Ile Gly Gly Gly Phe Phe Gly Ala Met Ala Asp Lys
 85           90           95
Tyr Gly Arg Lys Pro Met Met Met Trp Ala Ile Phe Ile Tyr Ser Val
100           105           110
Gly Thr Gly Leu Ser Gly Ile Ala Thr Asn Leu Tyr Met Leu Ala Val
115           120           125
Cys Arg Phe Ile Val Gly Leu Gly Met Ser Gly Glu Tyr Ala Cys Ala

```

130 135 140
 Ser Thr Tyr Ala Val Glu Ser Trp Pro Lys Asn Leu Gln Ser Lys Ala
 145 150 155 160
 Ser Ala Phe Leu Val Ser Gly Phe Ser Val Gly Asn Ile Ile Ala Ala
 165 170 175
 Gln Ile Ile Pro Gln Phe Ala Glu Val Tyr Gly Trp Arg Asn Ser Phe
 180 185 190
 Phe Ile Gly Leu Leu Pro Val Leu Leu Val Leu Trp Ile Arg Lys Ser
 195 200 205
 Ala Pro Glu Ser Gln Glu Trp Ile Glu Asp Lys Tyr Lys Asp Lys Ser
 210 215 220
 Thr Phe Leu Ser Val Phe Arg Lys Pro His Leu Ser Ile Ser Met Ile
 225 230 235 240
 Val Phe Leu Val Cys Phe Cys Leu Phe Gly Ala Asn Trp Pro Ile Asn
 245 250 255
 Gly Leu Leu Pro Ser Tyr Leu Ala Asp Asn Gly Val Asn Thr Val Val
 260 265 270
 Ile Ser Thr Leu Met Thr Ile Ala Gly Leu Gly Thr Leu Thr Gly Thr
 275 280 285
 Ile Phe Phe Gly Phe Val Gly Asp Lys Ile Gly Val Lys Lys Ala Phe
 290 295 300
 Val Val Gly Leu Ile Thr Ser Phe Ile Phe Leu Cys Pro Leu Phe Phe
 305 310 315 320
 Ile Ser Val Lys Asn Ser Ser Leu Ile Gly Leu Cys Leu Phe Gly Leu
 325 330 335
 Met Phe Thr Asn Leu Gly Ile Ala Gly Leu Val Pro Lys Phe Ile Tyr
 340 345 350
 Asp Tyr Phe Pro Thr Lys Leu Arg Gly Leu Gly Thr Gly Leu Ile Tyr
 355 360 365
 Asn Leu Gly Ala Thr Gly Gly Met Ala Ala Pro Val Leu Ala Thr Tyr
 370 375 380
 Ile Ser Gly Tyr Tyr Gly Leu Gly Val Ser Leu Phe Ile Val Thr Val
 385 390 395 400
 Ala Phe Ser Ala Leu Ile Leu Leu Val Gly Phe Asp Ile Pro Gly
 405 410 415
 Lys Ile Tyr Lys Leu Ser Val Ala Lys
 420 425

<210> 429

<211> 377

<212> PRT

<213> Escherichia coli

<400> 429

Met Ile Gly Gly Phe Met Ile Asn Tyr Gly Val Val Gly Val Gly Tyr
 1 5 10 15
 Phe Gly Ala Glu Leu Ala Arg Phe Met Asn Met His Asp Asn Ala Lys
 20 25 30
 Ile Thr Cys Val Tyr Asp Pro Glu Asn Gly Glu Asn Ile Ala Arg Glu
 35 40 45
 Leu Gln Cys Ile Asn Met Ser Ser Leu Asp Ala Leu Val Ser Ser Lys
 50 55 60
 Leu Val Asp Cys Val Ile Val Ala Thr Pro Asn Tyr Leu His Lys Glu
 65 70 75 80
 Pro Val Ile Lys Ala Ala Lys Asn Lys Lys His Val Phe Cys Glu Lys
 85 90 95
 Pro Ile Ala Leu Ser Tyr Glu Asp Cys Val Asp Met Val Lys Ala Cys
 100 105 110
 Lys Glu Ala Gly Val Thr Phe Met Ala Gly His Ile Met Asn Phe Phe
 115 120 125

```

Asn Gly Val Gln Tyr Ala Arg Lys Leu Ile Lys Glu Gly Val Ile Gly
130      135      140
Glu Ile Leu Ser Cys His Thr Lys Arg Asn Gly Trp Glu Asn Lys Gln
145      150      155      160
Glu Arg Leu Ser Trp Lys Lys Met Lys Glu Gln Ser Gly Gly His Leu
165      170      175
Tyr His His Ile His Glu Leu Asp Cys Val Gln His Leu Leu Gly Glu
180      185      190
Ile Pro Glu Thr Val Thr Met Ile Gly Gly Asn Leu Ala His Ser Gly
195      200      205
Pro Gly Phe Gly Asn Glu Asp Asp Met Leu Phe Met Thr Leu Glu Phe
210      215      220
Pro Ser Gly Lys Leu Ala Thr Leu Glu Trp Gly Ser Ala Phe Asn Trp
225      230      235      240
Pro Glu His Tyr Val Ile Ile Asn Gly Thr Lys Gly Ser Ile Lys Ile
245      250      255
Asp Met Gln Glu Thr Ala Gly Ser Leu Arg Ile Gly Gly Gln Thr Lys
260      265      270
His Phe Leu Val His Glu Thr Gln Glu Glu Asp Asp Asp Arg Arg Lys
275      280      285
Gly Asn Met Thr Ser Glu Met Asp Gly Ala Ile Ala Tyr Gly His Pro
290      295      300
Gly Lys Lys Thr Pro Leu Trp Leu Ala Ser Leu Ile Arg Lys Glu Thr
305      310      315      320
Leu Phe Leu His Asn Ile Leu Cys Gly Ala Lys Pro Glu Glu Asp Tyr
325      330      335
Ile Asp Leu Leu Asn Gly Glu Ala Ala Met Ser Ala Ile Ala Thr Ala
340      345      350
Asp Ala Ala Thr Leu Ser Arg Ser Gln Asp Arg Lys Val Lys Ile Ser
355      360      365
Glu Ile Ile Lys His Thr Ser Val Met
370      375

```

<210> 430

<211> 464

<212> PRT

<213> Escherichia coli

<400> 430

```

Met Ser Ala Gly Lys Leu Pro Glu Gly Trp Val Ile Ala Pro Val Ser
1      5      10      15
Thr Val Thr Thr Leu Ile Arg Gly Val Thr Tyr Lys Lys Glu Gln Ala
20      25      30
Ile Asn Tyr Leu Lys Asp Asp Tyr Leu Pro Leu Ile Arg Ala Asn Asn
35      40      45
Ile Gln Asn Gly Lys Phe Asp Thr Thr Asp Leu Val Phe Val Pro Lys
50      55      60
Asn Leu Val Lys Glu Ser Gln Lys Ile Ser Pro Glu Asp Ile Val Ile
65      70      75      80
Ala Met Ser Ser Gly Ser Lys Ser Val Val Gly Lys Ser Ala His Gln
85      90      95
His Leu Pro Phe Glu Cys Ser Phe Gly Ala Phe Cys Gly Val Leu Arg
100      105      110
Pro Glu Lys Leu Ile Phe Ser Gly Phe Ile Ala His Phe Thr Lys Ser
115      120      125
Ser Leu Tyr Arg Asn Lys Ile Ser Ser Leu Ser Ala Gly Ala Asn Ile
130      135      140
Asn Asn Ile Lys Pro Ala Ser Phe Asp Leu Ile Asn Ile Pro Ile Pro
145      150      155      160
Pro Leu Ala Glu Gln Lys Ile Ile Ala Glu Lys Leu Asp Thr Leu Leu

```

										165					170					175				
Ala	Gln	Val	Asp	Ser	Thr	Lys	Ala	Arg	Phe	Glu	Gln	Ile	Pro	Gln	Ile									
			180					185					190											
Leu	Lys	Arg	Phe	Arg	Gln	Ala	Val	Leu	Gly	Gly	Ala	Val	Asn	Gly	Lys									
			195				200					205												
Leu	Thr	Glu	Lys	Trp	Arg	Asn	Phe	Glu	Pro	Gln	His	Ser	Val	Phe	Lys									
			210			215					220													
Lys	Leu	Asn	Phe	Glu	Ser	Ile	Leu	Thr	Glu	Leu	Arg	Asn	Gly	Leu	Ser									
225					230					235					240									
Ser	Lys	Pro	Asn	Glu	Ser	Gly	Val	Gly	His	Pro	Ile	Leu	Arg	Ile	Ser									
			245					250						255										
Ser	Val	Arg	Ala	Gly	His	Val	Asp	Gln	Asn	Asp	Ile	Arg	Phe	Leu	Glu									
			260				265						270											
Cys	Ser	Glu	Ser	Glu	Leu	Asn	Arg	His	Lys	Leu	Gln	Asp	Gly	Asp	Leu									
			275			280					285													
Leu	Phe	Thr	Arg	Tyr	Asn	Gly	Ser	Leu	Glu	Phe	Val	Gly	Val	Cys	Gly									
			290			295					300													
Leu	Leu	Lys	Lys	Leu	Gln	His	Gln	Asn	Leu	Leu	Tyr	Pro	Asp	Lys	Leu									
305					310					315					320									
Ile	Arg	Ala	Arg	Leu	Thr	Lys	Asp	Ala	Leu	Pro	Glu	Tyr	Ile	Glu	Ile									
			325				330						335											
Phe	Phe	Ser	Ser	Pro	Ser	Ala	Arg	Asn	Ala	Met	Met	Asn	Cys	Val	Lys									
			340				345						350											
Thr	Thr	Ser	Gly	Gln	Lys	Gly	Ile	Ser	Gly	Lys	Asp	Ile	Lys	Ser	Gln									
			355			360					365													
Val	Val	Leu	Leu	Pro	Pro	Val	Lys	Glu	Gln	Ala	Glu	Ile	Val	Arg	Arg									
			370			375					380													
Val	Glu	Gln	Leu	Phe	Ala	Tyr	Ala	Asp	Thr	Ile	Glu	Lys	Gln	Val	Asn									
385					390					395					400									
Asn	Ala	Leu	Ala	Arg	Val	Asn	Asn	Leu	Thr	Gln	Ser	Ile	Leu	Ala	Lys									
			405					410					415											
Ala	Phe	Arg	Gly	Glu	Leu	Thr	Ala	Gln	Trp	Arg	Ala	Glu	Asn	Pro	Asp									
			420				425						430											
Leu	Ile	Ser	Gly	Glu	Asn	Ser	Ala	Ala	Ala	Leu	Leu	Glu	Lys	Ile	Lys									
			435			440					445													
Ala	Glu	Arg	Ala	Ala	Ser	Gly	Gly	Lys	Lys	Ala	Ser	Arg	Lys	Lys	Ser									
			450			455					460													

<210> 431

<211> 529

<212> PRT

<213> Escherichia coli

<400> 431

Met	Asn	Asn	Asn	Asp	Leu	Val	Ala	Lys	Leu	Trp	Lys	Leu	Cys	Asp	Asn
1				5				10					15		
Leu	Arg	Asp	Gly	Gly	Val	Ser	Tyr	Gln	Asn	Tyr	Val	Asn	Glu	Leu	Ala
			20					25					30		
Ser	Leu	Leu	Phe	Leu	Lys	Met	Cys	Lys	Glu	Thr	Gly	Gln	Glu	Ala	Glu
		35					40					45			
Tyr	Leu	Pro	Glu	Gly	Tyr	Arg	Trp	Asp	Asp	Leu	Lys	Ser	Arg	Ile	Gly
	50					55					60				
Gln	Glu	Gln	Leu	Gln	Phe	Tyr	Arg	Lys	Met	Leu	Val	His	Leu	Gly	Glu
65					70					75				80	
Asp	Asp	Lys	Lys	Leu	Val	Gln	Ala	Val	Phe	His	Asn	Val	Ser	Thr	Thr
			85						90					95	
Ile	Thr	Glu	Pro	Lys	Gln	Ile	Thr	Ala	Leu	Val	Ser	Asn	Met	Asp	Ser
			100					105					110		
Leu	Asp	Trp	Tyr	Asn	Gly	Ala	His	Gly	Lys	Ser	Arg	Asp	Asp	Phe	Gly
		115					120					125			

Asp Met Tyr Glu Gly Leu Leu Gln Lys Asn Ala Asn Glu Thr Lys Ser
 130 135 140
 Gly Ala Gly Gln Tyr Phe Thr Pro Arg Pro Leu Ile Lys Thr Ile Ile
 145 150 155 160
 His Leu Leu Lys Pro Gln Pro Arg Glu Val Val Gln Asp Pro Ala Ala
 165 170 175
 Gly Thr Ala Gly Phe Leu Ile Glu Ala Asp Arg Tyr Val Lys Ser Gln
 180 185 190
 Thr Asn Asp Leu Asp Asp Leu Asp Gly Asp Thr Gln Asp Phe Gln Ile
 195 200 205
 His Arg Ala Phe Ile Gly Leu Glu Leu Val Pro Gly Thr Arg Arg Leu
 210 215 220
 Ala Leu Met Asn Cys Leu Leu His Asp Ile Glu Gly Asn Leu Asp His
 225 230 235 240
 Gly Gly Ala Ile Arg Leu Gly Asn Thr Leu Gly Ser Asp Gly Glu Asn
 245 250 255
 Leu Pro Lys Ala His Ile Val Ala Thr Asn Pro Pro Phe Gly Ser Ala
 260 265 270
 Ala Gly Thr Asn Ile Thr Arg Thr Phe Val His Pro Thr Ser Asn Lys
 275 280 285
 Gln Leu Cys Phe Met Gln His Ile Ile Glu Thr Leu His Pro Gly Gly
 290 295 300
 Arg Ala Ala Val Val Val Pro Asp Asn Val Leu Phe Glu Gly Gly Lys
 305 310 315 320
 Gly Thr Asp Ile Arg Arg Asp Leu Met Asp Lys Cys His Leu His Thr
 325 330 335
 Ile Leu Arg Leu Pro Thr Gly Ile Phe Tyr Ala Gln Gly Val Lys Thr
 340 345 350
 Asn Val Leu Phe Phe Thr Lys Gly Thr Val Ala Asn Pro Asn Gln Asp
 355 360 365
 Lys Asn Cys Thr Asp Asp Val Trp Val Tyr Asp Leu Arg Thr Asn Met
 370 375 380
 Pro Ser Phe Gly Lys Arg Thr Pro Phe Thr Asp Glu His Leu Gln Pro
 385 390 395 400
 Phe Glu Arg Val Tyr Gly Glu Asp Pro His Gly Leu Ser Pro Arg Thr
 405 410 415
 Glu Gly Glu Trp Ser Phe Asn Ala Glu Glu Thr Glu Val Ala Asp Ser
 420 425 430
 Glu Glu Asn Lys Asn Thr Asp Gln His Leu Ala Thr Ser Arg Trp Arg
 435 440 445
 Lys Phe Ser Arg Glu Trp Ile Arg Thr Ala Lys Ser Asp Ser Leu Asp
 450 455 460
 Ile Ser Trp Leu Lys Asp Lys Asp Ser Ile Asp Ala Asp Ser Leu Pro
 465 470 475 480
 Glu Pro Asp Val Leu Ala Ala Glu Ala Met Gly Glu Leu Val Gln Ala
 485 490 495
 Leu Ser Glu Leu Asp Ala Leu Met Arg Glu Leu Gly Ala Ser Asp Glu
 500 505 510
 Ala Asp Leu Gln Arg Gln Leu Leu Glu Glu Ala Phe Gly Gly Val Lys
 515 520 525
 Glu

<210> 432

<211> 98

<212> PRT

<213> Escherichia coli

<400> 432

Met Lys Lys Glu Asn Tyr Ser Phe Lys Gln Ala Cys Ala Val Val Gly

1 5 10 15
 Gly Gln Ser Ala Met Ala Arg Leu Leu Gly Val Ser Pro Pro Ser Val
 20 25 30
 Asn Gln Trp Ile Lys Gly Val Arg Gln Leu Pro Ala Glu Arg Cys Pro
 35 40 45
 Ala Ile Glu Arg Ala Thr Arg Gly Glu Val Leu Cys Glu Glu Leu Arg
 50 55 60
 Pro Asp Ile Asp Trp Ser Tyr Leu Arg Arg Ser Ala Cys Cys Ser Gln
 65 70 75 80
 Asn Met Ser Val Lys Gln Leu Asn Asp Ser Asn Lys Ser Ser Phe Asp
 85 90 95
 His Thr

<210> 433
 <211> 140
 <212> PRT
 <213> Escherichia coli

<400> 433
 Met Lys Ile Lys His Glu His Ile Glu Ser Val Leu Phe Ala Leu Ala
 1 5 10 15
 Ala Glu Lys Gly Gln Ala Trp Val Ala Asn Ala Ile Thr Glu Glu Tyr
 20 25 30
 Leu Arg Gln Gly Gly Gly Glu Leu Pro Leu Val Pro Gly Lys Asp Trp
 35 40 45
 Asn Asn Gln Gln Asn Ile Tyr His Arg Trp Leu Lys Gly Glu Thr Lys
 50 55 60
 Thr Gln Arg Glu Lys Ile Gln Lys Leu Ile Pro Ala Ile Leu Ala Ile
 65 70 75 80
 Leu Pro Arg Glu Leu Arg His Arg Leu Cys Ile Phe Asp Thr Leu Glu
 85 90 95
 Arg Arg Ala Leu Leu Ala Ala Gln Glu Ala Leu Ser Thr Ala Ile Asp
 100 105 110
 Ala His Asp Asp Ala Val Gln Ala Val Tyr Arg Lys Ala His Phe Ser
 115 120 125
 Gly Gly Gly Ser Ser Asp Asp Ser Val Ile Val His
 130 135 140

<210> 434
 <211> 285
 <212> PRT
 <213> Escherichia coli

<400> 434
 Met Leu Phe Val Leu Ile Leu Ser His Arg Ala Ala Ser Tyr Gly Ala
 1 5 10 15
 Ile Met Ala Ala Leu Pro Tyr Met Gln Leu Tyr Ile Ala Asp Tyr Leu
 20 25 30
 Ala Asp Thr Met His Leu Ser Ala Glu Glu His Gly Ala Tyr Leu Leu
 35 40 45
 Leu Met Phe Asn Tyr Trp Gln Thr Gly Lys Pro Ile Pro Lys Asn Arg
 50 55 60
 Leu Ala Lys Ile Ala Arg Leu Thr Asn Glu Arg Trp Ala Asp Val Glu
 65 70 75 80
 Pro Ser Leu Gln Glu Phe Phe Cys Asp Asn Gly Glu Glu Trp Val His
 85 90 95
 Leu Arg Ile Glu Glu Asp Leu Ala Ser Val Arg Glu Lys Leu Thr Lys
 100 105 110
 Lys Ser Ala Ala Gly Lys Ala Ser Val Gln Ala Arg Arg Ser Arg Lys

```

      115              120              125
Glu Ala Asp Val Gln Thr Lys Gln Glu Arg Asn Leu Thr Gly Val Gln
  130              135              140
Thr Asp Val Glu Val Val Phe Glu His Asp Val Asn Thr Lys Ala Thr
 145              150              155              160
Asn Lys Asp Thr Asp Lys Asp Leu Lys Thr Asp Pro Pro Leu Asn Pro
      165              170              175
Pro Arg Gly Asn Arg Gly Val Lys Lys Phe Asp Pro Leu Asp Ile Thr
      180              185              190
Leu Pro Asn Trp Ile Ser Val Ser Leu Trp Arg Glu Trp Val Glu Phe
      195              200              205
Arg Gln Ala Leu Arg Lys Pro Ile Arg Thr Glu Gln Gly Ala Asn Gly
      210              215              220
Ala Ile Arg Glu Leu Glu Lys Phe Arg Gln Gln Gly Phe Ser Pro Glu
 225              230              235              240
Gln Val Ile Arg His Ser Ile Ala Asn Glu Tyr Gln Gly Leu Phe Ala
      245              250              255
Pro Lys Gly Val Arg Pro Glu Thr Leu Leu Arg Gln Val Asn Thr Val
      260              265              270
Ser Leu Pro Asp Ser Ala Ile Pro Pro Gly Phe Arg Gly
      275              280              285

```

<210> 435

<211> 248

<212> PRT

<213> Escherichia coli

<400> 435

```

Met Lys Asn Ile Ala Thr Gly Asp Val Leu Glu Arg Ile Arg Arg Leu
  1              5              10              15
Ala Pro Ser His Val Thr Ala Pro Phe Lys Thr Val Ala Glu Trp Arg
      20              25              30
Glu Trp Gln Leu Ser Glu Gly Gln Lys Arg Cys Glu Glu Ile Asn Arg
      35              40              45
Gln Asn Arg Gln Leu Arg Val Glu Lys Ile Leu Asn Arg Ser Gly Ile
      50              55              60
Gln Pro Leu His Arg Lys Cys Ser Phe Ser Asn Tyr Gln Val Gln Asn
      65              70              75              80
Glu Gly Gln Arg Tyr Ala Leu Ser Gln Ala Lys Ser Ile Ala Asp Glu
      85              90              95
Leu Met Thr Gly Cys Thr Asn Phe Ala Phe Ser Gly Lys Pro Gly Thr
      100              105              110
Gly Lys Asn His Leu Ala Ala Ala Ile Gly Asn Arg Leu Leu Lys Asp
      115              120              125
Gly Gln Thr Val Ile Val Val Thr Val Ala Asp Val Met Ser Ala Leu
      130              135              140
His Ala Ser Tyr Asp Asp Gly Gln Ser Gly Glu Lys Phe Leu Arg Glu
 145              150              155              160
Leu Cys Glu Val Asp Leu Leu Val Leu Asp Glu Ile Gly Ile Gln Arg
      165              170              175
Glu Thr Lys Asn Glu Gln Val Val Leu His Gln Ile Val Asp Arg Arg
      180              185              190
Thr Ala Ser Met Arg Ser Val Gly Met Leu Thr Asn Leu Asn Tyr Glu
      195              200              205
Ala Met Lys Thr Leu Leu Gly Glu Arg Ile Met Asp Arg Met Thr Met
      210              215              220
Asn Gly Gly Arg Trp Val Asn Phe Asn Trp Glu Ser Trp Arg Pro Asn
 225              230              235              240
Val Val Gln Pro Gly Ile Ala Lys
      245

```


<210> 436
 <211> 203
 <212> PRT
 <213> Escherichia coli

<400> 436
 Met Ser Ser Ser Gln Glu Leu Arg Ser Asn Phe Tyr Arg Glu Lys Asn
 1 5 10 15
 Leu Met Glu Thr Val Phe Asp Ala Leu Lys Ala Met Gly Lys Ala Thr
 20 25 30
 Ser Ile Glu Leu Ala Ala Arg Leu Asp Ile Ser Arg Glu Glu Val Leu
 35 40 45
 Asn Glu Leu Trp Glu Leu Lys Lys Ala Gly Phe Val Asp Lys Ser Ala
 50 55 60
 Tyr Thr Trp Arg Val Ala Asp Asn Asn Val Gln Gln Glu Gln Pro Ala
 65 70 75 80
 Gln Ala Glu Leu Pro Glu Glu Ile Thr Thr Ala Thr Val Ala Lys Ile
 85 90 95
 Ser Glu Cys Asp Leu Thr Ala Thr Ile Glu Gln Arg Gly Pro Gln Thr
 100 105 110
 Ala Asp Glu Leu Ala Thr Leu Phe Gly Thr Thr Ser Arg Lys Val Ala
 115 120 125
 Ser Thr Leu Ala Met Ala Ile Ser Lys Gly Arg Leu Ile Arg Val Asn
 130 135 140
 Gln Gly Gly Lys Phe Arg Tyr Cys Ile Pro Gly Asp Asn Leu Pro Ala
 145 150 155 160
 Glu Pro Lys Ala Ala Ser Val Ser Pro Leu Trp Leu Ser Ala Ser Ser
 165 170 175
 Ser Ala Cys His Gly Val Leu Ile Ile Thr Val Ile Thr Pro Ser Pro
 180 185 190
 Thr Lys Asn Ser Ala Thr Lys Met Pro Glu Asn
 195 200

<210> 437
 <211> 101
 <212> PRT
 <213> Escherichia coli

<400> 437
 Met Gln Met Arg Gln Arg Asp Val Ala Ala Leu Asp Ala Lys Tyr Thr
 1 5 10 15
 Lys Glu Leu Ala Asp Ala Lys Ala Glu Asn Asp Ala Leu Arg Asp Asp
 20 25 30
 Val Ala Ala Gly Arg Arg Arg Leu His Ile Lys Ala Val Cys Gln Ser
 35 40 45
 Val Arg Glu Ala Thr Thr Ala Ser Gly Val Asp Asn Ala Ala Ser Pro
 50 55 60
 Arg Leu Ala Asp Thr Ala Glu Arg Asp Tyr Phe Thr Leu Arg Glu Arg
 65 70 75 80
 Leu Val Met Met Gln Ala Gln Leu Glu Gly Ala Gln Gln Tyr Ile Thr
 85 90 95
 Glu Gln Cys Leu Lys
 100

<210> 438
 <211> 292
 <212> PRT
 <213> Escherichia coli

<400> 438

```

Met Lys Leu Gly Phe Ile Gly Leu Gly Ile Met Gly Thr Pro Met Ala
 1          5          10          15
Ile Asn Leu Ala Arg Ala Gly His Gln Leu His Val Thr Thr Ile Gly
          20          25          30
Pro Val Ala Asp Glu Leu Leu Ser Leu Gly Ala Val Ser Val Glu Thr
          35          40          45
Ala Arg Gln Val Thr Glu Ala Ser Asp Ile Ile Phe Ile Met Val Pro
          50          55          60
Asp Thr Pro Gln Val Glu Glu Val Leu Phe Gly Glu Asn Gly Cys Thr
65          70          75          80
Lys Ala Ser Leu Lys Gly Lys Thr Ile Val Asp Met Ser Ser Ile Ser
          85          90          95
Pro Ile Glu Thr Lys Arg Phe Ala Arg Gln Val Asn Glu Leu Gly Gly
          100          105          110
Asp Tyr Leu Asp Ala Pro Val Ser Gly Gly Glu Ile Gly Ala Arg Glu
          115          120          125
Gly Thr Leu Ser Ile Met Val Gly Gly Asp Glu Ala Val Phe Glu Arg
          130          135          140
Val Lys Pro Leu Phe Glu Leu Leu Gly Lys Asn Ile Thr Leu Val Gly
145          150          155          160
Gly Asn Gly Asp Gly Gln Thr Cys Lys Val Ala Asn Gln Ile Ile Val
          165          170          175
Ala Leu Asn Ile Glu Ala Val Ser Glu Ala Leu Leu Phe Ala Ser Lys
          180          185          190
Ala Gly Ala Asp Pro Val Arg Val Arg Gln Ala Leu Met Gly Gly Phe
          195          200          205
Ala Ser Ser Arg Ile Leu Glu Val His Gly Glu Arg Met Ile Lys Arg
          210          215          220
Thr Phe Asn Pro Gly Phe Lys Ile Ala Leu His Gln Lys Asp Leu Asn
225          230          235          240
Leu Ala Leu Gln Ser Ala Lys Ala Leu Ala Leu Asn Leu Pro Asn Thr
          245          250          255
Ala Thr Cys Gln Glu Leu Phe Asn Thr Cys Ala Ala Asn Gly Gly Ser
          260          265          270
Gln Leu Asp His Ser Ala Leu Val Gln Ala Leu Glu Leu Met Ala Asn
          275          280          285
His Lys Leu Ala
          290

```

<210> 439

<211> 92

<212> PRT

<213> Escherichia coli

<400> 439

```

Met Asn Arg Pro Ala Ile Leu Lys Lys Lys Ala Ala Lys Asp Val Ala
 1          5          10          15
Ser Val Leu Lys Ile Ile Phe Leu Phe Tyr Leu Phe Leu Ile Ala Arg
          20          25          30
Leu Lys Gln Arg Tyr Ser Ile Arg Glu Ile Lys Arg Asp Leu Trp Asn
          35          40          45
Ile Arg Glu Asn Tyr Ser Ser Asn Ala Ala Ile Ala Lys Ile Tyr Cys
          50          55          60
Arg Lys Arg Lys Ala Ser Gly Pro Gly Lys His Leu Thr Ile Leu Pro
65          70          75          80
Tyr Gly Trp Val Arg Phe Ile Thr Phe Pro Ile Met
          85          90

```

<210> 440

<211> 437

<212> PRT

<213> Escherichia coli

<400> 440

```

Met Val Gly Gly Phe Phe Ile Leu Gly Leu Ser Thr Phe Ser Ile Met
 1          5          10          15
Leu Ala Ile Ile Leu Ser Ala Phe Phe Ile Ala Ala Val Met Val Leu
          20          25          30
Asn Gly Ala Ala Gly Ser Lys Tyr Gly Val Pro Phe Ala Met Ile Leu
          35          40          45
Arg Ala Ser Tyr Gly Val Arg Gly Ala Leu Phe Pro Gly Leu Leu Arg
          50          55          60
Gly Gly Ile Ala Ala Ile Met Trp Phe Gly Leu Gln Cys Tyr Ala Gly
65          70          75          80
Ser Leu Ala Cys Leu Ile Leu Ile Gly Lys Ile Trp Pro Gly Phe Leu
          85          90          95
Thr Leu Gly Gly Asp Phe Thr Leu Leu Gly Leu Ser Leu Pro Gly Leu
          100          105          110
Ile Thr Phe Leu Ile Phe Trp Leu Val Asn Val Gly Ile Gly Phe Gly
          115          120          125
Gly Gly Lys Val Leu Asn Lys Phe Thr Ala Ile Leu Asn Pro Cys Ile
          130          135          140
Tyr Ile Val Phe Gly Gly Met Ala Ile Trp Ala Ile Ser Leu Val Gly
145          150          155          160
Ile Gly Pro Ile Phe Asp Tyr Ile Pro Ser Gly Ile Gln Lys Ala Glu
          165          170          175
Asn Gly Gly Phe Leu Phe Leu Val Val Ile Asn Ala Val Val Ala Val
          180          185          190
Trp Ala Ala Pro Ala Val Ser Ala Ser Asp Phe Thr Gln Asn Ala His
          195          200          205
Ser Phe Arg Glu Gln Ala Leu Gly Gln Thr Leu Gly Leu Val Val Ala
          210          215          220
Tyr Ile Leu Phe Ala Val Ala Gly Val Cys Ile Ile Ala Gly Ala Ser
225          230          235          240
Ile His Tyr Gly Ala Asp Thr Trp Asn Val Leu Asp Ile Val Gln Arg
          245          250          255
Trp Asp Ser Leu Phe Ala Ser Phe Phe Ala Val Leu Val Ile Leu Met
          260          265          270
Thr Thr Ile Ser Thr Asn Ala Thr Gly Asn Ile Ile Pro Ala Gly Tyr
          275          280          285
Gln Ile Ala Ala Ile Ala Pro Thr Lys Leu Thr Tyr Lys Asn Gly Val
          290          295          300
Leu Ile Ala Ser Ile Ile Ser Leu Leu Ile Cys Pro Trp Lys Leu Met
305          310          315          320
Glu Asn Gln Asp Ser Ile Tyr Leu Phe Leu Asp Ile Ile Gly Gly Met
          325          330          335
Leu Gly Pro Val Ile Gly Val Met Met Ala His Tyr Phe Val Val Met
          340          345          350
Arg Gly Gln Ile Asn Leu Asp Glu Leu Tyr Thr Ala Pro Gly Asp Tyr
          355          360          365
Lys Tyr Tyr Asp Asn Gly Phe Asn Leu Thr Ala Phe Ser Val Thr Leu
          370          375          380
Val Ala Val Ile Leu Ser Leu Gly Gly Lys Phe Ile His Phe Met Glu
385          390          395          400
Pro Leu Ser Arg Val Ser Trp Phe Val Gly Val Ile Val Ala Phe Ala
          405          410          415
Ala Tyr Ala Leu Leu Lys Lys Arg Thr Thr Ala Glu Lys Thr Gly Glu
          420          425          430
Gln Lys Thr Ile Gly

```

435

<210> 441
 <211> 464
 <212> PRT
 <213> Escherichia coli

<400> 441

Met	Leu	Leu	Leu	Asp	Ala	Cys	Ser	Gln	Met	Cys	Pro	Ser	Phe	Arg	Arg
1				5					10					15	
Phe	Gln	Thr	Val	Phe	His	Asn	Ser	Ser	Ile	Phe	Leu	Pro	Tyr	Trp	Leu
			20					25					30		
Ala	Thr	Leu	Val	Ser	Phe	Arg	Glu	Thr	Phe	Gln	Glu	Glu	Lys	Leu	Leu
		35					40					45			
Thr	Met	Lys	Gly	Ser	Tyr	Lys	Ser	Arg	Trp	Val	Ile	Val	Ile	Val	Val
	50					55					60				
Val	Ile	Ala	Ala	Ile	Ala	Ala	Phe	Trp	Phe	Trp	Gln	Gly	Arg	Asn	Asp
65				70					75					80	
Ser	Arg	Ser	Ala	Ala	Pro	Gly	Ala	Thr	Lys	Gln	Ala	Gln	Gln	Ser	Pro
			85						90					95	
Ala	Gly	Gly	Arg	Arg	Gly	Met	Arg	Ser	Gly	Pro	Leu	Ala	Pro	Val	Gln
			100					105						110	
Ala	Ala	Thr	Ala	Val	Glu	Gln	Ala	Val	Pro	Arg	Tyr	Leu	Thr	Gly	Leu
		115					120					125			
Gly	Thr	Ile	Thr	Ala	Ala	Asn	Thr	Val	Thr	Val	Arg	Ser	Arg	Val	Asp
	130					135					140				
Gly	Gln	Leu	Ile	Ala	Leu	His	Phe	Gln	Glu	Gly	Gln	Gln	Val	Lys	Ala
145				150					155					160	
Gly	Asp	Leu	Leu	Ala	Glu	Ile	Asp	Pro	Ser	Gln	Phe	Lys	Val	Ala	Leu
			165					170						175	
Ala	Gln	Ala	Gln	Gly	Gln	Leu	Ala	Lys	Asp	Lys	Ala	Thr	Leu	Ala	Asn
			180					185					190		
Ala	Arg	Arg	Asp	Leu	Ala	Arg	Tyr	Gln	Gln	Leu	Ala	Lys	Thr	Asn	Leu
	195						200					205			
Val	Ser	Arg	Gln	Glu	Leu	Asp	Ala	Gln	Gln	Ala	Leu	Val	Ser	Glu	Thr
	210					215					220				
Glu	Gly	Thr	Ile	Lys	Ala	Asp	Glu	Ala	Ser	Val	Ala	Ser	Ala	Gln	Leu
225				230					235					240	
Gln	Leu	Asp	Trp	Ser	Arg	Ile	Thr	Ala	Pro	Val	Asp	Gly	Arg	Val	Gly
			245					250						255	
Leu	Lys	Gln	Val	Asp	Val	Gly	Asn	Gln	Ile	Ser	Ser	Gly	Asp	Thr	Thr
		260					265					270			
Gly	Ile	Val	Val	Ile	Thr	Gln	Thr	His	Pro	Ile	Asp	Leu	Val	Phe	Thr
	275					280						285			
Leu	Pro	Glu	Ser	Asp	Ile	Ala	Thr	Val	Val	Gln	Ala	Gln	Lys	Ala	Gly
	290					295					300				
Lys	Pro	Leu	Val	Val	Glu	Ala	Trp	Asp	Arg	Thr	Asn	Ser	Lys	Lys	Leu
305				310					315					320	
Ser	Glu	Gly	Thr	Leu	Leu	Ser	Leu	Asp	Asn	Gln	Ile	Asp	Ala	Thr	Thr
			325					330						335	
Gly	Thr	Ile	Lys	Val	Lys	Ala	Arg	Phe	Asn	Asn	Gln	Asp	Asp	Ala	Leu
		340					345					350			
Phe	Pro	Asn	Gln	Phe	Val	Asn	Ala	Arg	Met	Leu	Val	Asp	Thr	Glu	Gln
		355					360					365			
Asn	Ala	Val	Val	Ile	Pro	Thr	Ala	Ala	Leu	Gln	Met	Gly	Asn	Glu	Gly
	370					375					380				
His	Phe	Val	Trp	Val	Leu	Asn	Ser	Glu	Asn	Lys	Val	Ser	Lys	His	Leu
385				390					395					400	
Val	Thr	Pro	Gly	Ile	Gln	Asp	Ser	Gln	Lys	Val	Val	Ile	Arg	Ala	Gly
			405					410						415	

Ile Ser Ala Gly Asp Arg Val Val Thr Asp Gly Ile Asp Arg Leu Thr
 420 425 430
 Glu Gly Ala Lys Val Glu Val Val Glu Ala Gln Ser Ala Thr Thr Pro
 435 440 445
 Glu Glu Lys Ala Thr Ser Arg Glu Tyr Ala Lys Lys Gly Ala Arg Ser
 450 455 460

<210> 442

<211> 1040

<212> PRT

<213> Escherichia coli

<400> 442

Met Gln Val Leu Pro Pro Ser Ser Thr Gly Gly Pro Ser Arg Leu Phe
 1 5 10 15
 Ile Met Arg Pro Val Ala Thr Thr Leu Leu Met Val Ala Ile Leu Leu
 20 25 30
 Ala Gly Ile Ile Gly Tyr Arg Ala Leu Pro Val Ser Ala Leu Pro Glu
 35 40 45
 Val Asp Tyr Pro Thr Ile Gln Val Val Thr Leu Tyr Pro Gly Ala Ser
 50 55 60
 Pro Asp Val Met Thr Ser Ala Val Thr Ala Pro Leu Glu Arg Gln Phe
 65 70 75 80
 Gly Gln Met Ser Gly Leu Lys Gln Met Ser Ser Gln Ser Ser Gly Gly
 85 90 95
 Ala Ser Val Ile Thr Leu Gln Phe Gln Leu Thr Leu Pro Leu Asp Val
 100 105 110
 Ala Glu Gln Glu Val Gln Ala Ala Ile Asn Ala Ala Thr Asn Leu Leu
 115 120 125
 Pro Ser Asp Leu Pro Asn Pro Pro Val Tyr Ser Lys Val Asn Pro Ala
 130 135 140
 Asp Pro Pro Ile Met Thr Leu Ala Val Thr Ser Thr Ala Met Pro Met
 145 150 155 160
 Thr Gln Val Glu Asp Met Val Glu Thr Arg Val Ala Gln Lys Ile Ser
 165 170 175
 Gln Ile Ser Gly Val Gly Leu Val Thr Leu Ser Gly Gly Gln Arg Pro
 180 185 190
 Ala Val Arg Val Lys Leu Asn Ala Gln Ala Ile Ala Ala Leu Gly Leu
 195 200 205
 Thr Ser Glu Thr Val Arg Thr Ala Ile Thr Gly Ala Asn Val Asn Ser
 210 215 220
 Ala Lys Gly Ser Leu Asp Gly Pro Ser Arg Ala Val Thr Leu Ser Ala
 225 230 235 240
 Asn Asp Gln Met Gln Ser Ala Glu Glu Tyr Arg Gln Leu Ile Ile Ala
 245 250 255
 Tyr Gln Asn Gly Ala Pro Ile Arg Leu Gly Asp Val Ala Thr Val Glu
 260 265 270
 Gln Gly Ala Glu Asn Ser Trp Leu Gly Ala Trp Ala Asn Lys Glu Gln
 275 280 285
 Ala Ile Val Met Asn Val Gln Arg Gln Pro Gly Ala Asn Ile Ile Ser
 290 295 300
 Thr Ala Asp Ser Ile Arg Gln Met Leu Pro Gln Leu Thr Glu Ser Leu
 305 310 315 320
 Pro Lys Ser Val Lys Val Thr Val Leu Ser Asp Arg Thr Thr Asn Ile
 325 330 335
 Arg Ala Ser Val Asp Asp Thr Gln Phe Glu Leu Met Met Ala Ile Ala
 340 345 350
 Leu Val Val Met Ile Ile Tyr Leu Phe Leu Arg Asn Ile Pro Ala Thr
 355 360 365
 Ile Ile Pro Gly Val Ala Val Pro Leu Ser Leu Ile Gly Thr Phe Ala

370		375		380
Val Met Val Phe Leu Asp Phe Ser Ile Asn Asn Leu Thr Leu Met Ala				
385		390		395
Leu Thr Ile Ala Thr Gly Phe Val Val Asp Asp Ala Ile Val Val Ile				
	405		410	415
Glu Asn Ile Ser Arg Tyr Ile Glu Lys Gly Glu Lys Pro Leu Ala Ala				
	420		425	430
Ala Leu Lys Gly Ala Gly Glu Ile Gly Phe Thr Ile Ile Ser Leu Thr				
	435		440	445
Phe Ser Leu Ile Ala Val Leu Ile Pro Leu Leu Phe Met Gly Asp Ile				
	450		455	460
Val Gly Arg Leu Phe Arg Glu Phe Ala Ile Thr Leu Ala Val Ala Ile				
	465		470	475
Leu Ile Ser Ala Val Val Ser Leu Thr Leu Thr Pro Met Met Cys Ala				
	485		490	495
Arg Met Leu Ser Gln Glu Ser Leu Arg Lys Gln Asn Arg Phe Ser Arg				
	500		505	510
Ala Ser Glu Lys Met Phe Asp Arg Ile Ile Ala Ala Tyr Gly Arg Gly				
	515		520	525
Leu Ala Lys Val Leu Asn His Pro Trp Leu Thr Leu Ser Val Ala Leu				
	530		535	540
Ser Thr Leu Leu Leu Ser Val Leu Leu Trp Val Phe Ile Pro Lys Gly				
	545		550	555
Phe Phe Pro Val Gln Asp Asn Gly Ile Ile Gln Gly Thr Leu Gln Ala				
	565		570	575
Pro Gln Ser Ser Ser Phe Ala Asn Met Ala Gln Arg Gln Arg Gln Val				
	580		585	590
Ala Asp Val Ile Leu Gln Asp Pro Ala Val Gln Ser Leu Thr Ser Phe				
	595		600	605
Val Gly Val Asp Gly Thr Asn Pro Ser Leu Asn Ser Ala Arg Leu Gln				
	610		615	620
Ile Asn Leu Lys Pro Leu Asp Glu Arg Asp Asp Arg Val Gln Lys Val				
	625		630	635
Ile Ala Arg Leu Gln Thr Ala Val Asp Lys Val Pro Gly Val Asp Leu				
	645		650	655
Phe Leu Gln Pro Thr Gln Asp Leu Thr Ile Asp Thr Gln Val Ser Arg				
	660		665	670
Thr Gln Tyr Gln Phe Thr Leu Gln Ala Thr Ser Leu Asp Ala Leu Ser				
	675		680	685
Thr Trp Val Pro Gln Leu Met Glu Lys Leu Gln Gln Leu Pro Gln Leu				
	690		695	700
Ser Asp Val Ser Ser Asp Trp Gln Asp Lys Gly Leu Val Ala Tyr Val				
	705		710	715
Asn Val Asp Arg Asp Ser Ala Ser Arg Leu Gly Ile Ser Met Ala Asp				
	725		730	735
Val Asp Asn Ala Leu Tyr Asn Ala Phe Gly Gln Arg Leu Ile Ser Thr				
	740		745	750
Ile Tyr Thr Gln Ala Asn Gln Tyr Arg Val Val Leu Glu His Asn Thr				
	755		760	765
Glu Asn Thr Pro Gly Leu Ala Ala Leu Asp Thr Ile Arg Leu Thr Ser				
	770		775	780
Ser Asp Gly Gly Val Val Pro Leu Ser Ser Ile Ala Lys Ile Glu Gln				
	785		790	795
Arg Phe Ala Pro Leu Ser Ile Asn His Leu Asp Gln Phe Pro Val Thr				
	805		810	815
Thr Ile Ser Phe Asn Val Pro Asp Asn Tyr Ser Leu Gly Asp Ala Val				
	820		825	830
Gln Ala Ile Met Asp Thr Glu Lys Thr Leu Asn Leu Pro Val Asp Ile				
	835		840	845
Thr Thr Gln Phe Gln Gly Ser Thr Leu Ala Phe Gln Ser Ala Leu Gly				

850		855		860	
Ser Thr Val Trp Leu Ile Val Ala Ala Val Val Ala Met Tyr Ile Val					
865		870		875	880
Leu Gly Ile Leu Tyr Glu Ser Phe Ile His Pro Ile Thr Ile Leu Ser					
	885		890		895
Thr Leu Pro Thr Ala Gly Val Gly Ala Leu Leu Ala Leu Leu Ile Ala					
	900		905		910
Gly Ser Glu Leu Asp Val Ile Ala Ile Ile Gly Ile Ile Leu Leu Ile					
	915		920		925
Gly Ile Val Lys Lys Asn Ala Ile Met Met Ile Asp Phe Ala Leu Ala					
	930		935		940
Ala Glu Arg Glu Gln Gly Met Ser Pro Arg Glu Ala Ile Tyr Gln Ala					
945		950		955	960
Cys Leu Leu Arg Phe Arg Pro Ile Leu Met Thr Thr Leu Ala Ala Leu					
	965		970		975
Leu Gly Ala Leu Pro Leu Met Leu Ser Thr Gly Val Gly Ala Glu Leu					
	980		985		990
Arg Arg Pro Leu Gly Ile Gly Met Val Gly Gly Leu Ile Val Ser Gln					
	995		1000		1005
Val Leu Thr Leu Phe Thr Thr Pro Val Ile Tyr Leu Leu Phe Asp Arg					
	1010		1015		1020
Leu Ala Leu Trp Thr Lys Ser Arg Phe Ala Arg His Glu Glu Glu Ala					
1025		1030		1035	1040

<210> 443

<211> 1025

<212> PRT

<213> Escherichia coli

<400> 443

Met Lys Phe Phe Ala Leu Phe Ile Tyr Arg Pro Val Ala Thr Ile Leu		
1	5	10
Leu Ser Val Ala Ile Thr Leu Cys Gly Ile Leu Gly Phe Arg Met Leu		
	20	25
Pro Val Ala Pro Leu Pro Gln Val Asp Phe Pro Val Ile Ile Val Ser		
	35	40
Ala Ser Leu Pro Gly Ala Ser Pro Glu Thr Met Ala Ser Ser Val Ala		
	50	55
Thr Pro Leu Glu Arg Ser Leu Gly Arg Ile Ala Gly Val Ser Glu Met		
65	70	75
Thr Ser Ser Ser Ser Leu Gly Ser Thr Arg Ile Ile Leu Gln Phe Asp		
	85	90
Phe Asp Arg Asp Ile Asn Gly Ala Ala Arg Asp Val Gln Ala Ala Ile		
	100	105
Asn Ala Ala Gln Ser Leu Leu Pro Ser Gly Met Pro Ser Arg Pro Thr		
	115	120
Tyr Arg Lys Ala Asn Pro Ser Asp Ala Pro Ile Met Ile Leu Thr Leu		
	130	135
Thr Ser Asp Thr Tyr Ser Gln Gly Glu Leu Tyr Asp Phe Ala Ser Thr		
145	150	155
Gln Leu Ala Pro Thr Ile Ser Gln Ile Asp Gly Val Gly Asp Val Asp		
	165	170
Val Gly Gly Ser Ser Leu Pro Ala Val Arg Val Gly Leu Asn Pro Gln		
	180	185
Ala Leu Phe Asn Gln Gly Val Ser Leu Asp Asp Val Arg Thr Ala Val		
	195	200
Ser Asn Ala Asn Val Arg Lys Pro Gln Gly Ala Leu Glu Asp Gly Thr		
	210	215
His Arg Trp Gln Ile Gln Thr Asn Asp Glu Leu Lys Thr Ala Ala Glu		
225	230	235
		240

Tyr	Gln	Pro	Leu	Ile	Ile	His	Tyr	Asn	Asn	Gly	Gly	Ala	Val	Arg	Leu	245	250	255
Gly	Asp	Val	Ala	Thr	Val	Thr	Asp	Ser	Val	Gln	Asp	Val	Arg	Asn	Ala	260	265	270
Gly	Met	Thr	Asn	Ala	Lys	Pro	Ala	Ile	Leu	Leu	Met	Ile	Arg	Lys	Leu	275	280	285
Pro	Glu	Ala	Asn	Ile	Ile	Gln	Thr	Val	Asp	Ser	Ile	Arg	Ala	Lys	Leu	290	295	300
Pro	Glu	Leu	Gln	Glu	Thr	Ile	Pro	Ala	Ala	Ile	Asp	Leu	Gln	Ile	Ala	305	310	315
Gln	Asp	Arg	Ser	Pro	Thr	Ile	Arg	Ala	Ser	Leu	Glu	Glu	Val	Glu	Gln	325	330	335
Thr	Leu	Ile	Ile	Ser	Val	Ala	Leu	Val	Ile	Leu	Val	Val	Phe	Leu	Phe	340	345	350
Leu	Arg	Ser	Gly	Arg	Ala	Thr	Ile	Pro	Ala	Val	Ser	Val	Pro	Val		355	360	365
Ser	Leu	Ile	Gly	Thr	Phe	Ala	Ala	Met	Tyr	Leu	Cys	Gly	Phe	Ser	Leu	370	375	380
Asn	Asn	Leu	Ser	Leu	Met	Ala	Leu	Thr	Ile	Ala	Thr	Gly	Phe	Val	Val	385	390	395
Asp	Asp	Ala	Ile	Val	Val	Leu	Glu	Asn	Ile	Ala	Arg	His	Leu	Glu	Ala	405	410	415
Gly	Met	Lys	Pro	Leu	Gln	Ala	Ala	Leu	Gln	Gly	Thr	Arg	Glu	Val	Gly	420	425	430
Phe	Thr	Val	Leu	Ser	Met	Ser	Leu	Ser	Leu	Val	Ala	Val	Phe	Leu	Pro	435	440	445
Leu	Leu	Leu	Met	Gly	Gly	Leu	Pro	Gly	Arg	Leu	Leu	Arg	Glu	Phe	Ala	450	455	460
Val	Thr	Leu	Ser	Val	Ala	Ile	Gly	Ile	Ser	Leu	Leu	Val	Ser	Leu	Thr	465	470	475
Leu	Thr	Pro	Met	Met	Cys	Gly	Trp	Met	Leu	Lys	Ala	Ser	Lys	Pro	Arg	485	490	495
Glu	Gln	Lys	Arg	Leu	Arg	Gly	Phe	Gly	Arg	Met	Leu	Val	Ala	Leu	Gln	500	505	510
Gln	Gly	Tyr	Gly	Lys	Ser	Leu	Lys	Trp	Val	Leu	Asn	His	Thr	Arg	Leu	515	520	525
Val	Gly	Val	Val	Leu	Leu	Gly	Thr	Ile	Ala	Leu	Asn	Ile	Trp	Leu	Tyr	530	535	540
Ile	Ser	Ile	Pro	Lys	Thr	Phe	Phe	Pro	Glu	Gln	Asp	Thr	Gly	Val	Leu	545	550	555
Met	Gly	Gly	Ile	Gln	Ala	Asp	Gln	Ser	Ile	Ser	Phe	Gln	Ala	Met	Arg	565	570	575
Gly	Lys	Leu	Gln	Asp	Phe	Met	Lys	Ile	Ile	Arg	Asp	Asp	Pro	Ala	Val	580	585	590
Asp	Asn	Val	Thr	Gly	Phe	Thr	Gly	Gly	Ser	Arg	Val	Asn	Ser	Gly	Met	595	600	605
Met	Phe	Ile	Thr	Leu	Lys	Pro	Arg	Asp	Glu	Arg	Ser	Glu	Thr	Ala	Gln	610	615	620
Gln	Ile	Ile	Asp	Arg	Leu	Arg	Val	Lys	Leu	Ala	Lys	Glu	Pro	Gly	Ala	625	630	635
Asn	Leu	Phe	Leu	Met	Ala	Val	Gln	Asp	Ile	Arg	Val	Gly	Gly	Arg	Gln	645	650	655
Ser	Asn	Ala	Ser	Tyr	Gln	Tyr	Thr	Leu	Leu	Ser	Asp	Asp	Leu	Ala	Ala	660	665	670
Leu	Arg	Glu	Trp	Glu	Pro	Lys	Ile	Arg	Lys	Lys	Leu	Ala	Thr	Leu	Pro	675	680	685
Glu	Leu	Ala	Asp	Val	Asn	Ser	Asp	Gln	Gln	Asp	Asn	Gly	Ala	Glu	Met	690	695	700
Asn	Leu	Val	Tyr	Asp	Arg	Asp	Thr	Met	Ala	Arg	Leu	Gly	Ile	Asp	Val	705	710	715
																		720


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<210> 444
<211> 471
<212> PRT
<213> Escherichia coli
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<400> 444																
Met	Thr	Asp	Leu	Pro	Asp	Ser	Thr	Arg	Trp	Gln	Leu	Trp	Ile	Val	Ala	
1				5					10					15		
Phe	Gly	Phe	Phe	Met	Gln	Ser	Leu	Asp	Thr	Thr	Ile	Val	Asn	Thr	Ala	
			20					25					30			
Leu	Pro	Ser	Met	Ala	Gln	Ser	Leu	Gly	Glu	Ser	Pro	Leu	His	Met	His	
		35					40					45				
Met	Val	Ile	Val	Ser	Tyr	Val	Leu	Thr	Val	Ala	Val	Met	Leu	Pro	Ala	
	50					55					60					
Ser	Gly	Trp	Leu	Ala	Asp	Lys	Val	Gly	Val	Arg	Asn	Ile	Phe	Phe	Thr	
65				70						75				80		
Ala	Ile	Val	Leu	Phe	Thr	Leu	Gly	Ser	Leu	Phe	Cys	Ala	Leu	Ser	Gly	
			85						90					95		
Thr	Leu	Asn	Glu	Leu	Leu	Leu	Ala	Arg	Ala	Leu	Gln	Gly	Val	Gly	Gly	

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      100      105      110
Ala Met Met Val Pro Val Gly Arg Leu Thr Val Met Lys Ile Val Pro
      115      120      125
Arg Glu Gln Tyr Met Ala Ala Met Thr Phe Val Thr Leu Pro Gly Gln
      130      135      140
Val Gly Pro Leu Leu Gly Pro Ala Leu Gly Gly Leu Leu Val Glu Tyr
      145      150      155      160
Ala Ser Trp His Trp Ile Phe Leu Ile Asn Ile Pro Val Gly Ile Ile
      165      170      175
Gly Ala Ile Ala Thr Leu Leu Leu Met Pro Asn Tyr Thr Met Gln Thr
      180      185      190
Arg Arg Phe Asp Leu Ser Gly Phe Leu Leu Leu Ala Val Gly Met Ala
      195      200      205
Val Leu Thr Leu Ala Leu Asp Gly Ser Lys Gly Thr Gly Leu Ser Pro
      210      215      220
Leu Thr Ile Ala Gly Leu Val Ala Val Gly Val Val Ala Leu Val Leu
      225      230      235      240
Tyr Leu Leu His Ala Arg Asn Asn Asn Arg Ala Leu Phe Ser Leu Lys
      245      250      255
Leu Phe Arg Thr Arg Thr Phe Ser Leu Gly Leu Ala Gly Ser Phe Ala
      260      265      270
Gly Arg Ile Gly Ser Gly Met Leu Pro Phe Met Thr Pro Val Phe Leu
      275      280      285
Gln Ile Gly Leu Gly Phe Ser Pro Phe His Ala Gly Leu Met Met Ile
      290      295      300
Pro Met Val Leu Gly Ser Met Gly Met Lys Arg Ile Val Val Gln Val
      305      310      315      320
Val Asn Arg Phe Gly Tyr Arg Arg Val Leu Val Ala Thr Thr Leu Gly
      325      330      335
Leu Ser Leu Val Thr Leu Leu Phe Met Thr Thr Ala Leu Leu Gly Trp
      340      345      350
Tyr Tyr Val Leu Pro Phe Val Leu Phe Leu Gln Gly Met Val Asn Ser
      355      360      365
Thr Arg Phe Ser Ser Met Asn Thr Leu Thr Leu Lys Asp Leu Pro Asp
      370      375      380
Asn Leu Ala Ser Ser Gly Asn Ser Leu Leu Ser Met Ile Met Gln Leu
      385      390      395      400
Ser Met Ser Ile Gly Val Thr Ile Ala Gly Leu Leu Leu Gly Leu Phe
      405      410      415
Gly Ser Gln His Val Ser Val Asp Ser Gly Thr Thr Gln Thr Val Phe
      420      425      430
Met Tyr Thr Trp Leu Ser Met Ala Leu Ile Ile Ala Leu Pro Ala Phe
      435      440      445
Ile Phe Ala Arg Val Pro Asn Asp Thr His Gln Asn Val Ala Ile Ser
      450      455      460
Arg Arg Lys Arg Ser Ala Gln
      465      470

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<210> 445

<211> 138

<212> PRT

<213> Escherichia coli

<400> 445

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Met Ile Ala Phe Glu Val Leu Lys Trp Ala Gly Ala Ala Tyr Leu Ile
1           5           10           15
Trp Leu Gly Ile Gln Gln Trp Arg Ala Ala Gly Ala Ile Asp Leu Lys
20           25           30
Ser Leu Ala Ser Thr Gln Ser Arg Arg His Leu Phe Gln Arg Ala Val
35           40           45

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Phe Val Asn Leu Thr Asn Pro Lys Ser Ile Val Phe Leu Ala Ala Leu
 50 55 60
 Phe Pro Gln Phe Ile Met Pro Gln Gln Pro Gln Leu Met Gln Tyr Ile
 65 70 75 80
 Val Leu Gly Val Thr Thr Ile Val Val Asp Ile Ile Val Met Ile Gly
 85 90 95
 Tyr Ala Thr Leu Ala Gln Arg Ile Ala Leu Trp Ile Lys Gly Pro Lys
 100 105 110
 Gln Met Lys Ala Leu Asn Lys Ile Phe Gly Ser Leu Phe Met Leu Val
 115 120 125
 Gly Ala Leu Leu Ala Ser Ala Arg His Ala
 130 135

<210> 446
 <211> 257
 <212> PRT
 <213> Escherichia coli

<400> 446
 Met Ala Arg Lys Trp Leu Asn Leu Phe Ala Gly Ala Ala Leu Ser Phe
 1 5 10 15
 Ala Val Ala Gly Asn Ala Leu Ala Asp Glu Gly Lys Ile Thr Val Phe
 20 25 30
 Ala Ala Ala Ser Leu Thr Asn Ala Met Gln Asp Ile Ala Thr Gln Phe
 35 40 45
 Lys Lys Glu Lys Gly Val Asp Val Val Ser Ser Phe Ala Ser Ser Ser
 50 55 60
 Thr Leu Ala Arg Gln Ile Glu Ala Gly Ala Pro Ala Asp Leu Phe Ile
 65 70 75 80
 Ser Ala Asp Gln Lys Trp Met Asp Tyr Ala Val Asp Lys Lys Ala Ile
 85 90 95
 Asp Thr Ala Thr Arg Gln Thr Leu Leu Gly Asn Ser Leu Val Val Val
 100 105 110
 Ala Pro Lys Ala Ser Val Gln Lys Asp Phe Thr Ile Asp Ser Lys Thr
 115 120 125
 Asn Trp Thr Ser Leu Leu Asn Gly Gly Arg Leu Ala Val Gly Asp Pro
 130 135 140
 Glu His Val Pro Ala Gly Ile Tyr Ala Lys Glu Ala Leu Gln Lys Leu
 145 150 155 160
 Gly Ala Trp Asp Thr Leu Ser Pro Lys Leu Ala Pro Ala Glu Asp Val
 165 170 175
 Arg Gly Ala Leu Ala Leu Val Glu Arg Asn Glu Ala Pro Leu Gly Ile
 180 185 190
 Val Tyr Gly Ser Asp Ala Val Ala Ser Lys Gly Val Lys Val Val Ala
 195 200 205
 Thr Phe Pro Glu Asp Ser His Lys Lys Val Glu Tyr Pro Val Ala Val
 210 215 220
 Val Glu Gly His Asn Asn Ala Thr Val Lys Ala Phe Tyr Asp Tyr Leu
 225 230 235 240
 Lys Gly Pro Gln Ala Ala Glu Ile Phe Lys Arg Tyr Gly Phe Thr Ile
 245 250 255
 Lys

<210> 447
 <211> 229
 <212> PRT
 <213> Escherichia coli

<400> 447

Met Ile Leu Thr Asp Pro Glu Trp Gln Ala Val Leu Leu Ser Leu Lys
 1 5 10 15
 Val Ser Ser Leu Ala Val Leu Phe Ser Leu Pro Phe Gly Ile Phe Phe
 20 25 30
 Ala Trp Leu Leu Val Arg Cys Thr Phe Pro Gly Lys Ala Leu Leu Asp
 35 40 45
 Ser Val Leu His Leu Pro Leu Val Leu Pro Pro Val Val Val Gly Tyr
 50 55 60
 Leu Leu Leu Val Ser Met Gly Arg Arg Gly Phe Ile Gly Glu Arg Leu
 65 70 75 80
 Tyr Asp Trp Phe Gly Ile Thr Phe Ala Phe Ser Trp Arg Gly Ala Val
 85 90 95
 Leu Ala Ala Ala Val Met Ser Phe Pro Leu Met Val Arg Ala Ile Arg
 100 105 110
 Leu Ala Leu Glu Gly Val Asp Val Lys Leu Glu Gln Ala Ala Arg Thr
 115 120 125
 Leu Gly Ala Gly Arg Trp Arg Val Phe Phe Thr Ile Thr Leu Pro Leu
 130 135 140
 Thr Leu Pro Gly Ile Ile Val Gly Thr Val Leu Ala Phe Ala Arg Ser
 145 150 155 160
 Leu Gly Glu Phe Gly Ala Thr Ile Thr Phe Val Ser Asn Ile Pro Gly
 165 170 175
 Glu Thr Arg Thr Ile Pro Ser Ala Met Tyr Thr Leu Ile Gln Thr Pro
 180 185 190
 Gly Gly Glu Ser Gly Ala Ala Arg Leu Cys Ile Ile Ser Ile Ala Leu
 195 200 205
 Ala Met Ile Ser Leu Leu Ile Ser Glu Trp Leu Ala Arg Ile Ser Arg
 210 215 220
 Glu Arg Ala Gly Arg
 225

<210> 448

<211> 352

<212> PRT

<213> Escherichia coli

<400> 448

Met Leu Glu Leu Asn Phe Ser Gln Thr Leu Gly Asn His Cys Leu Thr
 1 5 10 15
 Ile Asn Glu Thr Leu Pro Ala Asn Gly Ile Thr Ala Ile Phe Gly Val
 20 25 30
 Ser Gly Ala Gly Lys Thr Ser Leu Ile Asn Ala Ile Ser Gly Leu Thr
 35 40 45
 Arg Pro Gln Lys Gly Arg Ile Val Leu Asn Gly Arg Val Leu Asn Asp
 50 55 60
 Ala Glu Lys Gly Ile Cys Leu Thr Pro Glu Lys Arg Arg Val Gly Tyr
 65 70 75 80
 Val Phe Gln Asp Ala Arg Leu Phe Pro His Tyr Lys Val Arg Gly Asn
 85 90 95
 Leu Arg Tyr Gly Met Ser Lys Ser Met Val Asp Gln Phe Asp Lys Leu
 100 105 110
 Val Ala Leu Leu Gly Ile Glu Pro Leu Leu Asp Arg Leu Pro Gly Ser
 115 120 125
 Leu Ser Gly Gly Glu Lys Gln Arg Val Ala Ile Gly Arg Ala Leu Leu
 130 135 140
 Thr Ala Pro Glu Leu Leu Leu Asp Glu Pro Leu Ala Ser Leu Asp
 145 150 155 160
 Ile Pro Arg Lys Arg Glu Leu Leu Pro Tyr Leu Gln Arg Leu Thr Arg
 165 170 175
 Glu Ile Asn Ile Pro Met Leu Tyr Val Ser His Ser Leu Asp Glu Ile

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      180      185      190
Leu His Leu Ala Asp Arg Val Met Val Leu Glu Asn Gly Gln Val Lys
      195      200      205
Ala Phe Gly Ala Leu Glu Glu Val Trp Gly Ser Ser Val Met Asn Pro
      210      215      220
Trp Leu Pro Lys Glu Gln Gln Ser Ser Ile Leu Lys Val Thr Val Leu
      225      230      235
Glu His His Pro His Tyr Ala Met Thr Ala Leu Ala Leu Gly Asp Gln
      245      250      255
His Leu Trp Val Asn Lys Leu Asp Glu Pro Leu Gln Ala Ala Leu Arg
      260      265      270
Ile Arg Ile Gln Ala Ser Asp Val Ser Leu Val Leu Gln Pro Pro Gln
      275      280      285
Gln Thr Ser Ile Arg Asn Val Leu Arg Ala Lys Val Val Asn Ser Tyr
      290      295      300
Asp Asp Asn Gly Gln Val Glu Val Glu Leu Glu Val Gly Gly Lys Thr
      305      310      315
Leu Trp Ala Arg Ile Ser Pro Trp Ala Arg Asp Glu Leu Ala Ile Lys
      325      330      335
Pro Gly Leu Trp Leu Tyr Ala Gln Ile Lys Ser Val Ser Ile Thr Ala
      340      345      350

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<210> 449
 <211> 168
 <212> PRT
 <213> Escherichia coli

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<400> 449
Met Asn Ser Val Ile Thr Gln Lys Val Ser Ser Gly Val Thr Leu Tyr
  1      5      10      15
Ala Asp Thr Lys Thr Gly Gly Phe Met Asn Arg Thr Ile Leu Val Pro
      20      25      30
Ile Asp Ile Ser Asp Ser Glu Leu Thr Gln Arg Val Ile Ser His Val
      35      40      45
Glu Glu Glu Ala Lys Ile Asp Asp Ala Glu Val His Phe Leu Thr Val
      50      55      60
Ile Pro Ser Leu Pro Tyr Tyr Ala Ser Leu Gly Leu Ala Tyr Ser Ala
      65      70      75      80
Glu Leu Pro Ala Met Asp Asp Leu Lys Ala Glu Ala Lys Ser Gln Leu
      85      90      95
Glu Glu Ile Ile Lys Lys Phe Lys Leu Pro Thr Asp Arg Val His Val
      100      105      110
His Val Glu Glu Gly Ser Pro Lys Asp Arg Ile Leu Glu Leu Ala Lys
      115      120      125
Lys Ile Pro Ala His Met Ile Ile Ile Ala Ser His Arg Pro Asp Ile
      130      135      140
Thr Thr Tyr Leu Leu Gly Ser Asn Ala Ala Val Val Arg His Ala
      145      150      155      160
Glu Cys Ser Val Leu Val Val Arg
      165

```

<210> 450
 <211> 377
 <212> PRT
 <213> Escherichia coli

```

<400> 450
Met Lys Ser Lys Val Leu Ala Leu Leu Ile Pro Ala Leu Leu Ala Ala
  1      5      10      15
Gly Ala Ala His Ala Ala Glu Val Tyr Asn Lys Asp Gly Asn Lys Leu

```

```

      20      25      30
Asp Leu Tyr Gly Lys Val Asp Gly Leu His Tyr Phe Ser Asp Asn Ser
   35      40      45
Ala Lys Asp Gly Asp Gln Ser Tyr Ala Arg Leu Gly Phe Lys Gly Glu
   50      55      60
Thr Gln Ile Asn Asp Gln Leu Thr Gly Tyr Gly Gln Trp Glu Tyr Asn
   65      70      75      80
Ile Gln Ala Asn Asn Thr Glu Ser Ser Lys Asn Gln Ser Trp Thr Arg
      85      90      95
Leu Ala Phe Ala Gly Leu Lys Phe Ala Asp Tyr Gly Ser Phe Asp Tyr
      100      105      110
Gly Arg Asn Tyr Gly Val Met Tyr Asp Ile Glu Gly Trp Thr Asp Met
      115      120      125
Leu Pro Glu Phe Gly Gly Asp Ser Tyr Thr Asn Ala Asp Asn Phe Met
      130      135      140
Thr Gly Arg Ala Asn Gly Val Ala Thr Tyr Arg Asn Thr Asp Phe Phe
      145      150      155      160
Gly Leu Val Asn Gly Leu Asn Phe Ala Val Gln Tyr Gln Gly Asn Asn
      165      170      175
Glu Gly Ala Ser Asn Gly Gln Glu Gly Thr Asn Asn Gly Arg Asp Val
      180      185      190
Arg His Glu Asn Gly Asp Gly Trp Gly Leu Ser Thr Thr Tyr Asp Leu
      195      200      205
Gly Met Gly Phe Ser Ala Gly Ala Ala Tyr Thr Ser Ser Asp Arg Thr
      210      215      220
Asn Asp Gln Val Asn His Thr Ala Ala Gly Gly Asp Lys Ala Asp Ala
      225      230      235      240
Trp Thr Ala Gly Leu Lys Tyr Asp Ala Asn Asn Ile Tyr Leu Ala Thr
      245      250      255
Met Tyr Ser Glu Thr Arg Asn Met Thr Pro Phe Gly Asp Ser Asp Tyr
      260      265      270
Ala Val Ala Asn Lys Thr Gln Asn Phe Glu Val Thr Ala Gln Tyr Gln
      275      280      285
Phe Asp Phe Gly Leu Arg Pro Ala Val Ser Phe Leu Met Ser Lys Gly
      290      295      300
Arg Asp Leu His Ala Ala Gly Gly Ala Asp Asn Pro Ala Gly Val Asp
      305      310      315      320
Asp Lys Asp Leu Val Lys Tyr Ala Asp Ile Gly Ala Thr Tyr Tyr Phe
      325      330      335
Asn Lys Asn Met Ser Thr Tyr Val Asp Tyr Lys Ile Asn Leu Leu Asp
      340      345      350
Glu Asp Asp Ser Phe Tyr Ala Ala Asn Gly Ile Ser Thr Asp Asp Ile
      355      360      365
Val Ala Leu Gly Leu Val Tyr Gln Phe
      370      375

```

<210> 451

<211> 1122

<212> PRT

<213> Escherichia coli

<400> 451

```

Met Leu Arg Val Tyr His Ser Asn Arg Leu Asp Val Leu Glu Ala Leu
  1      5      10      15
Met Glu Phe Ile Val Glu Arg Glu Arg Leu Asp Asp Pro Phe Glu Pro
      20      25      30
Glu Met Ile Leu Val Gln Ser Thr Gly Met Ala Gln Trp Leu Gln Met
      35      40      45
Thr Leu Ser Gln Lys Phe Gly Ile Ala Ala Asn Ile Asp Phe Pro Leu
      50      55      60

```

Pro	Ala	Ser	Phe	Ile	Trp	Asp	Met	Phe	Val	Arg	Val	Leu	Pro	Glu	Ile	65	70	75	80
Pro	Lys	Glu	Ser	Ala	Phe	Asn	Lys	Gln	Ser	Met	Ser	Trp	Lys	Leu	Met	85	90	95	
Thr	Leu	Leu	Pro	Gln	Leu	Leu	Glu	Arg	Glu	Asp	Phe	Thr	Leu	Leu	Arg	100	105	110	
His	Tyr	Leu	Thr	Asp	Asp	Ser	Asp	Lys	Arg	Lys	Leu	Phe	Gln	Leu	Ser	115	120	125	
Ser	Lys	Ala	Ala	Asp	Leu	Phe	Asp	Gln	Tyr	Leu	Val	Tyr	Arg	Pro	Asp	130	135	140	
Trp	Leu	Ala	Gln	Trp	Glu	Thr	Gly	His	Leu	Val	Glu	Gly	Leu	Gly	Glu	145	150	155	160
Ala	Gln	Ala	Trp	Gln	Ala	Pro	Leu	Trp	Lys	Ala	Leu	Val	Glu	Tyr	Thr	165	170	175	
His	Gln	Leu	Gly	Gln	Pro	Arg	Trp	His	Arg	Ala	Asn	Leu	Tyr	Gln	Arg	180	185	190	
Phe	Ile	Glu	Thr	Leu	Glu	Ser	Ala	Thr	Thr	Cys	Pro	Pro	Gly	Leu	Pro	195	200	205	
Ser	Arg	Val	Phe	Ile	Cys	Gly	Ile	Ser	Ala	Leu	Pro	Pro	Val	Tyr	Leu	210	215	220	
Gln	Ala	Leu	Gln	Ala	Leu	Gly	Lys	His	Ile	Glu	Ile	His	Leu	Leu	Phe	225	230	235	240
Thr	Asn	Pro	Cys	Arg	Tyr	Tyr	Trp	Gly	Asp	Ile	Lys	Asp	Pro	Ala	Tyr	245	250	255	
Leu	Ala	Lys	Leu	Leu	Thr	Arg	Gln	Arg	Arg	His	Ser	Phe	Glu	Asp	Arg	260	265	270	
Glu	Leu	Pro	Leu	Phe	Arg	Asp	Ser	Glu	Asn	Ala	Gly	Gln	Leu	Phe	Asn	275	280	285	
Ser	Asp	Gly	Glu	Gln	Asp	Val	Gly	Asn	Pro	Leu	Leu	Ala	Ser	Trp	Gly	290	295	300	
Lys	Leu	Gly	Arg	Asp	Tyr	Ile	Tyr	Leu	Leu	Ser	Asp	Leu	Glu	Ser	Ser	305	310	315	320
Gln	Glu	Leu	Asp	Ala	Phe	Val	Asp	Val	Thr	Pro	Asp	Asn	Leu	Leu	His	325	330	335	
Asn	Ile	Gln	Ser	Asp	Ile	Leu	Glu	Leu	Glu	Asn	Arg	Ala	Val	Ala	Gly	340	345	350	
Val	Asn	Ile	Glu	Glu	Phe	Ser	Arg	Ser	Asp	Asn	Lys	Arg	Pro	Leu	Asp	355	360	365	
Pro	Leu	Asp	Ser	Ser	Ile	Thr	Phe	His	Val	Cys	His	Ser	Pro	Gln	Arg	370	375	380	
Glu	Val	Glu	Val	Leu	His	Asp	Arg	Leu	Leu	Ala	Met	Leu	Glu	Glu	Asp	385	390	395	400
Pro	Thr	Leu	Thr	Pro	Arg	Asp	Ile	Ile	Val	Met	Val	Ala	Asp	Ile	Asp	405	410	415	
Ser	Tyr	Ser	Pro	Phe	Ile	Gln	Ala	Val	Phe	Gly	Ser	Ala	Pro	Ala	Asp	420	425	430	
Arg	Tyr	Leu	Pro	Tyr	Ala	Ile	Ser	Asp	Arg	Arg	Ala	Arg	Gln	Ser	His	435	440	445	
Pro	Val	Leu	Glu	Ala	Phe	Ile	Ser	Leu	Leu	Ser	Leu	Pro	Asp	Ser	Arg	450	455	460	
Phe	Val	Ser	Glu	Asp	Val	Leu	Ala	Leu	Leu	Asp	Val	Pro	Val	Leu	Ala	465	470	475	480
Ala	Arg	Phe	Asp	Ile	Thr	Glu	Glu	Gly	Leu	Arg	Tyr	Leu	Arg	Gln	Trp	485	490	495	
Val	Asn	Glu	Ser	Gly	Ile	Arg	Trp	Gly	Ile	Asp	Asp	Asp	Asn	Val	Arg	500	505	510	
Glu	Leu	Glu	Leu	Pro	Ala	Thr	Gly	Gln	His	Thr	Trp	Arg	Phe	Gly	Leu	515	520	525	
Thr	Arg	Met	Leu	Leu	Gly	Tyr	Ala	Met	Glu	Ser	Ala	Gln	Gly	Glu	Trp	530	535	540	

Gln	Ser	Val	Leu	Pro	Tyr	Asp	Glu	Ser	Ser	Gly	Leu	Ile	Ala	Glu	Leu
545					550					555					560
Val	Gly	His	Leu	Ala	Ser	Leu	Leu	Met	Gln	Leu	Asn	Ile	Trp	Arg	Arg
				565					570						575
Gly	Leu	Ala	Gln	Glu	Arg	Pro	Leu	Glu	Glu	Trp	Leu	Pro	Val	Cys	Arg
			580					585					590		
Asp	Met	Leu	Asn	Ala	Phe	Phe	Leu	Pro	Asp	Ala	Glu	Thr	Glu	Ala	Ala
		595					600						605		
Met	Thr	Leu	Ile	Glu	Gln	Gln	Trp	Gln	Ala	Ile	Ile	Ala	Glu	Gly	Leu
	610					615					620				
Gly	Ala	Gln	Tyr	Gly	Asp	Ala	Val	Pro	Leu	Ser	Leu	Leu	Arg	Asp	Glu
625					630					635					640
Leu	Ala	Gln	Arg	Leu	Asp	Gln	Glu	Arg	Ile	Ser	Gln	Arg	Phe	Leu	Ala
				645					650						655
Gly	Pro	Val	Asn	Ile	Cys	Thr	Leu	Met	Pro	Met	Arg	Ser	Ile	Pro	Phe
			660					665						670	
Lys	Val	Val	Cys	Leu	Leu	Gly	Met	Asn	Asp	Gly	Val	Tyr	Pro	Arg	Gln
		675					680						685		
Leu	Ala	Pro	Leu	Gly	Phe	Asp	Leu	Met	Ser	Gln	Lys	Pro	Lys	Arg	Gly
	690					695					700				
Asp	Arg	Ser	Arg	Arg	Asp	Asp	Asp	Arg	Tyr	Leu	Phe	Leu	Glu	Ala	Leu
705					710					715					720
Ile	Ser	Ala	Gln	Gln	Lys	Leu	Tyr	Ile	Ser	Tyr	Ile	Gly	Arg	Ser	Ile
				725					730						735
Gln	Asp	Asn	Ser	Glu	Arg	Phe	Pro	Ser	Val	Leu	Val	Gln	Glu	Leu	Ile
				740				745							750
Asp	Tyr	Ile	Gly	Gln	Ser	His	Tyr	Leu	Pro	Gly	Asp	Glu	Ala	Leu	Asn
		755					760						765		
Cys	Asp	Glu	Ser	Glu	Ala	Arg	Val	Lys	Ala	His	Leu	Thr	Cys	Leu	His
	770					775					780				
Thr	Arg	Met	Pro	Phe	Asp	Pro	Gln	Asn	Tyr	Gln	Pro	Gly	Glu	Arg	Gln
785					790					795					800
Ser	Tyr	Ala	Arg	Glu	Trp	Leu	Pro	Ala	Ala	Ser	Gln	Ala	Gly	Lys	Ala
				805					810						815
His	Ser	Glu	Phe	Val	Gln	Pro	Leu	Pro	Phe	Thr	Leu	Pro	Glu	Thr	Val
			820					825						830	
Pro	Leu	Glu	Thr	Leu	Gln	Arg	Phe	Trp	Ala	His	Pro	Val	Arg	Ala	Phe
		835					840						845		
Phe	Gln	Met	Arg	Leu	Gln	Val	Asn	Phe	Arg	Thr	Glu	Asp	Ser	Glu	Ile
	850					855					860				
Pro	Asp	Thr	Glu	Pro	Phe	Ile	Leu	Glu	Gly	Leu	Ser	Arg	Tyr	Gln	Ile
865					870					875					880
Asn	Gln	Gln	Leu	Leu	Asn	Ala	Leu	Val	Glu	Gln	Asp	Asp	Ala	Glu	Arg
			885						890					895	
Leu	Phe	Arg	Arg	Phe	Arg	Ala	Ala	Gly	Asp	Leu	Pro	Tyr	Gly	Ala	Phe
			900					905						910	
Gly	Glu	Ile	Phe	Trp	Glu	Thr	Gln	Cys	Gln	Glu	Met	Gln	Gln	Leu	Ala
		915					920							925	
Asp	Arg	Val	Ile	Ala	Cys	Arg	Gln	Pro	Gly	Gln	Ser	Met	Glu	Ile	Asp
	930					935					940				
Leu	Ala	Cys	Asn	Gly	Val	Gln	Ile	Thr	Gly	Trp	Leu	Pro	Gln	Val	Gln
945					950					955					960
Pro	Asp	Gly	Leu	Leu	Arg	Trp	Arg	Pro	Ser	Leu	Leu	Ser	Val	Ala	Gln
				965					970						975
Gly	Met	Gln	Leu	Trp	Leu	Glu	His	Leu	Val	Tyr	Cys	Ala	Ser	Gly	Gly
			980					985						990	
Asn	Gly	Glu	Ser	Arg	Leu	Phe	Leu	Arg	Lys	Asp	Gly	Glu	Trp	Arg	Phe
		995					1000						1005		
Pro	Pro	Leu	Ala	Ala	Glu	Gln	Ala	Leu	His	Tyr	Leu	Ser	Gln	Leu	Ile
	1010						1015								1020

Glu Gly Tyr Arg Glu Gly Met Ser Ala Pro Leu Leu Val Leu Pro Glu
 1025 1030 1035 1040
 Ser Gly Gly Ala Trp Leu Lys Thr Cys Tyr Asp Ala Gln Asn Asp Ala
 1045 1050 1055
 Met Leu Asp Asp Asp Ser Thr Leu Gln Lys Ala Arg Thr Lys Phe Leu
 1060 1065 1070
 Gln Ala Tyr Glu Gly Asn Met Met Val Arg Gly Glu Gly Asp Asp Ile
 1075 1080 1085
 Trp Tyr Gln Arg Leu Trp Arg Gln Leu Thr Pro Glu Thr Met Glu Ala
 1090 1095 1100
 Ile Val Glu Gln Ser Gln Arg Phe Leu Leu Pro Leu Phe Arg Phe Asn
 1105 1110 1115 1120
 Gln Ser

<210> 452
 <211> 107
 <212> PRT
 <213> Escherichia coli

<400> 452
 Met Ser Ala Ser Leu Lys Asn Gln Gln Gly Phe Ser Leu Pro Glu Val
 1 5 10 15
 Met Leu Ala Met Val Leu Met Val Met Ile Val Thr Ala Leu Ser Gly
 20 25 30
 Phe Gln Arg Thr Leu Met Asn Ser Leu Ala Ser Arg Asn Gln Tyr Gln
 35 40 45
 Gln Leu Trp Arg His Gly Trp Gln Gln Thr Gln Leu Arg Ala Ile Ser
 50 55 60
 Pro Pro Ala Asn Trp Gln Val Asn Arg Met Gln Thr Ser Gln Ala Gly
 65 70 75 80
 Cys Val Ser Ile Ser Val Thr Leu Val Ser Pro Gly Gly Arg Glu Gly
 85 90 95
 Glu Met Thr Arg Leu His Cys Pro Asn Arg Gln
 100 105

<210> 453
 <211> 121
 <212> PRT
 <213> Escherichia coli

<400> 453
 Met Leu Leu Val Leu Gly Ser Leu Leu Leu Gln Gly Met Ser Gln Gln
 1 5 10 15
 Asp Arg Ser Phe Ala Ser Arg Val Ser Met Glu Ser Gln Ser Leu Arg
 20 25 30
 Arg Gln Ala Ile Val Gln Ser Ala Leu Ala Trp Gly Lys Met His Cys
 35 40 45
 Trp Gln Thr Gln Pro Ala Val Gln Cys Ser Gln Tyr Ala Glu Thr Asp
 50 55 60
 Ala Gln Val Cys Leu Arg Leu Leu Ala Asp Asn Glu Ala Leu Leu Ile
 65 70 75 80
 Ala Gly Tyr Glu Gly Val Ser Leu Trp Arg Thr Gly Glu Val Ile Asp
 85 90 95
 Gly Asn Ile Val Phe Ser Pro Arg Gly Trp Ser Asp Phe Cys Pro Leu
 100 105 110
 Lys Glu Arg Ala Leu Cys Gln Leu Pro
 115 120

<210> 454

<211> 187

<212> PRT

<213> Escherichia coli

<400> 454

```

Met Pro Val Lys Glu Gln Gly Phe Ser Leu Leu Glu Val Leu Ile Ala
 1          5          10          15
Met Ala Ile Ser Ser Val Leu Leu Leu Gly Ala Ala Arg Phe Leu Pro
          20          25          30
Ala Leu Gln Arg Glu Ser Leu Thr Ser Thr Arg Lys Leu Ala Leu Glu
          35          40          45
Asp Glu Ile Trp Leu Arg Val Phe Thr Val Ala Lys His Leu Gln Arg
          50          55          60
Ala Gly Tyr Cys His Gly Ile Cys Thr Gly Glu Gly Leu Glu Ile Val
          65          70          75          80
Gly Gln Gly Asp Cys Val Ile Val Gln Trp Asp Ala Asn Ser Asn Gly
          85          90          95
Ile Trp Asp Arg Glu Pro Val Lys Glu Ser Asp Gln Ile Gly Phe Arg
          100          105          110
Leu Lys Glu His Val Leu Glu Thr Leu Arg Gly Ala Thr Ser Cys Glu
          115          120          125
Gly Lys Gly Trp Asp Lys Val Thr Asn Pro Asp Ala Ile Ile Ile Asp
          130          135          140
Thr Phe Gln Val Val Arg Gln Asp Val Ser Gly Phe Ser Pro Val Leu
          145          150          155          160
Thr Val Asn Met Arg Ala Ala Ser Lys Ser Glu Pro Gln Thr Val Val
          165          170          175
Asn Ala Ser Tyr Ser Val Thr Gly Phe Asn Leu
          180          185

```

<210> 455

<211> 156

<212> PRT

<213> Escherichia coli

<400> 455

```

Met Lys Thr Gln Arg Gly Tyr Thr Leu Ile Glu Thr Leu Val Ala Met
 1          5          10          15
Leu Ile Leu Val Met Leu Ser Ala Ser Gly Leu Tyr Gly Trp Gln Tyr
          20          25          30
Trp Gln Gln Ser Gln Arg Leu Trp Gln Thr Ala Ser Gln Ala Arg Asp
          35          40          45
Tyr Leu Leu Tyr Leu Arg Glu Asp Ala Asn Trp His Asn Arg Asp His
          50          55          60
Ser Ile Ser Val Ile Arg Glu Gly Thr Leu Trp Cys Leu Val Ser Ser
          65          70          75          80
Ala Ala Gly Ala Asn Thr Cys His Gly Ser Ser Pro Leu Val Phe Val
          85          90          95
Pro Arg Trp Pro Glu Val Glu Met Ser Asp Leu Thr Pro Ser Leu Ala
          100          105          110
Phe Phe Gly Leu Arg Asn Thr Ala Trp Ala Gly His Ile Arg Phe Lys
          115          120          125
Asn Ser Thr Gly Glu Trp Trp Leu Val Val Ser Pro Trp Gly Arg Leu
          130          135          140
Arg Leu Cys Gln Gln Gly Glu Thr Glu Gly Cys Leu
          145          150          155

```

<210> 456

<211> 711

<212> PRT

<213> Escherichia coli

<400> 456

```

Met Ser Thr Ile Val Ile Phe Leu Ala Ala Leu Leu Ala Cys Ser Leu
 1           5           10           15
Leu Ala Gly Trp Leu Ile Lys Val Arg Ser Arg Arg Arg Gln Leu Pro
 20           25           30
Trp Thr Asn Ala Phe Ala Asp Ala Gln Thr Arg Lys Leu Thr Pro Glu
 35           40           45
Glu Arg Ser Ala Val Glu Asn Tyr Leu Glu Ser Leu Thr Gln Val Leu
 50           55           60
Gln Val Pro Gly Pro Thr Gly Ala Ser Ala Ala Pro Ile Ser Leu Ala
 65           70           75
Leu Asn Ala Glu Ser Asn Asn Val Met Met Leu Thr His Ala Ile Thr
 85           90           95
Arg Tyr Gly Ile Ser Thr Asp Asp Pro Asn Lys Trp Arg Tyr Tyr Leu
100           105           110
Asp Ser Val Glu Val His Leu Pro Pro Phe Trp Glu Gln Tyr Ile Asn
115           120           125
Asp Glu Asn Thr Val Glu Leu Ile His Thr Asp Ser Leu Pro Leu Val
130           135           140
Ile Ser Leu Asn Gly His Thr Leu Gln Glu Tyr Met Gln Glu Thr Arg
145           150           155
Ser Tyr Ala Leu Gln Pro Val Pro Ser Thr Gln Ala Ser Ile Arg Gly
165           170           175
Glu Glu Ser Glu Gln Ile Glu Leu Leu Asn Ile Arg Lys Glu Thr His
180           185           190
Glu Glu Tyr Ala Leu Ser Arg Pro Arg Gly Leu Arg Glu Ala Leu Leu
195           200           205
Ile Val Ala Ser Phe Leu Met Phe Phe Phe Cys Leu Ile Thr Pro Asp
210           215           220
Val Phe Val Pro Trp Leu Ala Gly Gly Ala Leu Leu Leu Leu Gly Ala
225           230           235
Gly Leu Trp Gly Leu Phe Ala Pro Pro Ala Lys Ser Ser Leu Arg Glu
245           250           255
Ile His Cys Leu Arg Gly Thr Pro Arg Arg Trp Gly Leu Phe Gly Glu
260           265           270
Asn Asp Gln Glu Gln Ile Asn Asn Ile Ser Leu Gly Ile Ile Asp Leu
275           280           285
Val Tyr Pro Ala His Trp Gln Pro Tyr Ile Ala Gln Asp Leu Gly Gln
290           295           300
Gln Thr Asp Ile Asp Ile Tyr Leu Asp Arg His Val Val Arg Gln Gly
305           310           315
Arg Tyr Leu Ser Leu His Asp Glu Val Lys Asn Phe Pro Leu Gln His
325           330           335
Trp Leu Arg Ser Thr Ile Ile Ala Ala Gly Ser Leu Leu Val Leu Phe
340           345           350
Met Leu Leu Phe Trp Ile Pro Leu Asp Met Pro Leu Lys Phe Thr Leu
355           360           365
Ser Trp Met Lys Gly Ala Gln Thr Ile Glu Ala Thr Ser Val Lys Gln
370           375           380
Leu Ala Asp Ala Gly Val Arg Val Gly Asp Thr Leu Arg Ile Ser Gly
385           390           395
Thr Gly Met Cys Asn Ile Arg Thr Ser Gly Thr Trp Ser Ala Lys Thr
405           410           415
Asn Ser Pro Phe Leu Pro Phe Asp Cys Ser Gln Ile Ile Trp Asn Asp
420           425           430
Ala Arg Ser Leu Pro Leu Pro Glu Ser Glu Leu Val Asn Lys Ala Thr
435           440           445
Ala Leu Thr Glu Ala Val Asn Arg Gln Leu His Pro Lys Pro Glu Asp

```

450	455	460
Glu Ser Arg Val Ser	Ala Ser Leu Arg Ser	Ala Ile Gln Lys Ser Gly
465	470	475
Met Val Leu Leu Asp	Asp Phe Gly Asp Ile	Val Leu Lys Thr Ala Asp
	485	490
Leu Cys Ser Ala Lys	Asp Asp Cys Val Arg	Leu Lys Asn Ala Leu Val
	500	505
Asn Leu Gly Asn Ser	Lys Asp Trp Asp Ala	Leu Val Lys Arg Ala Asn
	515	520
Ala Gly Lys Leu Asp	Gly Val Asn Val Leu	Leu Arg Pro Val Ser Ala
	530	535
Glu Ser Leu Asp Asn	Leu Val Ala Thr Ser	Thr Ala Pro Phe Ile Thr
545	550	555
His Glu Thr Ala Arg	Ala Ala Gln Ser Leu	Asn Ser Pro Ala Pro Gly
	565	570
Gly Phe Leu Ile Val	Ser Asp Glu Gly Ser	Asp Phe Val Asp Gln Pro
	580	585
Trp Pro Ser Ala Ser	Leu Tyr Asp Tyr Pro	Pro Gln Glu Gln Trp Asn
	595	600
Ala Phe Gln Lys Leu	Ala Gln Met Leu Met	His Thr Pro Phe Asn Ala
	610	615
Glu Gly Ile Val Thr	Lys Ile Phe Thr Asp	Ala Asn Gly Thr Gln His
625	630	635
Ile Gly Leu His Pro	Ile Pro Asp Arg Ser	Gly Leu Trp Arg Tyr Leu
	645	650
Ser Thr Thr Leu Leu	Leu Leu Thr Met Leu	Gly Ser Ala Ile Tyr Asn
	660	665
Gly Val Gln Ala Trp	Arg Arg Tyr Gln Arg	His Arg Thr Arg Met Met
	675	680
Glu Ile Gln Ala Tyr	Tyr Glu Ser Cys Leu	Asn Pro Gln Leu Ile Thr
	690	695
Pro Ser Glu Ser Leu	Ile Glu	
705	710	

<210> 457

<211> 237

<212> PRT

<213> Escherichia coli

<400> 457

Met Leu Pro Cys Arg	Ala Asn Cys Phe Thr	Leu Glu Ile Ser Leu Met
1	5	10
His Ile Asn Ile Ala	Trp Gln Asp Val Asp	Thr Val Leu Leu Asp Met
	20	25
Asp Gly Thr Leu Leu	Asp Leu Ala Phe Asp	Asn Tyr Phe Trp Gln Lys
	35	40
Leu Val Pro Glu Thr	Trp Gly Ala Lys Asn	Gly Val Thr Pro Gln Glu
	50	55
Ala Met Glu Tyr Met	Arg Gln Gln Tyr His	Asp Val Gln His Thr Leu
65	70	75
Asn Trp Tyr Cys Leu	Asp Tyr Trp Ser Glu	Gln Leu Gly Leu Asp Ile
	85	90
Cys Ala Met Thr Thr	Glu Met Gly Pro Arg	Ala Val Leu Arg Glu Asp
	100	105
Thr Ile Pro Phe Leu	Glu Ala Leu Lys Ala	Ser Gly Lys Gln Arg Ile
	115	120
Leu Leu Thr Asn Ala	His Pro His Asn Leu	Ala Val Lys Leu Glu His
	130	135
Thr Gly Leu Asp Ala	His Leu Asp Leu Leu	Leu Ser Thr His Thr Phe
145	150	155
		160

Gly Tyr Pro Lys Glu Asp Gln Arg Leu Trp His Ala Val Ala Glu Ala
 165 170 175
 Thr Gly Leu Lys Ala Glu Arg Thr Leu Phe Ile Asp Asp Ser Glu Ala
 180 185 190
 Ile Leu Asp Ala Ala Ala Gln Phe Gly Ile Arg Tyr Cys Leu Gly Val
 195 200 205
 Thr Asn Pro Asp Ser Gly Ile Ala Glu Lys Gln Tyr Gln Arg His Pro
 210 215 220
 Ser Leu Asn Asp Tyr Arg Arg Leu Ile Pro Ser Leu Met
 225 230 235

<210> 458

<211> 133

<212> PRT

<213> Escherichia coli

<400> 458

Met Lys Glu Lys Pro Ala Val Glu Val Arg Leu Asp Lys Trp Leu Trp
 1 5 10 15
 Ala Ala Arg Phe Tyr Lys Thr Arg Ala Leu Ala Arg Glu Met Ile Glu
 20 25 30
 Gly Gly Lys Val His Tyr Asn Gly Gln Arg Ser Lys Pro Ser Lys Ile
 35 40 45
 Val Glu Leu Asn Ala Thr Leu Thr Leu Arg Gln Gly Asn Asp Glu Arg
 50 55 60
 Thr Val Ile Val Lys Ala Ile Thr Glu Gln Arg Arg Pro Ala Ser Glu
 65 70 75 80
 Ala Ala Leu Leu Tyr Glu Glu Thr Ala Glu Ser Val Glu Lys Arg Glu
 85 90 95
 Lys Met Ala Leu Ala Arg Lys Leu Asn Ala Leu Thr Met Pro His Pro
 100 105 110
 Asp Arg Arg Pro Asp Lys Lys Glu Arg Arg Asp Leu Leu Arg Phe Lys
 115 120 125
 His Gly Asp Ser Glu
 130

<210> 459

<211> 294

<212> PRT

<213> Escherichia coli

<400> 459

Met Ile Met Pro Gln His Asp Gln Leu His Arg Tyr Leu Phe Glu Asn
 1 5 10 15
 Phe Ala Val Arg Gly Glu Leu Val Thr Val Ser Glu Thr Leu Gln Gln
 20 25 30
 Ile Leu Glu Asn His Asp Tyr Pro Gln Pro Val Lys Asn Val Leu Ala
 35 40 45
 Glu Leu Leu Val Ala Thr Ser Leu Leu Thr Ala Thr Leu Lys Phe Asp
 50 55 60
 Gly Asp Ile Thr Val Gln Leu Gln Gly Asp Gly Pro Met Asn Leu Ala
 65 70 75 80
 Val Ile Asn Gly Asn Asn Asn Gln Gln Met Arg Gly Val Ala Arg Val
 85 90 95
 Gln Gly Glu Ile Pro Glu Asn Ala Asp Leu Lys Thr Leu Val Gly Asn
 100 105 110
 Gly Tyr Val Val Ile Thr Ile Thr Pro Ser Glu Gly Glu Arg Tyr Gln
 115 120 125
 Gly Val Val Gly Leu Glu Gly Asp Thr Leu Ala Ala Cys Leu Glu Asp
 130 135 140

Tyr Phe Met Arg Ser Glu Gln Leu Pro Thr Arg Leu Phe Ile Arg Thr
 145 150 155 160
 Gly Asp Val Asp Gly Lys Pro Ala Ala Gly Gly Met Leu Leu Gln Val
 165 170 175
 Met Pro Ala Gln Asn Ala Gln Gln Asp Asp Phe Asp His Leu Ala Thr
 180 185 190
 Leu Thr Glu Thr Ile Lys Thr Glu Glu Leu Leu Thr Leu Pro Ala Asn
 195 200 205
 Glu Val Leu Trp Arg Leu Tyr His Glu Glu Glu Val Thr Val Tyr Asp
 210 215 220
 Pro Gln Asp Val Glu Phe Lys Cys Thr Cys Ser Arg Glu Arg Cys Ala
 225 230 235 240
 Asp Ala Leu Lys Thr Leu Pro Asp Glu Glu Val Asp Ser Ile Leu Ala
 245 250 255
 Glu Asp Gly Glu Ile Asp Met His Cys Asp Tyr Cys Gly Asn His Tyr
 260 265 270
 Leu Phe Asn Ala Met Asp Ile Ala Glu Ile Arg Asn Asn Ala Ser Pro
 275 280 285
 Ala Asp Pro Gln Val His
 290

<210> 460

<211> 120

<212> PRT

<213> Escherichia coli

<400> 460

Met Leu Lys Leu Phe Ala Lys Tyr Thr Ser Ile Gly Val Leu Asn Thr
 1 5 10 15
 Leu Ile His Trp Val Val Phe Gly Val Cys Ile Tyr Val Ala His Thr
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<211> 306

<212> PRT

<213> Escherichia coli

<400> 461

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 Ser Ile Ile Asn Ala Leu Ala Val Ser Asp Pro Leu Val Val Pro Leu
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 Ser Phe Thr Arg Asn Phe Gly Lys Glu Pro Ala Leu Phe Ala Gly Leu
 65 70 75 80

Asp His Ala Thr Gly Asp Ala Ile Ile Pro Ile Asp Val Asp Leu Gln
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 Asp Pro Ile Glu Val Ile Pro His Leu Ile Glu Lys Trp Gln Ala Gly
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 Arg Asp Val Val Glu Asn Ile Lys Leu Met Pro Glu Arg Asn Leu Phe
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 Met Lys Gly Ile Leu Ser Trp Val Gly Gly Lys Thr Asp Ile Val Glu
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 Tyr Val Arg Ala Glu Arg Ile Ala Gly Asp Thr Lys Phe Asn Gly Trp
 195 200 205
 Lys Leu Trp Asn Leu Ala Leu Glu Gly Ile Thr Ser Phe Ser Thr Phe
 210 215 220
 Pro Leu Arg Ile Trp Thr Tyr Ile Gly Leu Val Val Ala Ser Val Ala
 225 230 235 240
 Phe Ile Tyr Gly Ala Trp Met Ile Leu Asp Thr Ile Ile Phe Gly Asn
 245 250 255
 Ala Val Arg Gly Tyr Pro Ser Leu Leu Val Ser Ile Leu Phe Leu Gly
 260 265 270
 Gly Ile Gln Met Ile Gly Ile Gly Val Leu Gly Glu Tyr Ile Gly Arg
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 Lys Lys
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<211> 443

<212> PRT

<213> Escherichia coli

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 Leu Phe Leu Lys Val Ile Tyr Ile Tyr Ser Leu Tyr Ala Ile Phe Thr
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 Ser Tyr Ile Lys Thr Glu Arg Tyr Val Thr Leu Phe Thr Phe Phe Ile
 115 120 125
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 130 135 140
 Phe Tyr Gln Glu Gln Ile Val Ile Ile Phe Leu Pro Phe Leu Val Tyr
 145 150 155 160
 Ser Leu Thr Cys Lys Asn Asn Lys Ser Met Leu Leu Leu Phe Phe Ser
 165 170 175
 Leu Leu Ile Ile Ser Thr Ala Lys Asn Gln Phe Ile Leu Thr Pro Leu

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Ile	Val	Tyr	Ser	Tyr	Tyr	Ile	Phe	Phe	Asp	Arg	His	Lys	Leu	Ile	Ile	
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Lys	Ser	Val	Ile	Cys	Val	Val	Cys	Leu	Leu	Ala	Ser	Ile	Phe	Ala	Ile	
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Asp	Leu	Cys	Leu	Tyr	Ile	Thr	Val	Val	Phe	Leu	Ile	Tyr	Lys	Ile	Ile	
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<211> 148

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<213> Escherichia coli

<400> 464

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          35           40           45
Ser Leu Gly Gly Lys Tyr Leu Thr His Asp Leu Ser Ile Lys Ile Ala
          50           55           60
Asp Ile Ser Glu Glu Ile Ile Gln Gln Ala Ile Leu Ser Ala Met Ser
65           70           75           80
Ile Tyr Lys Phe Ser Ile Thr Asp Asp Leu Met Ser Met Ala Val Asn
          85           90           95
Glu Leu Ile Lys Leu Thr Lys Ile Glu Asn Asn Val Asp Leu Asn Lys
          100          105          110
Phe Thr Thr Ile Cys Thr Asp Val Leu Ser Pro Arg Val Thr Arg His
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<211> 167

<212> PRT

<213> Escherichia coli

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          35           40           45
Tyr Val Gly Ala Lys Ser Arg Gln Arg Trp Leu Phe Tyr Ala Tyr Asp
          50           55           60
Arg Leu Arg Lys Thr Val Val Ala His Val Phe Gly Glu Arg Thr Met
65           70           75           80
Ala Thr Leu Gly Arg Leu Met Ser Leu Leu Ser Pro Phe Asp Val Val
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Ile Trp Met Thr Asp Gly Trp Pro Leu Tyr Glu Ser Arg Leu Lys Gly
          100          105          110
Lys Leu His Val Ile Ser Lys Arg Tyr Thr Gln Arg Ile Glu Arg His
          115          120          125
Asn Leu Asn Leu Arg Gln His Leu Ala Arg Leu Gly Arg Lys Ser Leu
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<211> 91

<212> PRT

<213> Escherichia coli

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 35 40 45
 Gln Pro Gly Thr His Gln Lys Ile Ile Asp Met Ala Met Asn Gly Val
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<211> 1377

<212> PRT

<213> Escherichia coli

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 35 40 45
 Val Asn Pro Leu Leu Gly Ala Lys Val Leu Pro Gly Glu Thr Asp Ile
 50 55 60
 Ala Leu Pro Gly Pro Leu Pro Phe Ile Leu Ser Arg Thr Tyr Ser Ser
 65 70 75 80
 Tyr Arg Thr Lys Thr Pro Ala Pro Val Gly Ser Leu Gly Pro Gly Trp
 85 90 95
 Lys Met Pro Ala Asp Ile Arg Leu Gln Leu Arg Asp Asn Thr Leu Ile
 100 105 110
 Leu Ser Asp Asn Gly Gly Arg Ser Leu Tyr Phe Glu His Leu Phe Pro
 115 120 125
 Gly Glu Asp Gly Tyr Ser Arg Ser Glu Ser Leu Trp Leu Val Arg Gly
 130 135 140
 Gly Val Ala Lys Leu Asp Glu Gly His Arg Leu Ala Ala Leu Trp Gln
 145 150 155 160
 Ala Leu Pro Glu Glu Leu Arg Leu Ser Pro His Arg Tyr Leu Ala Thr
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 Asn Ser Pro Gln Gly Pro Trp Trp Leu Gly Trp Cys Glu Arg Val
 180 185 190
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 Glu Ala Ala Gly Glu Phe Ser Gly Glu Ile Thr Gly Val Thr Asp Gly
 225 230 235 240
 Ala Trp Arg His Phe Arg Leu Val Leu Thr Thr Gln Ala Gln Arg Ala
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 Glu Glu Ala Arg Gln Gln Ala Ile Ser Gly Gly Thr Glu Pro Ser Ala
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 Phe Pro Asp Thr Leu Pro Gly Tyr Thr Glu Tyr Gly Arg Asp Asn Gly
 275 280 285
 Ile Arg Leu Ser Ala Val Trp Leu Thr His Asp Pro Glu Tyr Pro Glu
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 Asn Leu Pro Ala Ala Pro Leu Val Arg Tyr Gly Trp Thr Pro Arg Gly
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 Glu Leu Ala Val Val Tyr Asp Arg Ser Gly Lys Gln Val Arg Ser Phe
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 Thr Tyr Asp Asp Lys Tyr Arg Gly Arg Met Val Ala His Arg His Thr

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Tyr Ile Thr Gln Asp Pro Ile Gly Leu Lys Gly Gly Trp Asn Phe Tyr		
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Gln Tyr Pro Leu Asn Pro Val Thr Asn Thr Asp Pro Leu Gly Leu Glu		
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Val Phe Pro Arg Pro Phe Pro Leu Pro Ile Pro Trp Pro Lys Ser Pro		
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Trp Asn Asp Thr Ala Ser Gln Arg Ile Phe Asp Ser Leu Ile Leu Asn		
	1285	1290
Asn Pro Gly Leu Ala Leu Asp Ile Thr Met Ile Ala Ser Arg Gly Asn		

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 1315 1320 1325
 Arg Phe Trp Ser Asp Gly Lys Lys Pro Asp Arg Cys Asp Val Leu Gln
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 Glu Leu Ile Asp Cys Gly Asp Ile Ser Ala Lys Asp Ala Lys Ser Thr
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 1365 1370 1375
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 100 105 110
 Glu Ser Thr Ala Gln Arg Cys Lys Lys Asn Pro Ile Tyr Ser Pro Lys
 115 120 125
 Ile Val Glu Gln Ser Gln Ile Thr Ala Phe Asp Lys Ser Thr Asn Val
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 145 150 155 160
 Ile Pro Leu Leu Ile Asn Leu Leu Lys Asp Pro Asn Gly Asp Val Arg
 165 170 175
 Asn Trp Ala Ala Phe Ala Ile Asn Ile Asn Lys Tyr Asp Asn Ser Asp
 180 185 190
 Ile Arg Asp Cys Phe Val Glu Met Leu Gln Asp Lys Asn Glu Glu Val
 195 200 205
 Arg Ile Glu Ala Ile Ile Gly Leu Ser Tyr Arg Lys Asp Lys Arg Val
 210 215 220
 Leu Ser Val Leu Cys Asp Glu Leu Lys Lys Asn Thr Val Tyr Asp Asp
 225 230 235 240
 Ile Ile Glu Ala Ala Gly Glu Leu Gly Asp Lys Thr Leu Leu Pro Val
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 260 265 270
 Ala Ile Asp Lys Leu Lys Arg Ser
 275 280

<210> 469
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 <212> PRT
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<400> 469

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Gln Met Lys Asn Gln Met Asp Pro Val Tyr Thr Pro Ala Arg Lys Ile
 35          40          45
His Leu Tyr His Cys Asp His Arg Gly Leu Pro Leu Ala Leu Ile Ser
 50          55          60
Lys Glu Gly Thr Thr Glu Trp Cys Ala Glu Tyr Asp Glu Trp Gly Asn
 65          70          75          80
Leu Leu Asn Glu Glu Asn Pro His Gln Leu Gln Gln Leu Ile Arg Leu
 85          90          95
Pro Gly Gln Gln Tyr Asp Glu Glu Ser Gly Leu Tyr Tyr Asn Arg His
100          105          110
Arg Tyr Tyr Asp Pro Leu Gln Gly Arg Tyr Ile Thr Gln Asp Pro Ile
115          120          125
Gly Leu Lys Gly Gly Trp Asn Phe Tyr Gln Tyr Pro Leu Asn Pro Val
130          135          140
Ile Asn Val Asp Pro Gln Gly Leu Val Asp Ile Asn Leu Tyr Pro Glu
145          150          155          160
Ser Asp Leu Ile His Ser Val Ala Asp Glu Ile Asn Ile Pro Gly Val
165          170          175
Phe Thr Ile Gly Gly His Gly Thr Pro Thr Ser Ile Glu Ser Ala Thr
180          185          190
Arg Ser Ile Met Thr Ala Lys Asp Leu Ala Tyr Leu Ile Lys Phe Asp
195          200          205
Gly Asn Tyr Lys Asp Gly Met Thr Val Trp Leu Phe Ser Cys Asn Thr
210          215          220
Gly Lys Gly Gln Asn Ser Phe Ala Ser
225          230

```

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International Bureau



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- (22) International Filing Date:
9 November 2000 (09.11.2000)
- (25) Filing Language: English
- (26) Publication Language: English
- (30) Priority Data:
60/164,415 9 November 1999 (09.11.1999) US
- (71) Applicant (for all designated States except US): **ELITRA PHARMACEUTICALS, INC.** [US/US]; Suite A, 3510 Dunhill Street, San Diego, CA 92121 (US).
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- (75) Inventors/Applicants (for US only): **FORSYTH, R., Allyn** [US/US]; 1135 Beryl Street, San Diego, CA 92116 (US). **OHLSEN, Kari** [US/US]; 3560 Vista de La Orilla, San Diego, CA 92117 (US). **ZYSKIND, Judith** [US/US]; 8415 La Jolla Scenic Drive, La Jolla, CA 92037 (US).
- (74) Agent: **HUNT, Dale, C.**; Knobbe, Martens, Olson & Bear, LLP, 16th Floor, 620 Newport Center Drive, Newport Beach, CA 92660 (US).
- (81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, CZ (utility model), DE, DE (utility model), DK, DK (utility model), DM, DZ, EE, EE (utility model), ES, FI, FI (utility model), GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KR (utility model), KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SK (utility model), SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.
- (84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).
- Published:
— with international search report
- (88) Date of publication of the international search report:
10 May 2002
- For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION

(57) Abstract: The sequences of nucleic acids encoding proteins required for E. coli proliferation are disclosed. The nucleic acids can be used to express proteins or portions thereof, to obtain antibodies capable of specifically binding to the expressed proteins, and to use those expressed proteins as a screen to isolate candidate molecules for rational drug discovery programs. The nucleic acids can also be used to screen for homologous genes that are required for proliferation in microorganisms other than E. coli. The nucleic acids can also be used to design expression vectors and secretion vectors. The nucleic acids of the present invention can also be used in various assay systems to screen for proliferation required genes in other organisms as well as to screen for antimicrobial agents.

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INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/30950

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/31 C12N15/11 C12N15/10 C07K14/245

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

SEQUENCE SEARCH, EPO-Internal, WPI Data, PAJ, BIOSIS

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE EM PRO [Online] EMBL; 29 January 1997 (1997-01-29) BLATTNER ET AL.: "Escherichia coli K12 MG1655 section 101 of 400 of the complete genome" retrieved from EBI, accession no. ECAE211 Database accession no. AE000211 XP002181472 the whole document	5,10,13, 14, 18-21, 124
Y		
X	-& DATABASE SWALL [Online] 15 July 1998 (1998-07-15) BLATTNER ET AL.: "Hypothetical protein YCFS precursor" retrieved from EBI, accession no. YCFS ECOLI Database accession no. P75954 XP002181473 the whole document	1-131 5,10,13, 14, 18-21, 124
-/--		

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

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"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

15 November 2001

Date of mailing of the international search report

30.11.01

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Fax: (+31-70) 340-3016

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Ceder, O

INTERNATIONAL SEARCH REPORT

International Application No.

PCT/US 00/30950

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	-& DATABASE EM PRO [Online] EMBL; 29 January 1997 (1997-01-29) BLATTNER ET AL.: "Escherichia coli K12 MG1655 section 305 of 400 of the complete genome" retrieved from EBI, accession no. ECAE415 Database accession no. AE000415 XP002181474 the whole document	5,10,13, 14, 18-21, 124
X	-& DATABASE SWALL [Online] 1 November 1995 (1995-11-01) BLATTNER ET AL.: "Hypothetical 79.5 kDa protein in MRCA-PCKA intergenic region (0711)" retrieved from EBI, accession no. YRFF ECOLI Database accession no. P45800 XP002181475 the whole document	5,10,13, 14, 18-21, 124
A	-& BLATTNER ET AL.: "The complete genome sequence of Escherichia coli K-12" SCIENCE, vol. 277, 5 September 1997 (1997-09-05), pages 1453-1462, FIGURES, XP002923023 the whole document	1,9
Y	WO 99 02673 A (DUGOURD DOMINIQUE ;WRIGHT JIM A (CA); YOUNG AIPING H (CA); GENESEN) 21 January 1999 (1999-01-21) page 7, line 25 -page 9, line 30; examples 2-6	1-131
X	--- DATABASE EM PRO [Online] EMBL; 31 October 1996 (1996-10-31) OSHIMA ET AL.: "Escherichia coli genomic DNA (25.2-25.6 min)" retrieved from EBI, accession no. ECD747 Database accession no. D90747 XP002181476 the whole document -& DNA RES.. vol. 3, 1996, pages 137-155, XP001040039	5,10,13, 14, 18-21, 124
X	--- DATABASE EM PRO [Online] EMBL; 30 December 1994 (1994-12-30) PLUNKETT, G: "Escherichia coli K-12 chromosomal region from 67.4 to 76 minutes" retrieved from EBI, accession no. ECUW67 Database accession no. U18997 XP002181477 the whole document --- -/--	5,10,13, 14, 18-21, 124

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/30950

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>POST L E ET AL: "NUCLEOTIDE SEQUENCE OF THE RIBOSOMAL PROTEIN GENE CLUSTER ADJACENT TO THE GENE FOR RNA POLYMERASE SUBUNIT BETA IN ESCHERICHIA COLI" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE USA,US,NEW YORK, NY, vol. 76, no. 4, 1 April 1979 (1979-04-01), pages 1697-1701, XP000574791 abstract</p> <p style="text-align: center;">---</p>	1
A	<p>WO 98 21366 A (Q B I ENTERPRISES LTD ;EINAT PAZ (IL); VASQUEZ IASLOP NORA CECILIA) 22 May 1998 (1998-05-22) page 8, line 9 - line 13 page 21, line 30 -page 27, line 35</p> <p style="text-align: center;">---</p>	1
A	<p>VAN HEESWIJK W C ET AL: "The genes of the glutamine synthetase adenylation cascade are not regulated by nitrogen in Escherichia coli" MOLECULAR MICROBIOLOGY,BLACKWELL SCIENTIFIC, OXFORD,GB, vol. 9, no. 3, 1993, pages 443-457, XP000926027 ISSN: 0950-382X</p> <p style="text-align: center;">---</p>	
A	<p>LEE N G ET AL: "Molecular cloning and characterization of the nontypable Haemophilus influenzae-2019 rfaE gene required for lipopolysaccharide biosynthesis" INFECTION AND IMMUNITY,AMERICAN SOCIETY FOR MICROBIOLOGY, WASHINGTON,US, vol. 63, no. 3, 1995, pages 818-824, XP000953326 ISSN: 0019-9567</p> <p style="text-align: center;">---</p>	
A	<p>AUSTIN A E ET AL: "Genetic analysis of lipopolysaccharide core biosynthesis by Escherichia coli k12 insertion mutagenesis of the RFA locus" JOURNAL OF BACTERIOLOGY,WASHINGTON, DC,US, vol. 172, no. 9, September 1990 (1990-09), pages 5312-5325, XP000926028 ISSN: 0021-9193</p> <p style="text-align: center;">---</p>	
T	<p>VALVANO M A ET AL: "The rfaE gene from Escherichia coli encodes a bifunctional protein involved in biosynthesis of the lipopolysaccharide core precursor ADP-L-glycero-D-manno-heptose" JOURNAL OF BACTERIOLOGY,WASHINGTON, DC,US, vol. 182, no. 2, January 2000 (2000-01), pages 488-497, XP000926030 ISSN: 0021-9193</p> <p style="text-align: center;">---</p>	
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INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/30950

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
E	<p>WO 01 48209 A (OHLSEN KARI L ;FORSYTH R ALLYN (US); ELITRA PHARMACEUTICALS INC (U) 5 July 2001 (2001-07-05) page 3 -page 14 seq id nos 274, 467 -----</p>	1-131

INTERNATIONAL SEARCH REPORT

In ternational application No.
PCT/US 00/30950

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.: -
because they relate to subject matter not required to be searched by this Authority, namely:
see FURTHER INFORMATION sheet PCT/ISA/210
2. ☒ Claims Nos.: -
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
see FURTHER INFORMATION sheet PCT/ISA/210
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

As a result of the prior review under R. 40.2(e) PCT,
part of the additional fees are to be refunded.

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
1-131 (Seq Id Nos 1, 116, 128, 285, 299, 456)
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☒ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.1

Although claims 129-131 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.

Continuation of Box I.1

Rule 39.1(iv) PCT - Method for treatment of the human or animal body by therapy

Continuation of Box I.2

Present claims 36, 44, 57, 95, 98, 109 and 117 relate to a compound defined by reference to a desirable characteristic or property, namely being identifiable by using the method of claims 28, 38, 45, 84, 96, 99, or 110, respectively. Present claims 125 and 126 relate to a compound defined by reference to a desirable characteristic or property, namely interacting with a gene or gene product or a polypeptide whose activity or expression is inhibited by an antisense nucleic acid comprising one of SEQ ID NOS 1-127.

The claims cover all compounds having this characteristic or property, whereas the application provides support within the meaning of Article 6 PCT and/or disclosure within the meaning of Article 5 PCT for only a very limited number of such compounds. In the present case, the claims so lack support, and the application so lacks disclosure, that a meaningful search over the whole of the claimed scope is impossible. Independent of the above reasoning, the claims also lack clarity (Article 6 PCT). An attempt is made to define the compound by reference to a result to be achieved. Again, this lack of clarity in the present case is such as to render a meaningful search over the whole of the claimed scope impossible. Consequently, the search has been carried out for those parts of the claims which appear to be clear, supported and disclosed, namely those parts relating to the sequences of claims 1, 9 and 19 .

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-8, 12-14, 45-124, 129-130 all partially

Invention 1:

A purified or isolated nucleic acid sequence, consisting of Seq Id No 1, a vector comprising said sequence, a host cell containing said vector, and their uses.

2. Claims: 1-8, 12-14, 45-124, 129-130 all partially

Inventions 2 to 127:

Idem as invention 1, but for Seq Id Nos 2-127, respectively.

3. Claims: 9-11, 15-44, 125-128 all partially

Invention 128:

A purified or isolated nucleic acid sequence consisting of Seq Id No 128, a vector comprising said sequence, a host cell containing said vector, a polypeptide encoded by said nucleic acid sequence and having Seq Id No 299, and an antibody binding said polypeptide, and their uses.

4. Claims: 9-11, 15-44, 125-128 all partially

Inventions 129 to 298:

Idem as invention 128, but for nucleic acid Seq Id Nos 129-298 and corresponding polypeptide Seq Id Nos 300-469, respectively.

INTERNATIONAL SEARCH REPORT

information on patent family members

International Application No

PCT/US 00/30950

Patent document cited in search report		Publication date	Patent family member(s)	Publication date
WO 9902673	A	21-01-1999	AU 8327798 A WO 9902673 A2 EP 1025219 A2	08-02-1999 21-01-1999 09-08-2000
WO 9821366	A	22-05-1998	AU 5442198 A EP 0960212 A1 JP 2001504694 T WO 9821366 A1 US 6057111 A	03-06-1998 01-12-1999 10-04-2001 22-05-1998 02-05-2000
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